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## C;Accession: JC5954 R;Tanaka, M.; Tanaka, T.; Harata, M.; Suzuki, T.; Mitsui, Y. Bicchem. Biophys. Res. Commun. 243, 531-537, 1998 A;Title: Triplet repeat-containing ribosomal protein L14 gene in immortalized human endt A;Reference number: JC5954; MUID:98153799; PMID:9480843 A;Accession: JC5954 A;Accession: S11563 A;Status: preliminary; nucleic acid sequence not shown A;Molecule type: mRNA A;Residues: 1-233 <-JOH> A;Residues: 1-233 <-JOH> A;Cross-references: UNIPROT:P19359; UNIPARC:UPI0000047567; EMBL:X53725; NID:g56630; PIDIC;Keywords: DNA binding A;Cross-references: UNIPARC:UPI000004E622; DDBJ:D87735; NID:g1620021; PIDN:BAA13443.1; C;Superfamily: rat ribosomal protein L14 C;Species: Homo sapiens (man) C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 02-Sep-2000 23-Jul-1999 #sequence\_revision 23-Jul-1999 #text\_change 09-Jul-2004 C;Accession: T12547 R;Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, submitted to the Protein Sequence Database, June 1999 A;Reference number: Z17528 A;Accession: T12547 A;Actus: preliminary A;Molecule type: mRNA A;Residues: 1-150 <OTT> A;Cross-references: UNIPROT:Q9Y4M1; UNIPARC:UPI0000071DDD; EMBL:AL080235 A;Experimental source: adult uterus; clone DKFZp586E1621 C;Genetics: 100.0%; Score 44; DB 2; Length 233; 84.6%; Pred. No. 15; ive 0; Mismatches 2; Indels 2; Length 150, DB 2; DB Score 44; DB Pred. No. 11; 0; Mismatches 0; Mismatches Score 44; Di Pred. No. 14; 100.0%; 84.6%; F Query Match Best Local Similarity 84.6%; Watches 11; Conservative 84.68; 150 AAAAAAAAAA 162 AAAAAAAAAAA 141 Query Match Best Local Similarity 84.0. The 11; Conservative 1 AAXAAAAAAAA 13 1 AAXAAAAAAAA 13 32 AAAAAAAAAAA 44 1 AAXAAAAAAAA 13 Query Match Best Local Similarity 84.6 Matches 11; Conservative ribosomal protein L14 - human A; Residues: 1-220 <TAN> A; Note: DKFZp586E1621.1 A; Status: preliminary A; Molecule type: DNA 129 g g ò ò 원 ò A;Accession: S12604 A;Molecule type: DNA A;Reses: 1-63,'V',65-91 <GAU> A;Cross-references: UNIPARC:UP10000001382; EMBL:X53718; NID:g64213; PIDN:CAA37754.1; PID C;Genetics: A; Molecule type: mRNA A; Residues: 1-91 - GGUJ-A; Cross-references: UNIPROT: P07835; UNIPARC: UPI0000125B4B; GB:M10148; NID:g213579; PIDN: R; Gauthier, S.; Wu, Y.; Davies, P.L. R; Gauthier, S.; Wu, Y.; Bavies, P.L. R; Gauthier, S.; Wu, Y.; Davies, P.L. A; Title: Nucleotide sequence of a variant antifreeze protein gene. A; Reference number: S12604; MUID: 90384854; PMID: 2402466 C;Species: Pseudopleuronectes americanus (winter flounder) C;Date: 01-Sep-1981 #sequence\_revision 01-Sep-1981 #text\_change 09-Jul-2004 C;Date: 01-Sep-1981 #sequence\_revision 01-Sep-1981 #text\_change 09-Jul-2004 C;Date: 01-Sep-1981 #sequence\_revision 01-Sep-1981 #text\_change 09-Jul-2004 R;Lin, Y; Gross, J.K. Proc. Natl. Acad. Sci. U.S.A. 78, 2825-2829, 1981 A;Tille: Molscular cloning and characterization of winter flounder antifreeze cDNA. A;Reference number: A03193; MUID:81247379; PMID:6265915 ö ö andifreeze protein IIA7 precursor - winter flounder) C;Species: Pseudopleuronectes americanus (winter flounder) C;Date: 05-Oct-1988 #sequence\_revision 05-Oct-1988 #text\_change 09-Jul-2004 C;Accession: A22592; S12604 R;Gourlie, B.; Lin, Y.; Price, J.; De Vries, A.L.; Powers, D.; Huang, R.C.C. J. Biol. Chem. 259, 14960-14965, 1984 A;Title: Winter flounder antifreeze proteins: a multigene family. A;Reference number: A22592; MUID:85084993; PMID:6548752 Gaps Gaps ;; 0 ; 0 C;Superfamily: antifreeze protein C;Keywords: antifreeze; tandem repeat F;1-21/Domain: signal sequence #status predicted <SIG> F;22-91/Product: antifreeze protein IIA7 #status predicted <MAT> 2; Length 91; Length 85; 2; Indels A;Cross-references: UNIPROT:P02734; UNIPARC:UPI0000174278 C;Superfamily: antifreeze protein C;Keywords: antifreeze F;1-21/Domain: signal sequence #status predicted <SIG> F;22-85/Product: antifreeze protein 4 #status predicted <MAT> 2; Indels hypothetical protein DKFZp586E1621.1 - human (fragment) C;Species: Homo sapiens (man) ; Score 44; DB 1; Pred. No. 7; 0; Mismatches 2, 100.0%; Score 44; DB 84.6%; Pred. No. 7.3; ive 0; Mismatches - winter flounder ALIGNMENTS 100.0%; Query Match 100.0%; Best Local Similarity 84.6%; Matches 11; Conservative 1 AAXAAAAAAAA 13 Query Match Best Local Similarity 84.6 Matches 11; Conservative 35 AATAAAAAATAA 47 AATAAAAAAAA 64 1 AAXAAAAAAAA 13 A; Molecule type: mRNA A; Residues: 1-85 <LIN> A; Introns: 19/2

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R.Yokoyama, M.; Nishi, Y.; Yoshii, J.; Okubo, K.; Matsubara, K.
DNA Res. 3, 311-320, 1996
A;Title: Identification and cloning of neuroblastoma-specific and nerve tissue-specific A;Reference number: JC5272; MUID:97191543; PMID:9039501
A;Contents: neuroblastma cell
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C;Species: Mus musculus (house mouse)
C;Date: 13-dan-1995 #sequence revision 13-Jan-1995 #text_change 05-Oct-2004
C;Accession: 516318; 540403; $57443
R;Izpisua-Belmonte, J.C.; Falkenstein, H.; Dolle, P.; Renucci, A.; Duboule, D.
EMBO J. 10, 2279-2289, 1991
A;Title: Murine genes related to the Drosophila AbdB homeotic gene are sequentially exp
A;Reference number: $16317; MUID:91293104; PMID:1676674
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B;Gerard, M.; Duboule, D.; Zakany, J.
B;MEO J. 12, 3539-3550, 1993
A;Title: Structure and activity of regulatory elements involved in the activation of the A;Reference number: S40403; MUID:94074553; PMID:7902810
A;Accession: S40403
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A,Cross-references: UNIPARC:UP10000026A38; EMBL:X60395; NID:g871427; PIDN:CAA42943.1; P
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A;Cross-references: UNIPARC:UPI000029F10; EMBL:X71422; NID:g397508; PIDN:CAA50553.1;
R;Takada, S.; Cook, M.; Kramlauf, R.; McMahon, A.P.
Submitted to the EMBL Data Library, May 1991
A;Description: Genomic sequence of mouse Hox-4.6.
A;Reference number: S57443
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C;Species: Homo sapiens (man)
C;Date: 16-Apr-1997 #sequence_revision 09-May-1997 #text_change 05-Oct-2004
C;Accession: JC5273
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C;Keywords: DNA binding; homeobox; nucleus; transcription regulation F;204-260/Domain: homeobox homology <HOX>
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84.6%; Pred. No. 19;
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A;Residues: 1-323 <IZP>
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                                                                                                                    C;Species: Homo sapiens (man)
C;Date: 31-May-1996 #text_change 09-Jul-2004
C;Accession: A48279
R;Ball, D.W.; Azzoli, C.G.; Baylin, S.B.; Chi, D.; Dou, S.; Donis-Keller, H.; Cumaraswam Proc. Natl. Acad. Sci. U.S.A. 90, 5648-5652, 1993
A;Title: Identification of a human achaete-scute homolog highly expressed in neuroendocx A;Reference number: A48279; MUID:93296195; PMID:8390674
A;Reference number: A48279
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Reference under: A48279
A;Reference: UNIPROT:P50553; UNIPARC:UPI0000047566; GB:L08424; NID:g306459; PID:g
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NyAlternate names: homeotic protein Hox 4.3

C;Species: Mus musculus (house mouse)

C;Species: Mus musculus (house mouse)

C;Accession: A43562

R;Izpisua-Belmonte, J.C.; Dolle, P.; Renucci, A.; Zappavigna, V.; Falkenstein, H.; Dubou Development 110, 733-745, 1990

A;Title: Primary structure and embryonic expression pattern of the mouse Hox-4.3 homeobc A;Reference number: A43562; MUID:91209232; PMID:1982431
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C;Species: Mus sp. (mouse)
C;Adzession: 157039
R;Hsieh-Li, H.M.; Witte, D.P.; Szucsik, J.C.; Weinstein, M.; Li, H.; Potter, Mech. Dev. 50, 177-186, 1995
A;Title: Gsh-2, a murine homeobox gene expressed in the developing brain.
A;Reference number: 157039; WUID:95344993; PMID:7619729
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A;Residues: 1-289 <1ZP>
A;Cross-references: UNIPROT:P23463; UNIPARC:UP10000177DA6
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A;Molecule type: mRNA
A;Residues: 1-305 <RES>
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0; Mismatches
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A;Cross-references: UNIPARC:UPI000016A2D0; EMBL:U48250; NID:g1199656; PIDN:AAC72247.1; P
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Plant J. 7, 927-938, 1995
A;Title: Alternative RNA products from a rice homeobox gene.
A;Reference number: Z15126; MUID:95322999; PMID:7599652
A;Accession: T03875
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Residues: 1-374 <TAM>
A;Cross-references: UNIPROT:P93423; UNIPARC:UPI00000AB610; EMBL:D49704; NID:g1805615; P:
A;Experimental source: cv. Nipponbare
C;Comment: For alternative splice forms, see PIR:T03874.
                                                                                              C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999
C;Accession: G02409
C; Kithroda, S.; Tokunaga, C.; Kiyohara, Y.; Konishi, H.; Kikkawa, U.
submitted to the EMBL Data Library, February 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene NKx6.1 protein - golden hamster
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Oct-2004
C;Accession: 148188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Species: Oryza sativa (rice)
;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-Oct-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Rudnick, A.; Ling, T.Y.; Odagiri, H.; Rutter, W.J.; German, M.S. Proc. Natl. Acad. Sci. U.S.A. 91, 12203-12207, 1994
A;Title: Pancreatic beta cells express a diverse set of homeobox genes. A;Reference number: 148185; MUD:95083670; PMID:7991607
A;Accession: 148188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Keywords: DNA binding; homeobox; nucleus; transcription regulation F;237-293/Domain: homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 44; DB 2; Length 334; 84.6%; Pred. No. 20; trive 0; Mismatches 2; Indels
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                                                               protein kinase C-binding protein RACK17 - human (fragment)
                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-334 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Gene: H45
A;Introns: 174/3; 215/1; 277/3; 321/3; 367/2
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Best Local Similarity 84.6
Matches 11; Conservative
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A;Accession: G02409
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B47236
zinc-finger protein Pur-1 - golden hamster
zinc-finger protein Pur-1 - golden hamster)
C;Species: Mesocricetus auratus (golden hamster)
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 05-Apr-1995
C;Accession: B47236
R;Kennedy, G.C.; Rutter, W.J.
R;Kennedy, G.C.; Rutter, W.J.
A;Kennedy, G.C.; Rutter, W.J.
A;Kennedy, G.C.; Rutter, W.J.
A;Keference number: A47236; MUID:93087555; PMID:1454839
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C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;46-102/Domain: homeobox homology <HOX>
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                                                                                                              binding; homeobox; nucleus; transcription regulation
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A,Status: preliminary; not compared with conceptual translation
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A;Cross-references: UNIPARC:UPI000017C615
A;Experimental source: insulinoma cell line T
A;Norce: sequence extracted from NCBI backbone (NCBIP:119832)
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84.6%; Pred. No. 20;
tive 0; Mismatches
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84.6%; Pred. No. 20;
:ive 0; Mismatches
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llarity 84.6%; Pred. No. 19;
Conservative 0; Mismatches
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                                                                   A;Introns: 246/1
C;Keywords: DNA binding; homeobox; nucleus
F;252-308/Domain: homeobox homology <HOX>
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Matches 11; Conserv
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Best Local Similarity
Matches 11; Conserv
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Best Local Similarity
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                                           A;Gene: Hoxd-11
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C; Genetics:
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C;Keywords: alternative initiators; alternative splicing; DNA binding; homeobox; nucleus
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C;Keywords: alternative initiators; alternative splicing; DNA binding; homeobox; nucleus
Fi.1375/Product: probable homeobox protein OSH45, splice form OSH44 #status predicted <M
F;197-367/Product: probable homeobox protein OSH45, splice form OSH42 #status predicted
F;291-352/Domain: homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Drosophila virilis
C;Species: Drosophila virilis
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 02-Jul-1998
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 02-Jul-1998
C;Accession: A4443
Mol. Cell. Biol. 12, 2475-2483, 1992
A;Title: Point mutations in the Drosophila hairy gene demonstrate in vivo requirements
A;Reference number: A44443; MUID:92269819; PMID:1588951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: UNIPARC: UPI00016DEBB; EMBL: D49704; NID: g1805615; PIDN: BAA08554.1; A; Experimental source: cv. Nipponbare; splice form OSH42 C; Comment: For an alternative splice form, see PIR: T03875.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: UNIPROT: P93424; UNIPARC: UPI00000AA5D5; EMBL: D49704; NID: 91805615;
                                                                                                                                                                                                                                                                                                                                                                    probable homeobox protein OSH45, splice form OSH44 [similarity] - rice
N;Contains: probable homeobox protein OSH45, splice form OSH42
C;Species: Oryza sativa (rice)
C;Species: Oxyza sativa (rice)
C;Accession: T03874; T03876
R;Tamaoki, M.; Tsugawa, H.; Minami, E.; Kayano, T.; Yamamoto, N.; Kano-Murakami, Y.; IPlant O. 7, 927-938, 1995
A;Title: Alternative RNA products from a rice homeobox gene.
A;Reference number: Z15126; MUID:95322999; PMID:7599652
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basic helix-loop-helix transcription repressor H - fruit fly (Drosophila virilis)
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A;Note: sequence extracted from NCBI backbone (NCBIN:102964, NCBIP:102966)
                                                                                                                                       Gaps
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                                                                                   Length 374;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                s; Score 44; DB
Pred. No. 21;
0; Mismatches
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A,Cross-references: FlyBase:FBgn0013115
                                                                                100.0%;
84.6%; F
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Conservative
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                                                                                                                                    11; Conservative
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A; Residues: 1-375 < TAM1>
                                                                                                           Similarity
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nes 11; Conserv
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A; Residues: 1-378 < WAI>
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Best Local
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C;Species: Mus musculus (house mouse)
C;Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 31-Dec-2004
C;Accession: A48423; S13009; A26629; A24778
R;Logan, C.; Hanks, M.C.; Noble-Topham, S.; Nallainathan, D.; Provart, N.J.; Joyner, A.Dev. Genet. 13, 345-358, 1992
A;Title: Cloning and sequence comparison of the mouse, human, and chicken engrailed gen A;Reference number: A48423; MUID:93185339; PMID:1363401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:P09065; UNIPARC:UPI00000299A1
A;Experimental source: CD-1, embryo
A;Experimental source: CD-1, embryo
A;Note: sequence extracted from NCB1 backbone (NCBIP:126620)
R;Holland, P.W.H.; Williams, N.A.
FEBS Lett. 277, 250-252, 1990
A;Title: Conservation of engrailed-like homeobox sequences during vertebrate evolution.
A;Reference number: $13009; MUID:91099509; PMID:1980115
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A; Title: En-1 and En-2, two mouse genes with sequence homology to the Drosophila engrain A; Reference number: A91620; MUID:88112776; PMID:2892757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Accession: A26629
A;Molecule type: DNA; mRNA
A;Residues: 278-401 < 2070
A;Residues: 278-401 < 2070
A;Cross-references: UNIPARC:UPI000016CA7C; GB:Y00201; GB:M11987; NID:g49587; PIDN:CAA68
Cross-references: UNIPARC:UPI000016CA7C; GCX, D.R.; Martin, G.R.
R;Joyner, A.L.; Kornberg, T.; Coleman, K.G.; Cox, D.R.; Martin, G.R.
A;Title: Expression during embryogenesis of a mouse gene with sequence homology to the A;Reference number: A24778; MUID:86079501; PMID:2416459
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C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 31-Dec-2004
                                                                 Gaps
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C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;313-369/Domain: homeobox homology <HOX>
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Length 378;
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A;Residues: 1-401 <LOG>
                                                                 Indels
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   DB 2;
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Pred. No. 22;
0; Mismatches
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0; Mismatches
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A,Residues: 321-380 440b.
A,Cross-references: UNIPARC:UP1000017A2AF
R,JOyner, A.L.; Martin, G.R.
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A;Residues: 311-401 <JO2>
A;Cross-references: UNIPARC:UP1000017A2B0
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                                  84.68;
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                                                                                                                                                                                                 269 AAAAAAAAAAA 281
                                                                                                                               1 AAXAAAAAAAAA 13
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                                                              11; Conservative
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homeotic protein HB9 - human
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Query Match 100.0%; Score 44; DB 2; Best Local Similarity 84.6%; Pred. No. 26; Matches 11; Conservative 0; Mismatches 2
                                                                                                                                                                    A;Gene: GDB:SOX3; SOX-3; SOXB
A;Cross-references: GDB:250376; OMIM:313430
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84.6%; I
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nes 11; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                          C;Genetics
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A;Accession: I38242
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                       R;Harrison, K.A.; Druey, K.M.; Deguchi, Y.; Tuscano, J.M.; Kehrl, J.H.
J. Biol. Chem. 269, 19968-19975, 1994
A;Title: A novel human homeobox gene distantly related to proboscipedia is expressed in
A;Reference number: A53662; MUID:94327547; PMID:7914194
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A,Note: the nucleotide sequence and conceptual translation as given are self-consistent
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T14911
T21911
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A;Note: CPR44b
C;Superfamily: BZIP G-box-binding protein; fos/jun DNA-binding domain homology
C;Keywords: DNA binding; leucine zipper
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Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
Cibate: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
Cisatesion: I38239; I38242; SG7816
Ristevanovic, M.; Lovell-Badge, R.; Collignon, J.; Goodfellow, P.N.
Hum. Mol. Genet. 2, 2013-2018, 1993
Airtle: SOX3 is an X-linked gene related to SRY.
Airtle: SOX3 is an X-linked gene related to SRY.
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C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;244-300/Domain: homeobox homology <HOX>
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A,Molecule type: DNA
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84.6%; Pred. No. 23;
ive 0; Mismatches
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0; Mismatches
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Best Local Similarity 84.0
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A;Cross-references: UNIP
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                                                                                                                                                                                                                                                                                           A; Residues: 1-403 <HAR>
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C; Accession: A53662
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: GDB:HLXB9
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 143-158,'P',160-218 <STE2>
A;Cross-references: UNIPARC:UPI0000071C8C; EMBL:X71137; NID:g468793; PIDN:CAA50467.1; PI
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K;Dush, M.K.; Martin, G.R.
Brobs, Biol. 151, 273-287, 1992
A;Title: Analysis of mouse Evx genes: Evx-1 displays graded expression in the primitive
A;Reference number: A43915; MUID:92249649; PMID:1349539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: DNA; mRNA
A;Residues: 1-475 - DUS.
A;Cross-references: UNIPROT:P49749; UNIPARC:UPI000020BC6; GB:S34322; NID:g249137; PIDN:
A;Cross-references: UNIPROT:P49749; UNIPARC:UPI0010478; NCBIN:100480; NCBIN:100482
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C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 05-Apr-1995
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 05-Apr-1995
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 05-Apr-1995
R;Accession: A47236
A;Accession: A47236
A;Accession: A47236
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N;Alternate names; mesodermal cell dorsoventral fates determinator Evx-2
C;Species: Mus musculus (house mouse)
C;Becies: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 31-Dec-2004
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A;Experimental source: islet cell line beta TC3
A;Note: sequence extracted from NCBI backbone (NCBIP:119831)
                                                                                                                                                                                                                                                                                                                                                 Score 44; DB 1;
Pred. No. 24;
0; Mismatches 2
                                                                                                                                                                                                                    A;Map position: Xq26-Xq27
C;Superfamily: human SOX3 protein; HMG box homology
F;136-211/Domain: HMG box homology <HMG>
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0; Mismatches
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Biochemistry 31, 4102-4110, 1992
Affile: Isolation of a novel cDNA encoding a zinc-finger protein that binds to two sit A;Title: Isolation of a novel cDNA encoding a zinc-finger protein that binds to two sit A;Reference number: A42170; MUID:92232709; PMID:1567856
A;Accession: A42170
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: I-494 <PKP>
                                                                                                                                                                                                                        Aicrossion: A46153 MUID: 956270; UNIPARC: UP1000017C427; GB:J05371
A;Note: it is uncertain whether Met-18 is the initiator or whether translation is initial R; Bossone, S.A.; Asselin, C.; Patel, A.J.; Marcu, K.B.
Proc. Natl. Acad. Sci. U.S.A. 89, 7452-7456, 1992
A;Title: MAZ, a zinc finger protein, binds to c-MYC and C2 gene sequences regulating transparence number: A46153; MUID:92366479; PMID:1502157
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A/Accession: 31223

A/Status: preliminary

A/Status: DNA

A/Cross-references: UNIPARC: UPI0000029AAF; EMBL: M88299; NID: G200444; PL.

C/Superfamily: transcription factor Brn-1; homeobox homology POU domain homology

C/Staywords: DNA binding; homeobox; nucleus; transcription regulation

C/Staywords: DNA binding; homeobox; nucleus; transcription regulation

C/Staywords: DNA binding; homeobox; nucleus; transcription regulation

F)210-112/Region: alanine-rich

F)162-180/Region: alanine-rich

F)216-21/Region: glycine-rich

F)216-23/Pregion: histidine/proline-rich

F)216-23/Domain: POU domain homology (POU)
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Proc. Natl. Acad. 821. U.5.A. 89, 3280-3284, 1992
A;Title: Structure and evolution of four POU domain genes expressed in mouse brain.
A;Reference number: S31223; MUID:92228768; PMID:1565620
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N;Alternate names: class III POU domain protein brain-1
C;Species: Mus musculus (house mouse)
C;Date: 02-Dec-1993 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S31223
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A; Residues: 18-417, 1, 1, 419-494 <BOS>
A; Cross-references: UNIPARC:UP100012ECF8; GB:M94046
A; Experimental source: HeLa cells
A; Note: sequence extracted from NCBI backbone (NCBIN:110666, NCBIP:110667)
C; Keywords: DNA binding: 2inc finger
F; 113-125/Region: alamine-rich
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Conservative 0; Mismatches
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F;296-318/Region: zinc finger
F;324-346/Region: zinc finger
F;354-368/Region: zinc finger
F;373-405/Region: zinc finger
F;409-430/Region: zinc finger
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Best Local Similarity 84.6
Matches 11; Conservative
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F;452-468/Region: alanine-rich
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les 11; Conserv
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 30-Uni-2001 #sequence_revision 30-Uni-2001 #text_change.09-Jul-2004
C;Accession: JC7583
R;Fujimoto, K.; Shen, M.; Noshiro, M.; Matsubara, K.; Shingu, S.; Honda, K.; Yoshida, E. Biochem. Biophys. Res. Commun. 280, 164-171, 2001
A;Title: Molecular cloning and characterization of DEC2, a new member of basic helix-lod A;Reference number: JC7583; MUID:21092582; PMID:11162494
A;Residues: 1-482 <FUJ>A;Residues: 1-482 <FUJ>A;Residues: 1-482 <FUJ>A;Cross-references: UNIPROT:Q9C0J9; UNIPARC:UPI0000052B52; DDBJ;AB044088
C;Comment: This protein, a novel member of the DEC subfamily of basic helix-loop-helix p
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C;Species: Chlamydomonas reinhardtii
C;Species: 1-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T09084
R;Molendijk, A.J.; Irvine, R.F.
R;Molendijk, A.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PI
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A;Cross-references: UNIPROT:O04270; UNIPARC:UPI00009C6FA; EMBL:U97663; NID:g2109290;
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N;Alternate names: MYC-associated zinc finger protein MAZ; zinc finger protein ZF87 C;Species: Homo sapiens (man)
C;Becies: Homo sapiens (man)
C;Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 09-Jul-2004
C;Accession: A42170; A46153
R;Pyrc, J.J.; Moberg, K.H.; Hall, D.J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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84.6%; Pred. No. 26;
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C;Keywords: transcription factor
F;1-173/Region: highly conserved #status predicted
F;130-173/Domain: Orange #status predicted <ORANS
F;286-411/Region: alanine and qlvcine-rich #status
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A;Molecule type: DNA
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0; Mismatches
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0; Mismatches
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C;Genetics:
A;Introns: 265/3; 331/3; 370/3; 455/1; 481/3
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                                                                          96 AAAAAAAAAAAA 108
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115 AATAAAAAAAA 127
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Best Local Similarity 84.6
Matches 11; Conservative
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C; Date: 27-Nov-1985 #sequence revision 27-Nov-1985 #text_change 09-Jul-2004
C; Accession: A90862; A93354; A03321; A03322; A25682; S03667
R; Poole, S.J.; Kauvar, L.M.; Drees, B.; Kornberg, T.
C[11 40, 37-43, 1985.
A; Title: The engrailed locus of Drosophila: structural analysis of an embryonic transcriA; Reference number: A90862; MUID:85099327; PMID:3917855
                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Mesidues: 1-522 < PRO>
A; Residues: 1-522 < PRO>
A; Residues: 1-522 < PRO>
A; Cross-references: UNIPROT: P02836; UNIPARC: UPI000012CA13; GB:M10017; NID:g157363; PIDN: R; Fjose, A.; McGinnis, W.J.; Gehring, W.J.
R; Fjose, A.; McGinnis, W.J.; Gehring, W.J.
A; Fjose, A.; McGinnis, W.J.; Gehring, W.J.
A; Fjose, A.; McGinnis, W.J.; Gehring, W.J.
A; Ffit: Isolation of a homoeo box-containing gene from the engrailed region of Drosophi A; Reference number: A93354; MUID:90114393; PMID:2481829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Accession: A93354
A,Molecule type: DNA
A,Residues: 447-485, E',487-518, WH' <FJO>
A,Residues: 477-485, E',487-518, WH' <FJO>
A,Cross-references: UNIPARC:UP100001745BF; GB:X01765; GB:K03059; NID:g8084; PIDN:CAA2590
A,Note: the translation of the nucleotide sequence from Fig. 5 is shown, not the transla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rykassis, J.A.; Poole, S.J.; Wright, D.K.; O'Farrell, P.H.

EMBO J. 5, 3583-5589, 1986

A;Title: Sequence conservation in the protein coding and intron regions of the engrailed A;Title: Sequence conservation in the protein coding and intron regions of the engrailed A;Reference number: A91059; MUD:218178; PMID:2881781

A;Contents: annotation; intron locations and sequences

R;Gay, N.J.; Poole, S.J.; Kornberg, T.B.

Nucleic Acids Res. 16, 6637-6647, 1988

A;Title: The Drosophila engrailed protein is phosphorylated by a serine-specific protein A;Reference number: 803667; MUID:88289425; PMID:2899884

A;Contents: annotation; potential phosphorylation sites; homeobox domain C;Comment: This protein specifies the body segmentation pattern.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Introns: 438/1, 470/3
C; Superfamily: engrailed homeotic protein; homeobox homology
C; Kaywords: DNA binding; embryo; homeobox; nucleus; segmentation; transcription regulati
F; 26-53/Region: glutamine-rich
F; 68-87/Region: alanine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: A39369
R;Kojima, T.; Ishimaru, S.; Higashijima, S.; Takayama, E.; Akimaru, H.; Sone, M.; Emori, Proc. Natl. Acad. Sci. U.S.A. 88, 4343-4347, 1991
A;Title: Identification of a different-type homeobox gene, BarHI, possibly causing Bar A;Reference number: A39369; MUID:91239564; PMID:1674606
A;Accession: A39369
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A;Molecule type: DNA
A;Residues: 1-604 <KOJ>
A;Cross-references: UNIPROT:Q23838; UNIPARC:UPI0000075A37; GB:M59962; GB:M59963; NID:gl
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C,Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 31-Dec-2004
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A,Cross-references: FlyBase:FBgn0012114
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
C;Keywords: DNA binding; homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: FlyBase: FBgn0000577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Map position: 2R, 62.0 (48A1-4)
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Best Local Similarity
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myc-associated zinc-finger protein - human
MyAlterrate names: MAZ protein
NyAlterrate names: MAZ protein
Cispecies: Homo sapiens (man)
Cispecies: Judan-1997 #sequence_revision 31-Jan-1997 #text_change 05-Nov-1999
CyAccession: JC5076
RyTsutsui, H.; Sakatsume, O.; Itakura, K.; Yokoyama, K.K.
Biochem: Biophys. Res. Commun. 226, 801-809, 1996
AyTitle: Members of the MAZ family: A novel cDNA clone for MAZ from human pancreatic isl
AyReference number: JC5076; MUID:96428591; PMID:8831693
AyAccession: JC5076
AyAccession: JC5076
AyAccession: JC5076
AyAccession: JC5076
AyAccession: JC5076
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A;Experimental source: pancreatic islet
C;Comment: This protein plays a role in the control of transcriptional initiation of gen
and between the introns of the mouse gene for immunoglobulin M-D.
C;Keywords: phosphoprotein; zinc finger
F;146,204,480/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status pre
F;349/Binding site: phosphate (Tyr) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polygomavirus enhancer-binding protein 2 alpha chain type 1 - mouse
NyAlternate names: PEA2 alpha chain type 1; PEA2 alpha chain type 2; PEBP2 alpha chain type (5;Species: Mus musculus (house mouse)
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Jul-2004
C;Accession: A48233; B48233
R;Ogawa, E.; Maruyama, M.; Kagoshima, H.; Inuzuka, M.; Lu, J.; Satake, M.; Shigesada, K. Proc. Nall. Acad. Sci. U.S.A. 90, 6859-6863, 1993
A;Title: PEBP2/PEA2 represents a family of transcription factors homologous to the produ A;Reference number: A48233; MUID:93342088; PMID:8341710
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C;Superfamily: transcription factor CBF alpha 2
C;Keywords: alternative splicing; DNA binding; T-cell; transcription factor; transcripti
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A;Molecule type: mRNA
A;Residues: 1-513 <OGA>
A;Cross-references: UNIPROT:Q08775; UNIPARC:UPI000002B2F8; GB:D14636; NID:g391766; PIDN:A;Status: preliminary
A;Status: preliminary
A;Molecule type: mRNA
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A;Cross-references: UNIPARC:UPI000002B2F9; GB:D14637; NID:9391768; PIDN:BAA03486.1; PID:
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0; Mismatches
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C;Accession: S40382
R;Abel, T.; Michelson, A.M.; Maniatis, T.
Development 119, 623-633, 1993
A;Title: A Drosophila GATA family member that binds to Adh regulatory sequences is expri
A;Reference number: S40382; MUID:94244465; PMID:8187633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-779 <ABE>
A;Cross-references: UNIPROT:P52172; UNIPARC:UPI0000135F5F; EMBL:X76217; NID:g441491; PII
C;Comment: This transcriptional activator is the earliest known marker of the developin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: box A-binding factor; GATA-type zinc finger homology ckeywords: DNA binding; nucleus; transcription factor; transcription regulation; zinc F;316-369/Domain: GATA-type zinc finger homology <GZF> F;319-343/Region: zinc finger GATA motif
                                                                                                                                                                                                                                                                                                                                                                                                                                         Riwinmer, B.A.; Jaeckle, H.; Pfeifle, C.; Cohen, S.M.
Nature 366, 690-694, 1993
A;Title: A Drosophila homologue of human Spl is a head-specific segmentation gene.
A;Reference number: S39356; MUID:94081952; PMID:8259212
A;Accession: S39356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-644 <WIM>
A,Cross-references: UNIPARC:UP10000124C17; EMBL:Z29361; NID:g441283; PID:g441284
                                                                                                                                                                                                                                                                                                                                                                   C;Species: Drosophila sp.
C;Date: 18-Feb-1994 #sequence_revision 01-Dec-1995 #text_change 07-May-1999
C;Accession: S39356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            box A-binding factor - fruit fly (Drosophila melanogaster)
NiAlternate names: ABF; transcription factor dGATAb
C.Species: Drosophila melanogaster
C.Species: 13-Jan-1995 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
                                                                                                              Gaps
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     C;Superfamily: FtsH/SEC18/CDC48-type ATP-binding domain homology
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                                                           В
                                                        100.0%; Score 44; DE
84.6%; Pred. No. 32;
:ive 0; Mismatches
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84.6%; Pred. No. 37;
tive 0; Mismatches
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Pred. No. 32;
0; Mismatches
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A;Introns: 245/2
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A;Cross-references: FlyBase:FBgn0003507
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84.6%; I
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598 AAAAAAAAAA 610
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                                                     Query Match
Best Local Similarity 84.6
Matches 11; Conservative
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Best Local Similarity 84..
The 11; Conservative
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Best Local Similarity 84.6
Matches 11; Conservative
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A,Gene: FlyBase:btd
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                                                                                                                                                                                                                                                                          0m(1D) protein - fruit fly (Drosophila ananassae)
C)Species: Drosophila ananassae
C)Species: Drosophila ananassae
C)Species: Drosophila ananassae
C)Accession: S13367
R)Tanda, S.; Corces, V.G.
EMBO J. 10, 407-417, 1991
A;Title: Retrotransposon-induced overexpression of a homeobox gene causes defects in eye A;Reference number: S13367; MUID:91122048; PMID:1671353
A;Accession: S13367
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-606 < TAN>
A;Residues: UNIPROT:P22544; UNIPARC:UPI000012C97A; EMBL:X56682; NID:97146; PIDN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-627 <ROU>
A;Cross-references: UNIPROT:O80983; UNIPARC:UPI000017885F; EMBL:AC004747; NID:g3413696;
A;Experimental source: cultivar Columbia
B;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Uniture 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable YME1 ATP-dependant proteinase [imported] - Arabidopsis thaliana
N;Alternate names: YTA11 protein homolog T19L18.5
Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 24-Mar-1999 #text_change 31-Dec-2004
C;Accession: T02610; H84656
E;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, August 1998
A;Description: Arabidopsis thaliana chromosome II BAC T19L18 genomic sequence.
A;Reference number: Z14681
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A; Accession: H84656
A; Status: preliminary
A; Molecule type: DNA
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A;Introns: 307/1; 383/2
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation E;332-388/Domain: homeobox homology <HOX>
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                          Length 604;
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                                DB 2;
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     Score 44; Db
                                                                                0; Mismatches
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live 0; Mismatches
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A;Status: translated from GB/EMBL/DDBJ
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A, Introns: 40/1; 119/1; 160/3; 319/3
                             100.0%;
84.6%; I
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234 AAAAAAAAASAA 246
1 AAXAAAAAAAA 13
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Best Local Similarity 84.6
Matches 11; Conservative
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A;Gene: T19L18.5; At2g26140
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A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www sanger.ac.uk/Projects/C ele A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Accession: C88402
A;Status: preliminary
A;Molecule type: DNA
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R;Burtis, K.C.; Thummel, C.S.; Jones, C.W.; Karim, F.D.; Hogness, D.S.
Cell 61, 85-99, 1990
A;Title: The Drosophila 74EF early puff contains E74, a complex ecdysone-inducible gene A;Reference number: A90912; MUID:90199900; PMID:2107982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:Q9TXU2; UNIPARC:UPI000007CE2B; GB:chr_III; PIDN:AAC68790.1;
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C;Keywords: alternative splicing; DNA binding; nucleus; transcription regulation
F;735-815/Domain: ets DNA-binding domain homology <FTS>
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A;Residues: 1-829 <BUR>
A;Cross-references: UNIPARC:UP10000077909; GB:M37082; NID:g157307; PID:g157308
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N;Alternate names: ets-related protein E74A
C;Species: Drosophila melanogaster
C;Species: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 15-Mar-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Č;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                      Gaps
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Pred. No. 38;
0; Mismatches 2; Indels
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R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
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Pred. No. 39;
0; Mismatches
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Best Local Similarity 84.6%; Pred. No. 39;
Matches 11; Conservative 0; Mismatches
                      A;Cross_references: FlyBase:FBgn0025833
A;Introns: 37/3; 448/3; 611/2; 690/3
A;Note: EG:EG0003.2
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U16755
C140rf4 protein - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens
C;Accession: U77555
R;Rampazzo, A.; Pivotto, F.; Occhi, G.; Tiso, N.; Bortoluzzi, S.; Rowen, L.; Hood, L.; N
Biochem. Biophys. Res. Commun. 278, 766-774, 2000
A;Title: Characterization of C14orf4, a novel intronless human gene containing a polyglu
A;Reference number: U7555; MUID: 20549026; PMID:11095982
A;Accession: U7755
A;Accession: U77555
A;Residues: 1-796 <RAM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:09H1B7; UNIPARC:UPI00000738BA; GB:AJ277365
C;Comment: This protein, a proline-rich nuclear protein, functions as a transcriptional
s and undergoes rapid degradation.
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c;Species: Drosophila melanogaster
c;Species: Drosophila melanogaster
c;Date: 13-Mag-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: T1869
R;Murphy, L.; Harris, D.; Barrell, B.
submitted to the BMBL Data Library, November 1998
A;Description: Sequencing the distal X chromosome of Drosophila melanogaster.
A;Reference number: Z17699
A;Accession: T1869
A;Accession: T1869
A;Accession: T1869
A;Molecule type: DNA
A;Residues: L960 cMMRA
A
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C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
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DB 2;

Score 44;

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Query Match

A;Map position: 6 A;Introns: 54/3; 212/3 A; Gene: NCSP:B1D1.390

C;Genetics:

DB 2;

Score 44; Db

100.08; 84.68;

Pred. No. 38; 0; Mismatches

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1 AAXAAAAAAAA 13

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A,Gene: Cl4orf4 A,Map position: 14q24.3

C, Genetics:

Search completed: September 9, 2006, 23:01:51 Job time: 15.8101 secs

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ALIGNMENTS

Gaps

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Length 71;

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Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE [MRNA].
MEDLINE=81247379; PubMed=6265915;
Lin Y., Gross J.K.;
"Molecular cloning and characterization of winter flounder antifreeze
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1995, sequence version 2.
07-FEB-2006, entry version 35.
Ice-structuring protein 2A7 precursor (ISP 2A7) (Antifreeze protein IIA7) (AFP).
                                                                                                                                                                                                                                                                                                                                                             07-FBB-2006, entry version 32.
Ice-structuring protein 4 precursor (ISP 4) (Antifreeze peptide 4).
Pseudopleuronectes americanus (Winter flounder) (Pleuronectes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. (Natl. Acad. Sci. U.S.A. 78:2825-2829(1981).
-!- FUNCTION: Antifreeze proteins lower the blood freezing point.
-!- SIMILARITY: Belongs to the type-I AFP family.
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                   6958 MW; 3A0B336CD1048D99 CRC64;
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PRINTS; PR00308; ANTIFREEZEI.
Antifreeze protein; Repeat; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       americanus)
  NON TER
SEQUENCE
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P07835;
                                                             Query Match
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                   Totoki Y., Seki M., Ishida J., Nakajima M., Enju A., Kamiya A.,
Narusaka M., Shin-i T., Nakagawa M., Sakamoto N., Oishi K., Kohara Y.,
Kobayashi M., Toyoda A., Sakaki Y., Sakurai T., Iida K., Akiyama K.,
Satou M., Toyoda T., Konagaya A., Carninci P., Kawai J.,
Hayashizaki Y., Shinozaki K.,
"Large-scale analysis of RIKEN Arabidopsis full-length (RAFL) cDNAs.";
Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                              Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, AK220842; BAD94171.1; -; mRNA.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0005840; C:ribosome; IEA.
GO; GO:000823; F:peptidase activity; IEA.
GO; GO:0003735; F:structural constituent of ribosome; IEA.
GO; GO:0006412; P:protein biosynthesis; IEA.
InterPro; IPRO0456; Ribosomal P2.
PRINTS; PR00456; RIBOSOMALP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 44; DB 2; Length 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang A., Gonzalez-Santos J.M., Hu J.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 1
52 AA; 4750 MW; D8B358D27E6813B1 CRC64;
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                                                                                                            10-MAY-2005, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF261889; AAM21972.1; -; Genomic_DNA.
Ensembl; ENSG0000163694; Homo sapiens.
NON_TER
                                                                   52 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 40;
0; Mismatches
                                                                                                                                                                                          Name=At2g26140;
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                   PRT;
                                                                                                                             10-MAY-2005, sequence version 1. 07-FEB-2006, entry version 3. FtsH like protease (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 AAAAAAAAAAA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AAXAAAAAAAA 13
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                                                                                                                                                                                                                                                                                                  NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QBNIS3 HUMAN
QBNIS3;
                                                           QS6ZWB_ARATH
QS6ZWB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C57BL/63; TISSUE=Thymus; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninoi P., Hayashizaki Y.; Hayashizaki Y.; Hidih-efficiency Hayashizaki Y.; Methods Enzymol. 303:19-44(1999).
                                                                            MEDLINE-85054999; PubMed=6548752; Gourlie B., Lin Y., Price J., Devries A.L., Powers D., Huang R.C.C.; "Winter flounder antifreeze proteins: a multigene family."; J. Biol. Chem. 259:14960-14965(1984).
-!- FUNCTION: Antifreeze proteins lower the blood freezing point.
-!- SIMILARITY: Belongs to the type-I AFP family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 days neonate thymus cDNA, RIKEN full-length enriched library, clone:Al30089M21 product:HBV pX associated protein 8 large isoform
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0
                                                                                                                                                                                                                                                                                                                                                                                                     Removed by a dipeptidylpeptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 91;
                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
Pleuronectoidei; Pleuronectidae; Pseudopleuronectes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-OCT-2005, integrated into UniProtKB/TrEMBL.
11-OCT-2005, sequence version 1.
07-FEB-2006, entry version 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-C57BL/6J; TISSUE-Thymus;
PubMed=16141072; DOI=10.1126/science.1112014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 63;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 44;
                                                                                                                                                                                                                                                                                                                                                                                  Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                    InterPro; IPR000104; Antifreeze 1. PRINTS; PR00308; ANTIFREEZEI.
                                                                                                                                                                                                                                                                             EMBL; M10148; AAA49465.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                             Antifreeze protein; Repeat; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8326 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84.68;
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                                                       NUCLEOTIDE SEQUENCE [MRNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AAXAAAAAAAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 84.6
nes 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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As Georgii-Hemming P., Gingerse T.R., Golobort T., Green R.E.,

Antinical S., Markers W., Hayabii Y., Hanchy T.K., Hinchas N.,

Antinical S., Marker M., Hayabii Y., Hanch T.K., Hinchas N.,

Antinical S., Marker M., Marker M., Kangar S., Kammerfeld S. K.,

Antinical S., Mallan S., Walden Babu M., Madera M., Marchini L.,

Antinical S., Mallan S., Walden Babu M., Madera M., Marchini E., Marchini S.,

Antinical S., Mallan S., Walden Babu M., Madera M., Marchini E., Marchini S.,

Antinical S., Mallan S., Mallan S., Mark H., Mignone F., Miyake S., Morris K.,

Antinical S., Mallan S., Mallan S., Mark H., Mignone F., Miyake S., Morris K.,

Antinical S., Mallan S., Mallan S., Mark H., Mignone F., Miyake S., Morris K.,

Antinical S., Man Y., Gallaberg S.L., Sandellin A., Schneider C.,

B. Schonberl C., Sedigue E., Sandellin A., Schneider C.,

B. Schonberl C., Sedigue E., Sandellin A., Schneider C.,

B. Minha S., Man Y., Sallaberg S.L., Sandellin A., Schneider C.,

B. Malland S.M., Tasardia R., Shimda K., Silva D., Sinclair B.,

B. Malland S.M., Tasardia R., Shimda K., Silva D., Sinclair B.,

B. Malland S.M., Tasardia R. D., Liu E.T., Brusic V., Gasaki D., Tonari V.,

M. Malland S.M., Tasardia R. D., Liu E.T., Brusic V., Gasaki D., Tonari V.,

M. Malland M., Mak K., Watahiki A., Moki J., Arakawa T.,

B. Marker S., Kanamori-Katayama M., Suuxiki M., Aoki J., Arakawa T.,

M. Malland M., Mak K., Watahiki A., Dammura Chio, V., Suzuki M., Maka M.,

M. Malland M., Mak K., Watahiki A., Dammura Chio, Y., Suzuki M., Maka M.,

M. Malland M., Mak K., Watahiki A., Dammura Chio, W., Suzuki M., Malland M.,

M. Malland M., Mak K., Matahiki A., Dammura Chio, W., Suzuki M., Malland M.,

M. Malland M., Mak K., Matahiki A., Dammura Chio, W., Suzuki M., Malland M.,

M. Malland M., Mak K., Matahiki A., Dammura Chio, Malland M.,

M. Malland M., Mak K., Matahiki A., Dammura Chio, Malland M.,

M. Malland M., Malland
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Oryza sativa (japonica cultivar-group). Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta; Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP clade,

NUCLEOTIDE SEQUENCE.

NCBI\_TaxID=39947;

25-OCT-2004, integrated into UniProtKB/TrEMBL

25-OCT-2004, sequence version 1.

07-FEB-2006, entry version

Cell division protein (FtsH) - like. Name=B1151A10.24-1;

PRT;

PRELIMINARY;

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MEDLINE=22337376; PubMed=12447438; DOI=10.1038/nature01184;
A Sasaki T., Mateumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
Sasaki T., Mateumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
A Gamoto M., Ando T., Aoki H., Arikawa K., Chiden Y., Hayashi M.,
A Hijishita S., Honda M., Ichikawa K., Idonuma A., Iijima M., Ikeda M.,
Hijishita S., Honda M., Ichikawa Y., Ito Y., Iwabuchi A., Kamiya K.,
A Ikeno M., Ito S., Ito T., Ito Y., Ito Y., Iwabuchi A., Kamiya K.,
A Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
A Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
A Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
A Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuli K., Yamangata H., Yamane H., Yamane H., Yoshihara R., Yukawa K.,
A Maki K., Yamangata H., Yamane H., Yoshihara R., Yukawa K.,
A Man M., Jiang J., Gojobori T.;
A Man M., Jiang J., Gojobori T.;
A Man M., Jiang J., Gojobori T.;
DDT THE BEAR AND T
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                Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Komo H., Adachi J., Fukuda S., Alawaa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., A Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., A Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Kaho B., Kochiwa H., Kelischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kohrim L.M., Staubli F., Suruki R., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suruki R., Paldarelli R., Bareh G., Bake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Austincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Iyons P., Marchionni L., Mashima J., Mazzarelli J., Sakamoto N., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Nasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Whinhaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Havashizaki V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C57BL/6J; IISSUB=Thywnus; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y., Muramatsu M., Hayashizaki Y.; Shibata K., Itoh M., Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K., Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K., Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S., Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N., Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D., Shibata K., Shizaki T., Tagami M., Tagami Y., Waki K., Watahiki A., Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibate K., Titoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibate X., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Hazama M., Tashiro H., Itoh M., Sumi N., Ishii K., Makamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Pujiwake S., Inoue K., Togawa W., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rikik lintegrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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      MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82305; Hbxap.
112 AA; 11657 MW; 3F364EA14DDFD076 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 44; DB 2;
Pred. No. 74;
0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, AK138087, BAE23549.1; -; mRNA.
MGI; MGI:2682305; HDXAD.
SEQUENCE 112 AA; 11657 MW: 3F74AE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
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EMBL; AP003413; BAD45189.1; -; Genomic\_DNA

Gramene; Q656T8; -

"The genome sequence and structure of rice chromosome 1."; Nature 420:312-316(2002)

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Euarchontoglires, Glires, Rodentia, Sciurognathi;
                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                           11-0CT-2005, integrated into UnibrotKB/TrEMBL.
11-0CT-2005, sequence version 1.
07-FEB-2006, entry version 5.
Adult male testis CDNA, RIKEN full-length enriched library, clone:4933416E08 product:hypothetical Proline-rich region profile/Alanine-rich region profile containing protein, full insert
                                                                                                                                                                                          ö
                                                                                                                                                         Length 115;
                                                                                                                                                                                          Indels
                                                                                                                      115 AA; 11813 MW; B64A595C9756DEC5 CRC64;
Gramment; would, and the binding; IEA. GO; GO:0004222; F:metalloendopeptidase activity; IEA. GO; GO:0051301; F:metalloendopeptidase activity; IEA. GO; GO:0051301; P:cell division; IEA. GO; GO:006508; P:proteolysis; IEA. InterPro; IPRO0642; Peptidase M41.
                                                                                                                                                                                          5;
                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                117 AA.
                                                                                                                                         100.0%; Score 44; DE
                                                                                                                                                                          Pred. No. 75;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Muridae; Murinae; Mus.
                                                                                        Pfam; PF01434; Peptidase_M41;
                                                                                                                                                                                                                                                                                                                                                Q3V062_MOUSE PRELIMINARY;
Q3V062;
                                                                                                                                                                                                                               1 AAXAAAAAAAA 13
                                                                                                                                                                                                                                                             85 AASAAAAAATAA 97
                                                                                                                                                                                                11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE
                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                             Cell division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sednence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Muroidea;
                                                                                                                             SEQUENCE
                                                                                                                                                              Query Match
                                                                                                                                                                                                 Matches
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Gaps

; 0

Indels

2;

84.6%;

4 AAAAAAAAAAAA 16

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RESULT 6 Q656T8 ORYSA

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RC STRAIN-GC7BL/G01 TISSUB-Testis;

RX PAUCEGC7BL SEQUENCE.

RX PARIN-GC7BL/G01 TISSUB-Testis;

RX PARIN-GC7BL/G01 TISSUB-Testis;

RA Davis M.J. Rarasi T. Lenard B., Wells C., Kodzius R., Shimokawa K., Ra Bajic V. B., Bernner S. B., Batalvo S., Forrest A.R., Zavolan M., Davis M.J., Wilning L.G., Addinis V., Allen J.E.,

RA Davis M.J., Wilning L.G., Addinis V., Allen J.E.,

RA Davis M.J., Dalla E., Dalrymple B.P., Ge Bono B., Della Gatta G., Christoffels A., Clutterbuck D.R.,

Christoffels A., Clutterbuck D.R.,

RA Grow M.L., Dalla E., Dalrymple B.P., Red Bono B., Della Gatta G.,

RA Georgii-Hemming P., Gingeras T.R., Golobori T. Green R.B.,

Authoritical S., Harbors M., Hayashi Y., Hensch T.K., Hirokawa N.,

RA Jak M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,

RA Jak M., Marapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,

RA Jak M., Marapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,

RA Jak M., Matula G., Krishman S.P., Kruger A., Kummerfeld S.K.,

Liuni S., McWilliam S., Maddan Babu M., Madera M., Marchionni L.,

Matsuda H., Matulawa S., Miki H., Mignone F., Miyake S., Morris K.,

RA RA Bartowsky N., Fiazza S., Reed J., Reid J.F., Rings J.S., Ringwald M.,

RA RA RA B. Runn Y., Salzberg S.L., Sandelin A., Schneider C., Sekiguchi K., Samale C.J., Seno S., Sessa L., Sheng Y.,

RA Forowsky N., Fiazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,

RASARI Y., Shimada H., Shimada K., Sillan B., Tawanishi H.,

Schonbach C., Sekiguchi K., Sample C.A., Seno S., Sessa L., Sheng Y.,

RA Tammoja K., Tan S.L., Tang S.L., Sandelin A., Schneider C.,

Ranneja K., Tan S.L., Tang S.L., Sandelin A., Schneider C.,

Ranneja K., Tan S.L., Tang S.L., Sandelin A., Sandelin S.,

Rannishi H., Van Niwesgen E., Sugiuer K., Sillan B.,

Rannishi H., Van Niwesgen E., Sugiuer K., Sillan B.,

Ranneja K., Tan S.L., Tang S., Ranner A., Hide W.,

Rawashima T., Kojiam M., Kono S., Konno H., Makano Y., Shiraki J.,

Rasahaima W., Shiraki Y., Rasadiak Y.,

Rasahaima Y., Shiraki Y., Rasadiak Y., Rasahima T., Suzuki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAINS-ESTBL/61; TISSUB=Testis;

X MEDLINE=22354683; PubMed=12466881; DOI=10.1038/nature01266;

MEDLINE=22354683; PubMed=12466881; DOI=10.1038/nature01266;

A Nikaido I., Osatuo M., Kasukawa T., Adachi J., Bono H., Kondo S.,

Nikaido I., Osatuo N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

Schriml L.M., Kanapin A., Matuada H., Batalov S., Beisel K.W.,

Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

A Gasterland T.A., Fletcher C.F., Forrest A., Frazer K.S.,

Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,

Konaja A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

Maglott D.R., Maltais L., Marchionni L., Miki H.,

Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
                          MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=CS7BL/6J; TISSUE=Testis; PubMed=16141073; DOI=10.1126/science.1112009; RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium; "Antisense Transcription in the Mammalian Transcriptome."; Science 309:1564-1566(2005).
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                                             Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Methods Enzymol. 303:19-44(1999).
  STRAIN=C57BL/6J; TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 309:1559-1563(2005)
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Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
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Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
Sultana R., Takenaka Y., Taylor M.S., Teadale R.D., Tomita M.,
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Yan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
Ahiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
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Birney B., Hayashizaki Y.,
Birney E., Hayashizaki Y.,
Birney E., Hayashizaki Y.,
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Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
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Radota K., Matsuda H.A., Ashburner M., Batalov S., Yamanaka I.,
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Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Radota K., Matsuda H.A., Suzuki R., Tomita M., Wagner L., Washio T.,
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Rakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Rawatein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Iyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Toyo-oka K., Hang K.H., Weitz C., Whittaker C., Wilming L.,
Mynshaw-Borish A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carninci P., Shibata Y., Hayateu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Shibata K., Itoh M., "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630 (2000).
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Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CS7BL/6J; TISSUB=Testis;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=CS7BL/6J; TISSUE=Testis;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
                                                                                                                                                                                                                                                                                                                                                                                       full-length cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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NUCLEOTIDE SEQUENCE
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nes 11; Conser
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              Felinae; Felis.
NCBI_TaxID=9685;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
MEDLINE=20122168; PubMed=10656931; DOI=10.1007/s003350010029;
MOTILOCK D.P., Satesh P., Innis J.W.;
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MEVOLUTION OF N-terminal sequences of the Vertebrate HOXA13 protein.";
Mamm. Genome 11:151-158(2000).
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                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Laurasiatheria, Carnivora, Fissipedia, Canidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Felis silvestris catus (Cat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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                                                                                                                                                             DB 2; Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF083096; AAD54641.1; -; Genomic_DNA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005840; C:ribosome; IEA.
GO; GO:0003735; F:structural constituent of ribosome; IEA.
GO; GO:0006412; P:protein biosynthesis; IEA.
InterPro; IPR001859; Ribosomal_P2.
PRINTS; PR00456; RIBOSOMALP2.
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                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 AA; 10975 MW; CCCA1A7B52221394 CRC64;
                                                                                                                       61282448B68F9365 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
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01-MAY-2000, sequence version 1.
07-FEB-2006, entry version 16.
Transcription factor HOXA13 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 AA.
                                                                                                                                                                                                                                                                                                                                                                                        130 AA.
                                                                                                                                                             s; Score 44; DB
Pred. No. 76;
0; Mismatches
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transcription factor HOXA13 (Fragment).
                                                                               EMBL; AK133410; BAE21643.1; -; mRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000, sequence version 1. 07-FEB-2006, entry version 15.
                                                                                                    Hypothetical protein.
SEQUENCE 117 AA; 12609 MW;
                                                                                                                                                             100.0%;
84.6%;
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Q9TST8;
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Q9TUC9;
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                                                                                                                                                Query Match
Best Local Similarity 84.6
                                                                                                                                                                                                                                              1 AAXAAAAAAAA 13
                                                                                                                                                                                                                                                                                    AASAAAAAAAA 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Canis familiaris (Dog)
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DT 011
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RX DubMed=15496914; DOI=10.1038/nature031025;

RA Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N., RA Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N., Maillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N., RA Maucell E., Bouneau L., Fisher S., Lutfalla G., Dossat C., Segurens B., RA Matchouard V., Jubin C., Castelli V., Katinka M., Vacherie B., Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B., Ra Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V., RA Enud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J., RA Kellis M., Volff J.-N., Gilgo R., Zody M.C., Mesban P., Bosak S., Lindblad-Toh K., Birren B., Nuchaum C., Kahn D., Robinson-Rechavi M., Lindblad-Toh K., Birren B., Nuchaum C., Kahn D., Robinson-Rechavi M., Lander P., Lander E.S., Weissenbach J., Roest Crollius H.;

Ry "Genome duplication in the teleost fish Tetraodon nigroviridis reveals T. Nature 431:946-957(2004).
                                                                                                                                                                                                                                                                                                                                                                                         Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                 Mortlock D.P., Sateesh P., Innis J.W.; "Evolution of N-terminal sequences of the vertebrate HOXA13 protein."; Mamm. Genome 11:151-158(2000).
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tetraodon nigroviridis (Green puffer).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-JUL-2005, sequence version 1.
07-FEB-2006, entry version 3.
Chromosome undetermined SCAF7119, whole genome shotgun sequence.
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                                                                                                                                                                                                    MEDLINE=20122168; PubMed=10656931; DOI=10.1007/s003350010029;
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Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AF083095; AAD54640.1; -; Genomic_DNA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005840; C:ribosome; IEA.
GO; GO:0003735; F:structural constituent of ribosome; IEA.
GO; GO:000412; P:protein biosynthesis; IEA.
InterPro; IPRO01859; Ribosomal_P2.
PRINTS; PR00456; RIBOSOMALP2.
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131 AA; 11046 MW; 950562B80E529D4F CRC64;
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84.6%; Pred. No. 83;
cive 0; Mismatches
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Distributed under the Creative Commons Attribution-NoDerive License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anopheles gambiae str. PEST.
Eukaryota; Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
Anophelinae; Anopheles.
                                                       PubMed=16292255;
Fry B.G., Vidal N., Norman J.A., Vonk F.J., Scheib H., Ramjan S.F., Kuruppu S., Fung K., Blair Hedges S., Richardson M.K., Hodgson W.C. Ignjatovic V., Summerhayes R., Kochva E.;
"Early evolution of the venom system in lizards and snakes.";
Nature 439:584-588(2006).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, AAAB01008944; EAA10278.2; -; Genomic_DNA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The Anophales gambiae Sequence Committee;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 44; DB 2; Length 149;
Best Local Similarity 84.6%; Pred. No. 92;
Matches 11; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
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149 AA; 15582 MW; 6EA2E6044F4ED59C CRC64;
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                                                                                                                                                                                                                                                                                                                                                  ; Score 44; DB
Pred. No. 90;
0; Mismatches
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PANTHER, PTHR11267; TF T-box, 1.
Pfam; PF00907; T-box; T.
PROSITE, PS50252; TBOX_3; 1.
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Best Local Similarity 84.0.,
Best Local 11; Conservative
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                                           NUCLEOTIDE SEQUENCE.
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   MCBI_TaxID=51957;
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                                                     Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Identification of Pax2-regulated genes by expression profiling of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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Lepidosauria, Squamata, Scleroglossa, Anguimorpha, Anguidae,
Anniellinae, Anniella.
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Bouchard M., Grote D., Craven S.E., Sun Q., Steinlein P.,
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143 AA; 14137 MW; 5C1818C8EC2121F4 CRC64;
                                                                                                       EMBL; CAAE01007119; CAF89724.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-MAY-2005, integrated into UniProtKB/TrEMBL. 24-MAY-2005, sequence version 1. 07-FBB-2006, entry version 3. Pou3f3 (Fragment).
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84.6%; Pred. No. 89;
tive 0; Mismatches
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Q2XYX3;
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Development 132:2633-2643(2005).
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Gallus gallus (Chicken).
                                                                                                                                                     132
                     preliminary data.
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NCBI_TaxID=9031;
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RESULT 11
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RESULT 12
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                                                                                                                                                                                                                                                                                         Homo sapions (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ottenwaelder B., Obermaier B., Deutschenbaur S., Schaipp A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S., Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Osteoblast;
Dohi Y., Ohgushi H., Nakajima H., Ikeuchi M., Shimaoka H.,
Yonemasu K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      150 AA; 15110 MW; BOC80E466FCAB03E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-FEB-2006, entry version 9.
Core binding factor alphal subunit type I (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ensembl; ENSRNOG00000020193; Rattus norvegicus.
GO; GO:0005634; C:nucleus; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUL-2004, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                       01-NOV-1999, sequence version 1.
07-FRB-2006, entry version 19.
Hypothetical protein DKFZp586E1621 (Fragment)
Name-DKFZp586E1621;
                                                                                                                                                                                    01-NOV-1999, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         %; Score 44; DB
; Pred. No. 93;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        153 AA
                                                                                                                                              150 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AL080235; CAB45781.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AB115745; BAD08305.1; -; mRNA.
SMR; Q765Q0; 93-153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY; PRT;
                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004, sequence version 1. 07-FEB-2006, entry version 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
84.6%; E
                                                                                                                                            Q9Y4M1 HUMAN PRELIMINARY;
Q9Y4M1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    German cDNA Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 AAAAAAAAAAAA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AAXAAAAAAAXAA 13
    1 AAXAAAAAAAA 13
                                         10 AAAAAAAAAAA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; T12547; T12547.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
ses 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Uterus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q76500_RAT
Q765Q0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=CBFA1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                           HUMAN
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(276500 RAT

DT 076500

DT 05-JUL

DT 07-PEB

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PURMATCC 23344;

PubMed=1537793; DOI=10.1073/pnas.0403306101;

PubMed=1537793; DOI=10.1073/pnas.0403306101;

PubMed=1537793; DOI=10.1073/pnas.0403306101;

PubMyn T.V. Ulrich R.L., Ronning C.M., Brinkac L.M.,

Daugherty S.C., Davidsen T.D., DeBoy R.T., Dimitrov G., Dodson R.J.,

Durkin A.S., Gwinn M.L., Haft D.H., Khouri H.M., Kolonay J.F.,

Madupu R., Mohammoud Y., Nelson W.C., Radune D., Romero C.M.,

Sarria S., Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y.,

Sarria N., Zhou L., Fraser C.M.,

Structural flexibility in the Burkholderia mallei genome.";

Proc. Natl. Acad. Sci. U.S.A. 101:14246-14251(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
GO, GO:0005524; F:ATP binding; IEA.

GO; GO:0003700; F:transcription factor activity; IEA.

GO; GO:0006355; F:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR000040; AMI, Runt.

InterPro; IPR012346; PS3 RUNT DNA_bd.

PANTHER; PTHR11950; AMI, Runt; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Acetyl-CoA carboxylase, biotin carboxyl carrier protein.
Name=accB, OrderedLocusNames=BMA2501;
Burkholderia mallei (Pseudomonas mallei).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiaceae; Burkholderiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 157;
                                                                                                                                                                                                                                                                                                                                                                                       Score 44; DB 2; Length 153;
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R GO; GO:000317; C:acetyl-CoA carboxylase complex; IEA.

R GO; GO:000379; F:biotin binding; IEA.

R GO; GO:000573; F:biotin binding; IEA.

R GO; GO:000663; P:fatty acid biosynthesis; IEA.

R GO; GO:000663; P:fatty acid biosynthesis; IEA.

R InterPro; IPR00188; AccoAbiotinCC.

R InterPro; IPR00188; Biotin BS.

R InterPro; IPR00188; Biotin Ilpoyl.

Pfam; PF00364; Biotin Ilpoyl;

PRINTS; PR01071; ACOABIOTINCC.

PRINTS; PR01071; ACOABIOTINCC.

PROSITE; PS00188; BIOTINYL LIPOYL; 1.

PROSITE; PS00188; BIOTINYL LIPOYL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16082 MW; A0B41233C5AE51B0 CRC64;
                                                                                                                                                                                                                                                                                                                             SEQUENCE 153 AA; 16521 MW; D8A2B1598C1EC364 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-OCT-2004, integrated into UniProtKB/TrBMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           157 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 44; DE
84.6%; Pred. No. 96;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; CP000010; AAUS0135.1; -; Genomic_DNA.
TIGR; BMA2501; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                           94;
                                                                                                                                                                                                                                                                                                                                                                                                                        84.6%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q62GX4_BURMA PRELIMINARY; PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-OCT-2004, sequence version 1. 07-FEB-2006, entry version 11.
                                                                                                                                                                                                Pfam; PF00853; Runt; 1.
PRINTS; PR00967; ONCOGENEAML1.
PROSITE; PS51062; RUNT; 1.
                                                                                                                                                                                                                                                                                                                                                                                           100.08;
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SEQUENCE 157 AA; 16082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AAXAAAAAAAAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 AAAAAAAAAAAA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                               11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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2; Indels

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TEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 19
CORRHES MOUT
DE ORBENHES MOUT
DT 01-MA
MAN
RE STRAIL
RA CARNI
RA CARNI
RA CARNI
RA BAJIC
RA BAJIC
RA BAJIC
RA BANDAR
RA GEORG
RA A KITAN
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셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0005694; C:chromosome; IEA.
GO; GO:0005694; C:nucleosome; IEA.
GO; GO:00005634; C:nucleosome; IEA.
GO; GO:0005634; C:nucleosome; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0007001; P:chromosome organization and biogenesis (sen. . .; IEA.
GO; GO:000534; P:nucleosome assembly; IEA.
InterPro; IPR007124; Hist_TAF.
InterPro; IPR007125; Histone Gore D.
InterPro; IPR007125; Histone H2B.
PANTHER; PTHR11425; Histone H2B.
PANTHER; PTHR11425: FF4; Histone H2B; 1.
PANTHER; PTHR11425: FF4; Histone H2B; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                       L1J
NUCLEOTIDE SEQUENCE.
MEDLINE=20252564; PubMed=10794571; DOI=10.1007/s004120050401;
Ueda K., Kinoshita Y., Xu Z.-J., Ide N., Ono M., Akahori Y.,
Tanaka I., Inoue M.;
"Unusual core histones specifically expressed in male gametic cells of
                                                                                                                                                                                                                                                                                                                                           Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Liliales, Liliaceae, Lilium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lilium longiflorum.";
Chromosoma 108:491-500(2000).
-!- SUBUNIT: The nucleosome is an octamer containing two molecules each of H2A, H2B, H3 and H4. The octamer wraps approximately 146 bp of DNA (By similarity).
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anopheles gambiae str. PEST.
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Culicidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chromosomal protein; DNA-binding; Nuclear protein; Nucleosome core. SEQUENCE 158 AA; 17249 MW; 37A96D6D9117A0BD CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                           01-OCT-2000, integrated into UniProtKB/TrEMBL. 01-OCT-2000, sequence version 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-DEC-2003, integrated into UniProtKB/TrEMBL. 07-DEC-2004, sequence version 2. 07-PEB-2006, entry version 8. 07-PEB-2006, entry version 8. OR-SANGPO0000015660 (Fragment).
                                                                                                                                                            158 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 44; DB
84.6%; Pred. No. 96;
:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AB003780; BAA96095.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q7Q9M3 ANOGA PRELIMINARY; PRT; Q7Q9M3;
                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00621; HISTONEH2B.
ProDom; PD000497; Histone_H2B; 1.
                                                                                                                                                                                                                                                                                                                     Lilium longiflorum (Trumpet lily).
                                                                                                                                                                                                                                                                21-FEB-2006, entry version 25
                                                                                                                                                         PRELIMINARY;
                         64 AASAAAAAAAA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AAXAAAAAAAA 13
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les 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4690;
                                                                                                                                                         Q9MBF7 LILLO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6
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0709M3 ANO
1D 0709M
AC 0709M
DT 15-DE
DT 07-DE
DE ROSAM
GN ORFNA
OS ANOPA
OC NEOPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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NUCLEUING: STUCENCE.

WITH NUCLEUR STUCENCE.

WAS GARDING: TISSUE=Whole body;

WA Carninci P., Kasukwam T., Katayama S., Gough J., Frith M.C., Maeda N.,

A Carninci P., Kasukwam T., Katayama S., Gough J., Frith M.C., Maeda N.,

A Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,

Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,

A mabesi-Impiombato A., Apweller R., Aturaliya R.N., Bailey T.L.,

A mabesi-Impiombato A., Apweller R., Aturaliya R.N., Bailey T.L.,

A mabesi-Impiombato A., Apweller R., Aturaliya R.N., Bailey T.L.,

A mabesi-Impiombato A., Apweller R., Aturaliya R.N., Bailey T.L.,

A chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,

Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,

Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,

A Crow M.L., Dalla E., Dallymple B.P., de Bono B., Della Gatta G.,

A Crow M.L., Dalla E., Dallymple B.P., de Bono B., Della Gatta G.,

A Bernardo D., Down T., Engerrom P., Fagiolini M., Petaki S., Gariboldi M.,

Georgii-Hemming P., Gingeras T.R., Golobori T., Green R.E.,

A Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa T.,

A Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,

Xitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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Mammalia, Butheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-C57BL/61; TISSUE-Whole body;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003, integrated into UniProtKB/TrEMBL.
01-MAR-2003, sequence version 1.
07-FBS-2006, entry version 13.
9 days embryo whole body cDNA, RIKEN full-length enriched library, clone:D030067F24 product:hypothetical protein, full insert sequence. Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                               STRAIN=PEST;
The Anopheles gambiae Sequence Committee;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                               "Anopheles gambiae re-annotation.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           164 AA; 16803 MW; 2D1BAC62C087BBAC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AAAB01008900; EAA09564.2; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Methods Enzymol. 303:19-44(1999).
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0; Mismatches
                                                                                                                                                                                           The Anopheles gambiae Sequence Committee;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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Anophelinae; Anopheles.
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                                       NCBI_TaxID=180454;
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RETAINSCIPEL(61) TISSUE=Whole body;

MULINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

A OKAZAKI Y., Furuno M., Kasukawa T., Adachi J., Rondo H., Kondo S.,

A Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

Radi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

Radiake J.A., Eradt D., Brattor C.F., Forrest A., Frazer K.S.,

Baldarelli R., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,

Radiake J., Mirchiboli M., Gissi C., Godzi A., Gough J.,

Ranai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

Ronagaya A., Kurcchkin IV., Lee Y., Lenhard B., Lyons P.H.,

RA Agashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

RA Ravasi T., Reed J.C., Reed D.J., Ring B.Z., Ringwald M.,

Radashima T., Numata K., Pontius J.U., Oi D., Ramachandran S.,

Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,

Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,

Milming L.G., Wynshaw-Boris A., Vanagisawa M., Rangawa T., Konno H., Nakamura M., Saro K.,

RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Radawa T., Konno H., Nakamura M., Sarawa T., Konno H., Nakamura M., Sarawa T., Konno H., Nakamura M., Sarawa T., Radawa T., Konno H., Nakawa T., Kanada J., Aizawa K., Aradawa T., Kanada J., Aizawa K., Aradawa T., Kayawa T.,

Rayazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

Rayazaki A., Sokai K., Sasaki D., Shibata K., Shinagawa J.,

Rayaraki Y., Yanagisaki Y.,

Rayaraki W., Yangi L., Pilli Y., Ilohi Y., Sirok Y., Reilli Y., Ilohi Y., Shinaka Y., Hayasaki J., Ilohi W., Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
Mottagui-Tabar S., Miki H., Mignone F., Miyake S., Morris K.,
Mottagui-Tabar S., Miki H., Mignone F., Miyake S., Morris K.,
Mottagui-Tabar S., Miki H., Mignone F., Miyake S., Morris K.,
Mottagui-Tabar S., Miki H., Mignone F., Miyake S., Morris K.,
Mottagui-Tabar S., Miki H., Morris F., Ohara O.,
Mottagui-Tabar S., Nishikawa S., Nori F., Ohara O.,
Mottagui-Tabar S., Reed J., Reid J.F., Pavan W.J., Pavesi G.,
Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
Schonbach C., Sekjuchi K., Semple C.A., Sessa L., Sheng Y.,
Schonbach C., Stingada H., Shimada K., Silva D., Sinclair B.,
Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
Tamaoja K., Tan S.L., Tang S., Taghar J., Teichmann S.A.,
Mader H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
Vamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
Mahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
Mahlestedt C., Mattick J.S., Hume D.A., Kawagashira N.,
Mahlestedt C., Mattick J.S., Hume D.A., Kawagashira N.,
Mahlestedt C., Mattick J.S., Hume D.A., Kawagashira N.,
Mishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki H., Kawai J.,
Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J., STRAIN=CS7BL/GJ; TISSUE=Whole body;
PubMed=16141073; DOI=10.1126/science.1112009;
RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium;
"Antisense Transcription in the Mammalian Transcriptome."; "The transcriptional landscape of the mammalian genome."; Science 309:1564-1566(2005). Science 309:1559-1563(2005). full-length cDNAs."; Nature 420:563-573(2002). NUCLEOTIDE SEQUENCE NUCLEOTIDE SEQUENCE NUCLEOTIDE SEQUENCE Hayashizaki 

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MEDLINE=21085660; PubMed=11217851; DOI=10.1038/3505500;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Stahli S., Matsuo Y., Nikaido I., Pasole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Bataki K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M., F., Gustinici B., Hill D., Hoffmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamcto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Hasselawa Poris A., Yoshida K., Hassegawa Y., Kawaji H., Kohtsuki S., STRAIN=C57BL/61; TISSUE=Whole body;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
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RESULT 20

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Q96NI3_HUMAN
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   Gramene;
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                                                                                      Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP clade,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                           Ensembl; ENSRNOG0000020193; Rattus norvegicus.
Ensembl; ENSRNOG0000020193; Rattus norvegicus.
GO; GO:0005534; C:nucleus; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR000040; AML1 Runt.
InterPro; IPR012346; P53_RUNT_DNA_bd.
PANTHER; PTRR112346; P53_RUNT_DNA_bd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 44; DB 2; Length 167; 84.6%; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
Wing R.A., Yu Y., Soderlund C., Kim H.-R., Rambo T., Saski
Currie J., Collura K.;
                                                                                                                                                                                     Dohi Y., Ohgushi H., Nakajima H., Ikeuchi M., Shimaoka H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                           Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                     167 AA; 18085 MW; E3C437F8F04BE74A CRC64;
                                                       07-FEB-2006, entry version 9.

Core binding factor alphal subunit type II (Fragment).

Name=CBFA1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-WAR-2003, integrated into UniProtKB/TrEMBL. 01-MAR-2003, sequence version 1. 21-FEB-2006, entry version 10. Putative KNOX family class 2 homeodomain protein.
                                  05-JUL-2004, integrated into UniProtKB/TrEMBL
            167 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QBH8GG_ORYSA PRELIMINARY; PRT; 171 AA.
Q8H8GG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AC098695; AAN74840.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84.6%; Pred. No. 1e+0
ive 0; Mismatches
                                                                                                                                                                                                                                                                    EMBL; AB115746; BAD08306.1; -; mRNA.
            PRT;
                                            05-JUL-2004, sequence version 1.
                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00967; ONCOGENEAML1.
          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS51062; RUNT; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Conservative
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                                                                                                                                                               NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                        rissum=Osteoblast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=OJ1126B12.15;
                                                                                                                                        NCBI_TaxID=10116;
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            Q765P9_RAT
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SEQUENCE
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MEDLINE=2233736. PubMed=12447438; DOI=10.1038/nature01184; Sasaki T. Matsumoto T. Yamamoto K. Sakata K. Baba T. Katayose Y. M. U., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H., Hosokawa S., Magukawa M., Arikawa K., Chiden Y., Hayashi M., Ando T., Aoki H., Arita K., Hamada M., Harada C., Hishawa S., Honda M., Ichikawa Y., Idonuma A., Iijina M., Ikeda M., Aikeno M., Ito Y., Ito Y., Iwabuchi A., Kamiya K., Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I., Machita K., Machara T., Mixuno H., Mizubayashi T., Mukai Y., Nakamura M., Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M., Animokawa T., Shomura A., Song J., Takazaki Y., Tarasawa K., Terusawa K., Tarasawa K., Taniyi K., Waki K., Yamagata H., Yamane H., Yashiki S., Yoshihara R., Yukawa K., Alanog H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.-I., Eun M.-Y., A. Yano M., Jiang J., Gojobori T.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                 ; Score 44; DB 2; Length 171;
Pred. No. 1e+02;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The genome sequence and structure of rice chromosome 1."; Nature 420:312-316 (2002).
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SEQUENCE 175 AA; 18520 MW; 2FFF4E34C0E89871 CRC64;
                                                                                                                                                                                               171 AA; 17982 MW; 647C830E1C22B8F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-2005, integrated into UniProtKB/TrEMBL.
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     175 AA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-FEB-2006, entry version 5.
Hypothetical protein P0406G08.29.
Name=P0406G08.29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-2005, sequence version 1.
                                                                                                                                                                                                                                                       100.08;
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                                                 InterPro, IPR005540; KNOX1.
InterPro, IPR005541; KNOX2.
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                                                                                                                                                                                                                    Query Match

Best Local Similarity 84.00.,

Best 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                     1 AAXAAAAAAAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                       24 AAAAAAAAAAA 36
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                                                                                 InterPro; IPR005541; KNO>
Pfam; PF03790; KNOX1; 1.
Pfam; PF03791; KNOX2; 1.
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NUCLEOTIDE SEQUENCE
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                                                                                                                                                                  Nuclear protein.
SEQUENCE 171 A
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PRT;

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                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                               01-DEC-2001, integrated into UniProtKB/TrEMBL.
01-DEC-2001, sequence version 1.
07-MAR-2006, entry version 21.
Hypothetical protein FLJ30829 (Hypothetical protein RBM24)
(OTTHUMP0000001016067).
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                                                                                                                                                                                                                                                                                                               Name=RBM24; ORFNames=RP1-259A10.1-002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA sequences."
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NUCLEOTIDE SEQUENCE

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The pubmed-1546914; DOI-10.1038/nature03025;

The bubmed-1546914; DOI-10.1038/nature03025;

The bubmed-1546914; DOI-10.1038/nature03025;

The bubmed-1546914;

The bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,

Mauceli E., Bouneau L., Fischer C., Lutfalla G., Dossat C., Segurens B.,

The basilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,

Anthousad V., Jubin C., Castelli V., Katinka M., Vacherie B.,

Anthousad V., Jubin C., Cattolico L., Poulain J., De Berardinis V.,

Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,

R. Biran G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,

R. Alis M., Volff J.-M., Guigo R., Zody M.C., Mesirov J.,

Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Scarpelli C.,

Mincker P., Lander B.S., Weissenbach J., Roest Crollius H.,

"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
                                                                                                                                                                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-JUL-2005, sequence version 1.
07-FBB-2006, entry version 3.
Chromosome 2 SCAF150132, whole genome shotgun sequence. (Fragment).
ORFNames=GSTENG00031100001;
Tetraodon nigroviridis (Green puffer).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 44; DB 2; Length 191; 84.6%; Pred. No. 1.1e+02; ive 0; Mismatches 2; Indels
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-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry whi.
                                               to the EMBL/GenBank/DDBJ databases.
                                                                                                                                       Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                191 AA; 19599 MW; 89E4D14E3DA941F7 CRC64;
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PROSITE; PSO0178; AA_TRNA_LIGASE_I; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                199 AA.
                                                                                                                                                                                                                                                                                                                    EMBL, BC104810; AA104811.1; -; mRNA.
EMBL, AL136305; CA119958.1; -; Genomic_DNA.
Ensembl; ENSG0000112183; Homo sapiens.
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0; Mismatches
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Nature 431:946-957(2004).
                                                                                                                                                                                                                                                                    EMBL; AK055391; BAB70914.1; -; mRNA.
EMBL; BC104808; AAI04809.1; -; mRNA.
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InterPro; IPR001412; tRNA-synt_I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein. seguence 191 AA; 1
                                             Submitted (SEP-2005)
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                                                                                            NUCLEOTIDE SEQUENCE.
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                           NIH MGC Project;
rissum=Brain;
                                                                                                                        Babbage A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Mamm. Genome 11:151-158(2000).
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213
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NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                            Best Local Similarity
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Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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Mortlock D.P., Sateesh P., Innis J.W.;
"Evolution of N-terminal sequences of the vertebrate HOXA13 protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Metatheria, Didelphimorphia, Didelphidae, Monodelphis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Falvella F.S., Manenti G., Spinola M., Pignatiello C., Ravagnani Conti B., Pastorino U., Dragani T.A.;
"Population-based association study on two candidate lung adenocarcinoma modifier genes flanking the Di2Si034 locus.";
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                      Length 199;
                                                                                                                                                    ; Score 44; DB 2; Length 19
Pred. No. 1.2e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AY665466; AAV54601.1; -; mRNA.
Ensembl; ENSG00000123095; Homo sapiens.
SEQUENCE 203 AA; 19438 MW; 02625F0B557CB263 CRC64;
                                                                                                             199 AA; 21690 MW; FB839A4F470FFD5D CRC64;
                                                           EMBL; CAAE01015032; CAG11205.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                              QSCI4_HUMAN PRELIMINARY; PRT; 203 AA. QSC14_7
21-DEC-2004, integrated into UniprotKB/TrEMBL.
07-FEB-2006, entry version 1.
07-FEB-2006, entry version 5.
Basic_helix-loop-helix protein 3 isoform 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000, integrated into UniFrotKB/TrEMBL. 01-MAY-2000, sequence version 1. 07-FEB-2006, entry version 16. Transcription factor HOXA13 (Fragment).
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                                                                                                                                                        100.08;
                                                                                                                                                                             84.68;
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                                                                                                                                                                                                                                                                                        147 AAAAAAAAAA 159
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                                                                                                                                                                                                                                            1 AAXAAAAAAAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AAXAAAAAAAA 13
                                                                                                                                                                                                 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                             Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=13616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=BHLHB3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=HOXA13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rissue=Lung;
                                                                                                           SEQÜENCE
                                                                                                                                                        Query Match
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025C14 HUM
025C11 AC
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DT 21-DE
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DT 21-DE
DT 07-FE
DGN Mamma
OC BUKAT
OC BUKAT
OC HUMON
OX NCBI
RN [1]
RN [1]
RN NUCLE
RR TISSU
RR TISSU
RR TISSU
RR CONTI
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CC COPY
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Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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Distributed under the Creative Commons Attribution-NoDerivs License
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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MEDLINE=94171032; PubMed=8125298; DOI=10.1016/0378-1119(94)90802-8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [3]
NUCLEOTIDE SEQUENCE.
Suzuki Y., Sugano S., Totoki Y., Toyoda A., Takeda T., Sakaki Y.,
Tanaka A., Yokoyama S.,
Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Maruyama K., Sugano S.; Olydo-capping: a simple method to replace the cap structure of eucaryotic mRNAs with oligoribonucleotides."; Gene 138:171-174(1994).
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                                                                                                                                                                                                                                                                                                                          100.0%; Score 44; DB 2; Length 213; 84.6%; Pred. No. 1.2e+02; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, AK223111; BAD96831.1; -; mRNA.
Ensembl; ENSG00000139239; Homo sapiens.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0005840; C:ribosome; IEA.
GO; GO:0003735; F:structural constituent of ribosome; IEA.
GO; GO:000412; P:protein biosynthesis; IEA.
                                                                                                                                                                                                                                                                213 AA; 19165 MW; EDEC8B40FCACADE9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           218 AA; 23645 MW; 3DESCB1F97345E78 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-MAY-2005, integrated into UniProtKB/TrEMBL. 24-MAY-2005, sequence version 1. 07-FBB-2006, entry version 4. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                218 AA.
                                                                                              EMBL; AF083097; AAD54642.1; -; Genomic_DNA.
GO; GO:0005634; C:nucleus; IEA.
Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q53G20 HUMAN PRELIMINARY;
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Alusner R.D., Collins F.S., Wagner L., Sheamen C.W., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Rena S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan R.D., Mullahy S.J.,
A Norley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Sakalska U., Smailus D.E.,
A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
Schnerch A., Schein J.E., Schults J. Schults J
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Suzuki Y., Sugano S., Totoki Y., Toyoda A., Takeda T., Sakaki Y.,
Tanaka A., Yokoyama S.,
Submitted A., Yokoyama S.,
Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IISSUE=Dermoid cancer;
MEDLINE=98038986; PubMed=9373149; DOI=10.1016/S0378-1119(97)00411-3;
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Director MGC Project;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                           10-MAY-2005, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                       RPL14 protein (Ribosomal protein L14 variant)
Name=RPL14;
                                                                                                                                                                                                         220 AA.
                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                  10-MAY-2005, sequence version 1.
07-MAR-2006, entry version 8.
                                                                                                                                                                                                     PRELIMINARY;
150 AAAAAAAAAAA 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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QEIPH7;
                                                                                                                                                                   HUMAN
                                                                                                                                RESULT 28
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EMBL; BC071913; AAH71913.1; -; mRNA.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=15620360; DOI=10.1016/j.cell.2004.11.040;
Dorus S., Vallender B.J., Evans P.D., Anderson J.R., Gilbert S.L.,
Mahowald M., Wyckoff G.J., Malcom C.M., Lahn B.T.;
"Accelerated evolution of nervous system genes in the origin of Homo
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-FBB-2005, sequence version 1.
07-FBB-2006, entry version 6.
Achaete-scute complex protein (Fragment).
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapiens.";
Cell 119:1027-1040(2004).
-!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
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                                                                                                                                                                                                                                                                                                                                                    Score 44; DB 2; Length 220;
Pred. No. 1.2e+02;
; Mismatches 2; Indels
                                                                                      ribosome; IEA.
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GO; GO:0005634; C:nucleus; IEA.
GO; GO:0030528; F:transcription regulator activity; IEA.
GO; GO:0045449; P:regulation of transcription; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23804 MW; CD0D8E7C9F4F1063 CRC64;
                                                                                                                                                                                                                                                                                                220 AA; 23787 MW; 0FD8AA7FC191E864 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IS-FEB-2005, integrated into UniProtKB/TrEMBL.
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EMBL, AK222750; BAD96470.1; -; mRNA.
Ensembl, RNSG00000139239; Homo sapiens.
GO; GO:0005840; C:ribosome; IEA.
GO; GO:0003735; F:structural constituent of
GO; GO:000412; P:structural biosynthesis; IEA.
InterPro; IPR005824; KOW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             223 AA.
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 1.2e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cercopithecidae; Cercopithecinae; Macaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                      Pfam; PF00467; KOW; 1.
Pfam; PF01929; Ribosomal_L14e; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001092; HLH basic.
InterPro; IPR011598; HLH DNA bd
                                                                                                                                                                                                                                                                                                                                                              100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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QTQT06 ANGGA PRELIMINARY;
QTQT06;
                                                                                                                                                                                                                                                                                                                                                                                             84.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           150 AAAAAAAAAAA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR011598; HLH_I
Pfam; PF00010; HLH; 1.
SMART; SM00353; HLH; 1.
PROSITE; PS50888; HLH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AAXAAAAAAAAA 13
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Best Local Similarity 84.6
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AAXAAAAAAAA 13
                                                                                                                                                                                                                                                                                                                                                              Query Match 100.
Best Local Similarity 84.6
Matches 11; Conservative
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                                                                                                                                                                                                                                                                          Ribosomal protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9541;
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Q7Q706_ANO
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Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae; Potexvirus; unclassified Potexvirus.
                                                                             GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0003577; F:Edvelopment; IEA.
GO; GO:0006355; P:regulation; IEA.
GO; GO:0006359; P:transcription; IEA.
InterPro; IPR001523; Paired box N.
InterPro; IPR011991; Wing_hlx_DNA_bd.
                                                                                                                                                                                                                                                                Pfam; PF00292; PAX; 1.

PRINTS; PR00027; PAIREDBOX.
SMART; SM00351; PAX; 1.

PROSTIE: PS51057; PAIRED 2; 1.

DNA-binding; Developmental protein; Nuclear protein; Paired box;
Transcription; Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Ohio;
PubMed=16096710; DOI=10.1007/s00705-005-0586-x;
Tzanetakis I.E., Postman J.D., Martin R.R.;
"Mint virus X: a novel potexvirus associated with symptoms in 'Variegata' mint.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 44; DB 2; Length 228; 84.6%; Pred. No. 1.3e+02; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 44; DB 2; Length 228; 84.6%; Pred. No. 1.38+02; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7CCA50757B2ACDE9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AY921610; AAX19351.1; -; Genomic_RNA.
GO; GO: 0019028; C: viral capsid; IEA.
GO; GO: 0005198; F: structural molecule activity; IEA.
InterPro; IPR00055; Pltvir_coat.
PRINTS; PR00236; Virus P-coat; 1.
PRINTS; PR00232; POTXCARLCOAT.
PROSITE; PS00418; POTEX_CARLAVIRUS_COAT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-APR-2005, integrated into UniProtKB/TrEMBL.
12-APR-2005, sequence version 1.
07-FBB-2006, entry version 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         228 AA.
                           EMBL; AJ579865; CAE30302.1; -; mRNA.
SMR; Q5K4L2; 1-103.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        228 228
228 AA; 24289 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QSBQDS_9VIRU PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.68;
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hes 11; Conservative
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NUCLEOTIDE SEQUENCE.
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Best Local Similarity
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SEQUENCE 228
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Mint virus X.
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SEQUENCE
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QSBQD5_9VI
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                                                                                                                                 Anopheles gambiae str. PEST.
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
Anophelinae; Anopheles.
NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glomeris marginata.
Bukaryota, Metazoa, Arthropoda, Myriapoda, Diplopoda, Pentazonia,
Glomerida, Glomeridae, Glomeris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 44; DB 2; Length 22
Pred. No. 1.3e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                             The Anopheles gambiae Sequence Committee; "Anopheles gambiae re-annotation."; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            227 227
227 AA; 25069 MW; C14D4245AF45563C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, AAAB01008960; BAA11077.2; -; Genomic_DNA.GO; GO:0005614; C:nucleus; IEA.GO; GO:0005674; C:nucleus acid binding; IEA.GO; GO:0008270; F:nucleic acid binding; IEA.InterPro; IPR007087; Znf C2H2. Beam; PR00096; Zc-C2H2; 3. PROSITE; PS00028; ZINC_FINGER_C2H2]; 3. PROSITE; PS00028; ZINC_FINGER_C2H2]; 3. PROSITE; PS20157; ZINC_FINGER_C2H2]; 3. NON_TER 227 227 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=16351954; DOI=10.1016/j.zool.2004.11.003;
15-DEC-2003, integrated into UniProtKB/TrEMBL. 07-DEC-2004, sequence veraion 2. 07-EBS-2006, entry version 10. ENSANGPO0000017596 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-FEB-2005, integrated into UniProtKB/TrEMBL.
15-FEB-2005, sequence version 1.
07-FEB-2006, entry version 8.
Pax6.2 protein (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The Anopheles gambiae Sequence Committee;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                        ORFNames=ENSANGG00000015107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 AAAAAAAAAAA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AAXAAAAAAAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        preliminary data.
                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
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Best Local Similarity
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Q5K4L2;
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Capsid protein.
SEQUENCE 228
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Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
Potexvirus; unclassified Potexvirus.
                                                                                                                                                             Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
Potexvirus; unclassified Potexvirus.
NCBI_TaxID=301865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=15664053; DOT=10.1016/j.jviromet.2004.11.006; Tzanetakis I.E., Keller K.E., Martin R.R.; "The use of reverse transcriptase for efficient first- and secondstrand cDNA synthesis from single- and double-stranded RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
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                                                                                                                                                                                                                                                                              STRAIN=Maryland;
PubMed=16096710; DOI=10.1007/s00705-005-0586-x;
PubMed=16096710; DOI=10.1007/s00705-005-0586-x;
Tzanetakis I.E., Postman J.D., Martin R.R.;
"Mint virus I.E. a novel potexvirus associated with symptoms in 'Variegata' mint.'
Arch. Virol. 151:143-153(2006).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 44; DB 2; Length 22
84.6%; Pred. No. 1.3e+02;
tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            228 AA; 23843 MW; 8076F49DE5EB1A96 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AY921609; AAX19348.1; -; Genomic_RNA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR000062; Pltvir_cat.
PF00286; Virus_P-coat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Oregon;
PubMed=16096710; DOI=10.1007/s00705-005-0586-x;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-WAR-2005, integrated into UniProtKB/TrEMBL. 01-WAR-2005, sequence version 1. 07-FEB-2006, entry version 7.
                                                             12-APR-2005, integrated into UniProtKB/TrEMBL
12-APR-2005, sequence version 1.
07-FEB-2006, entry version 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             228 AA.
                       228 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00232; POTXCARLCOAT.
PROSITE; PS00418; POTEX_CARLAVIRUS_COAT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QSG1G9 9VIRU PRELIMINARY; PRT;
QSG1G9;
                       PRELIMINARY; PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        templates.";
J. Virol. Methods 124:73-77(2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Variegata' mint.";
Arch. Virol. 151:143-153(2006).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AAXAAAAAAAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 AAAAAAAAAASAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 84.6
ses 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=301865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tzanetakis I.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coat protein.
Mint virus X.
                     QSBQD8_9VIRU
QSBQD8;
                                                                                                                                Coat protein.
                                                                                                                                                      Mint virus X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Capsid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Q5G7G9_9VI
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"Two rat homologues of Drosophila achaete-scute specifically expressed in neuronal precursors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata; Craniata, Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILĀRITY: Contains 1 basic helix-loop-helix (bHLH) domain.
                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                             100.0%; Score 44; DB 2; Length 228; 84.6%; Pred. No. 1.3e+02; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Sprague-Dawley;
MEDLINE=90363294; PubMed=2392153; DOI=10.1038/346858a0;
                                                                                                                                                                                                                                  228 AA; 23834 MW; A56CCC8FD0F12A81 CRC64;
EMBL; AY789138; AAW67750.1; -; Genomic_RNA.

EMBL; AY921611; AAX19354.1; -; Genomic_RNA.

GO; GO: 00190218; F: Structural capacid; IEA.

InterPro; IPR000052; Pitvir_coat.

Pfam; PR00286; Virus P-coat; 1.

PRINTS; PR00232; POTXCRLCOAT.

PRODOM; P0000603; Pitvir_coat; 1.

PRODOM; P0000603; Pitvir_coat; 1.

PROSITE; PG00189; POTEX_CARLAVIRUS_COAT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1990, integrated into UniProtKB/Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X53725; CAA37760.1; -; mRNA.
PIR; S11563; S11563.
TRANSFAC; T00484; -.
Ensembl; ENSRNOG0000004294; Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       233 AA.
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GO; GO:0007399; P:neurogenesis; IDA.
InterPro; IPR001092; HLH_basic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1990, sequence version 1.

07-WAR-2006, entry version 46.

Achaete-scute homolog 1.

Name=Ascll; Synonyms=Ashl, Mash-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE [MRNA].
                                                                                                                                                                                                                                                                                                                                                                           1 AAXAAAAAAAA 13
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                                                                                                                                                                                                                                                                                                         Sest Local Similarity 84.6
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                                          Oryza satīva (japonīca cultivar-group).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                     Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J., Liu Y., Hu X., Jia P., Zhang S., Fu G., Huang Y., Li Y., Zhu J., Liu Y., Hu X., Jia P., Zhao Q., Ying K., Yu Z., Tang Y., Weng Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D., Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J., Ru M., Zhang R., Zhou B., Chen L., Jin Z., Wang R., Yin H., Cai Z., Ren S., Lo G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y., Chen J., Xhang Y., Chen J., Xhang Y., Chen J., Zhang Y., Zhang W., Zhu Q., Zhang Y., Jia J., Zhang Y., Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y., Han B.;
                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
        Hash, Course of SYRYV6; -... GO; GO:0005634; C:nucleus; IEA. GO; GO:0005634; C:nucleus; IEA. GO; GO:0005100; F:transcription factor activity; IEA. GO; GO:0006155; P:regulation of transcription, DNA-dependent; IEA. InterPro; IPR001471; TF_ERF.
                                                                                                                                                                      ;
0
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0
                                                                                                                                                 Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 233;
                                                                                                                                     Score 44; DB 1; Lengtn 25.
Pred, No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMAKI; DINGGOGG, ......
PROSITE; PS51032; AP2_ERF; 1.
GEGITENCE 233 AA; 25434 MW; 90B3BF38A3A4A419 CRC64;
                                                                                                                            036BDAC8E2D23274 CRC64;
                                                            Achaete-scute homolog 1.
/FTId=PRO 0000127128.
Helix-loop-helix motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 44; DB 2; Le
84.6%; Pred. No. 1.38+02;
live 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Sequence and analysis of rice chromosome 4.";
                                                                                                                                                                                                                                                                                        01-OCT-2003, integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                                                                                                   233 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AL606635; CAD41708.2; -; Genomic_DNA.
HSSP; O80337; 1GCC.
                                                                                                                                                                      0; Mismatches
                                                                                             Basic motif.
                                                                                                      Poly-Ala.
Poly-Gln.
                                                                                                                                                                                                                                                                   Q7XTV6_ORYSA PRELIMINARY; PRT;
Q7XTV6;
                                                                                                                                                                                                                                                                                                01-MAR-2004, sequence version 2.
07-FEB-2006, entry version 14.
OSJNBa0010D21.10 protein.
InterPro; IPR011598; HLH_DNA_bd
                                                                                 129 168 He.
118 128 Bat
30 44 Po.
48 54 Po.
233 AA; 24972 MW; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00367; ETHRSPELEMNT.
ProDom; PD001423; TF ERF; 1.
SMART; SM00380; AP2; 1.
                                                                                                                                                100.0%;
84.6%; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 420:316-320(2002).
                                                                                                                                                                                          1 AAXAAAAAAAA 13
                                                                                                                                                                                                               32 AAAAAAAAAAAA 44
                                                                                                                                                                     11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Conservative
                                                              233
                                                                                                                                                                                                                                                                                                                                  Name=OSJNBa0010D21.10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
                                                                                                                                                Query Match
Best Local Similarity
                                                                                          DNA BIND
COMPBIAS
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                                                                                                                COMPBIAS
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MEDLINE-22388257; PubMed-12477932; DOI=10.1073/pnas.242603899;

MEDLINE-22388257; PubMed-12477932; DOI=10.1073/pnas.242603899;

Atlausner R.D., Collins F.S., Wagner L., Derge J.G.,

Alusner R.D., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Alusthan R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,

Alachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

And Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.U.,

Rabas S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Allalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Anterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Broc. Natl. Acad. Sci. U.S.A., 99:16899-16903(2002).

Frunction may play a role at early stages of development of several lineages in most regions of the CNS, and of Sci. U.S.A., Besential for the generation of Clastocox and authonomic, Commons.
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLECTIDE SEQUENCE FORMAN.
MEDLINE=91296195; PubMed=8190674;
MEDLINE=91296195; PubMed=81910674;
Ball D.W., Azzoli C.G., Baylin S.B., Chi D., Dou S., Donis-Keller H.,
Cumaraswamy A., Borges M., Nelkin B.D.;
"Identification of a human achaete-scute homolog highly expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         binding to the B box (5 -CANNTG-3').
-!-SUBBUNIT: Efficient DNA binding requires dimerization with another bHLH protein. Forms a heterodimer with E12/B47.
-!-SUBCELLULAR LOCATION: Nucleus (Probable).
-!-SUBCELLULAR: Contains 1 basic helix-loop-helix (bHLH) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                ASCLI HUMAN STANDARD; PRT; 236 AA. P50553; Q9BQ30; 01-0CT-1996, integrated into UniProtKB/Swiss-Prot. 07-MAY-2002, sequence version 2. 07-MAX-2006, entry version 46. Achaete-scute homolog 1 (HASH1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neuroendocrine tumors.";
Proc. Natl. Acad. Sci. U.S.A. 90:5648-5652(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; BC001638; -; NOT ANNOTATED CDS; MENA, EMBL; BC002341; AAH02341.1; -; MENA. EMBL; BC002341; AAH02341.1; -; MENA. EMBL; BC003134; AAH01134.1; -; MENA. EMBL; BC004125; AAH0425.1; -; MENA. EMBL; BC013299; AAH31299.1; -; MENA. ENR, AAH379; AAH31299.1; -; MENA. ENR, ENR, AAH379; AAH379.1; -; MENA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; L08424; AAA58376.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=ASCL1; Synonyms=ASH1;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE [MRNA]
13
                                                                                  14 AASAAAAAAAA 26
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Gaps

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Indels

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                                                                                                                                                                            01-UUN-2001, integrated into UniProtKB/TrEMBL.
01-UUN-2001, sequence version 1.
01-UUN-2001, sequence version 2.
01-FEB-2006, entry version 28.
0T-FEB-2006, entry version 28.
0T-FHUMPO000016066.
ORFNames=RP1-259A10.1-001;
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kluyveromyces lactis (Yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1] — NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=CBS 2359 / IFO 1267 / NRRL Y-1140 / WM37;
PubMed=15229592; DOI=10.1038/nature02579;
Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 44; DB 2; Length 236; 84.6%; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-AUG-2004, integrated into UniProtKB/TrEMBL.
16-AUG-2004, sequence version 1.
07-FEB-2006, entry version 11.
Similarities with sp|Q9YAC5 Aeropyrum pernix Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24776 MW; 1CFB5AEBD4E3AA24 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ensembl. ENSGO0000112183, Homo sapiens.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:000166; F:nucleicide binding; IEA.
InterPro; IPR012677; a b plait nuc bd.
InterPro; IPR001778; POA_allergen_C.
InterPro; IPR001778; POA_allergen_C.
InterPro; IPR001712; tRNPI_RNA_bd.
InterPro; IPR001912; tRNPI_RNA_bd.
InterPro; IPR001912; tRNPI_RNA_bd.
IPR01076; RRM 1; 1.
PRINTS; PR00833; POAALLERGEN.
SWART; SW00336; RRM; 1.
PROSITE; PS001078; AA TRNA_LIGASE_I; UNKNOWN_I.
PROSITE; PS00102; RRW; 1.
SEQUENCE 236 AA; 24776 MW; 1CFBSAEBD4E3AA24 C.
                                                                                                                                                 236 AA.
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0; Mismatches
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HSSP; P09651; 1L3K.
Mismatches
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                                                                                                                                               PRT;
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                                                                                                                                               O9BX46 HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 KLULA
QGCNB7 KLULA PRELIMINARY;
QGCNB7;
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                                                               209 AAAAAAAAAAA 221
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                                  1 AAXAAAAAAAA 13
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   11; Conservative
                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                     Babbage A.;
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
Li H., Zhong G., Zhou G., Wang C., Shen C., Ke R., Li M., Xiao W.,
Lin L., Yang S.;
                                                                                                                                     PROSITE; PS50888; HLH; 1.
Developmental protein; Differentiation; DNA-binding; Neurogenesis;
Nuclear protein; Polymorphism.
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                                                                                                                                                                                                                                                                                                                                                                    ; Score 44; DB 1; Length 236;
Pred. No. 1.3e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                   Poly-Ala.
Poly-Gln.
E -> G (in dbSNP:1803157).
FrId=VAR 013179.
Q -> QQQ (in Ref. 1).
W; A7D784329305B49A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lin L., Yang S.;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
SEQUENCE 236 AA; 24740 MW; 9B550B5232E3AA3D CRC64;
                                                                                                                                                                                   Achaete-scute homolog 1.
/FTId=PRO 0000127126.
Helix-loop-helix motif.
Basic motif.
                 HGNC; HGNC:738; ASCLI.
MIM; 100790; gene.
GO; 0003700; F:transcription factor activity; NAS.
InterPro; IPR01159; HLH basic.
InterPro; IPR011599; HLH DNA_bd.
Pfam; PP00010; HLH; 1.
SWART; SM00353; HLH; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL-2004, integrated into UniProtKB/TrEMBL. 05-JUL-2004, sequence version 1. 05-JUL-2004, extra version 16. Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO0833; PŌAALLERGEN.
SMART; SMO0360; RRM; 1.
PROSITE; PSO1018; AA TRNA_LIGASE_I; UNKNOWN_1.
PROSITE; PS50102; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HGNC; HGNC: 21539; RBM24.

GO; GO:0003676; F:nucleic acid binding; IEA.

GO; GO:000166; F:nucleotide binding; IEA.

InterPro; IPR01267; a b plait_nuc bd.

InterPro; IPR001778; POA allergen_C.

InterPro; IPR001778; POA allergen_C.

InterPro; IPR001478; RNPI_RNA_bd.

InterPro; IPR001412; tRNA_Synt_I.
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Ensembl; ENSG0000112183; Homo sapiens.
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                                                                                                                                                                                                                                                                                                                     62 Q
25454 MW;
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QGQDA4;
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      H-InvDB; HIX0010931; -.
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236 AA;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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COMPBIAS
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Gaps

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Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E., Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V., Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C., Boisrame A., Bloyer J., Cattolico L., Confanioleri F., Ge Daruvar A., Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R., Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R., Kerrest A., Koszul R., Lemaire M., Lesur I., Muller H., Nicola J.-M., Nikolski M., Ozier-Kalogeropoulos O., Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A., Swennen D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B., Zeniou-Meyer M., Zivanovic Y., Bolocin-Fukuhara M., Thierry A., Buchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J., Wincker P., Souciet J.-L.;
I'm "Genome evolution in yeasts.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; CR382125; CAG99659.1; -; Genomic DNA.
Complete proteome; Hypothetical protein.
SEQUENCE 244 AA; 24930 MW; CC83CACE35423EE2 CRC64;
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Search completed: September 9, 2006, 23:00:22 Job time : 120.139 secs

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                                                                                            9, 2006, 22:48:41 ; Search time 14.8101 Seconds
                                                                                                           (without alignments)
84.457 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                      Fotal number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 100 summaries
                                                            protein search, using sw model
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A32380
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Gapop 10.0 , Gapext 0.5
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G81655
E71497
H83324
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Maximum DB seq length: 200000000
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54
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Match Length
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A;Residues: 1-470 -WIL>
A;Cross-references: UNIPROT:Q9XUY1; UNIPARC:UPI000007519F; EMBL:Z81552; PIDN:CAB04486.1;
A;Experimental source: clone.F56G4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: JH0797
R;Mellerick, D.M.; Kassis, J.A.; Zhang, S.D.; Odenwald, W.F.
R;Mellerick, D.M.; Kassis, J.A.; Zhang, S.D.; Odenwald, W.F.
A;Title: Castor encodes a novel zinc finger protein required for the development of a su A;Reference number: JH0797; MUID:93040222; PMID:1418995
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Datesion: ACIDS
C;Accession: ACIDS
C;Accession: ACIDS
C;Accession: ACIDS
C;Accession: ACIDS
C; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Makathors: Kreft, J.; Simose, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Molecule type: DNA,
A,Residues: 1-79 «MEL.
A,Gross-references: UNIPROT:07M3MB; UNIPARC:UP1000017BEED; GB:L04487
C,Comment: This protein is required for the development of embryonic CNS neurons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein lmo2643 [imported] - Listeria monocytogenes (strain EGD-e)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Introns: 17/3; 152/1; 241/3; 339/1; 449/3
C;Superfamily: hypothetical protein F56G4.4; WW repeat homology
F;177-216/Domain: WW repeat homology <WWR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 799;
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Pred. No. 69;
3; Mismatches
                                                  A,Status: preliminary, translated from GB/EMBL/DDBJ
A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                        5
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Pred. No. 42;
1; Mismatches
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A;Introns: 284/3; 515/3; 660/3
C;Rywords: metal binding; zinc finger
F;236-242/Region: acidic
F;363-421/Region: zinc finger
F;422-482/Region: zinc finger
F;483-541/Region: zinc finger
F;542-600/Region: zinc finger
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Best Local Similarity 75.0%;
Matches 9; Conservative
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A; Reference number: Z19615
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Best Local Similarity
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                               A; Accession: T22785
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                                                                                                                                                                                                                                        Cjacession: AB1781
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsini, H. D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mak, C.; Schlueter, T.; Simces, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference mumber: AB1077; MUID:21537279; PMID:11679669
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-128 «GLA»
A;Cross-references: UNIPROT:Q927J6; UNIPARC:UPI00000CC998; GB:AL592022; PIDN:CAC98018.1;
A;Experimental source: strain Clip11262
C;Genetics:
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C;Species: Drosophila melanogaster
C;Accession: A32380
R;Weigel, D.; Juergens, G.; Kuettner, F.; Seifert, E.; Jaeckle, H.
Cell 57, 645-658, 1989
A;Title: The homeoric gene fork head encodes a nuclear protein and is expressed in the A;Reference number: A32380; WUID:89249328; PMID:2566386
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                                                                                                                       AB1781
hyporhetical protein lin2792 [imported] - Listeria innocua (strain Clip11262)
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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C;Keywords: DNA binding; transcription regulation
F;210-301/Domain: fork head DNA-binding domain homology <FHD>
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      ALIGNMENTS
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313 AAMSAAAAASAAA 325
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Matches 9; Conservative
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A;Molecule type: DNA; mRNA
A;Residues: 1-510 <WEI>
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Gaps

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hypothetical 31.3K protein in agaI-mtr intergenic region (f286) [imported] - Agrobacter
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Accession: D97395

R; Goodner, B.; Hinkle, G; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman R; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B. Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tu
A,Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:Q8UIJ3; UNIPARC:UPI0000164347; GB:AE007869; PIDN:AAK86117.1
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C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
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C;Species: Galleria mellonella (greater wax moth)
C;Date: 18-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 09-Jul-2004
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                                                                                                                            Length 375;
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R; Zurovec, M.; Sehnal, F.; Scheller, K.; Kumaran, A.K.
Insect Biochem. Mol. Biol. 22, 55-67, 1992
A; Title: Silk gland specific CDNAs from Galleria mellonella L.
A; Reference number: A61615
                                                                                                                                                                                 1; Indels
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A;Cross-references: UNIPROT:Q7M468; UNIPARC:UP1000017CAA4
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72;
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1; Mismatches
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                                                                                                                              Score 37;
Pred. No.
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Pred. No.
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C;Superfamily: methyltransferase, YraL type
                   C,Genetics:
A,Gene: YPO3978
C,Superfamily: hypothetical protein HI0093
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69.2%;
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Similarity 90.0%;
9; Conservative
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Best Local Similarity 69.2
Matches 9; Conservative
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Matches 10; Conservative
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                                                                                                                            Query Match
Best Local Similarity
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A;Molecule type: DNA
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C;Species: Yersinia pestis
C;Accession: AC0484
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Residues: preliminary
A;Molecule type: DNA
A;Residues: 1-375 < KUR>
A;Cross-references: UNIPROT:QBZA42; UNIPARC:UPI0000DC955; GB:AL590842; PIDN:CAC93439.1;
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-328 <GLA>
A;Cross-references: UNIPROT:Q8Y431; UNIPARC:UPI00000556C4; GB:NC_003210; PIDN:CAD00721.1
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo2643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fork head domain protein crocodile - fruit fly (Drosophila melanogaster)

C;Species: Drosophila melanogaster

C;Species: Jo-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Oct-2004

C;Accession: S59870; A46178

R;Haecker, U.; Kaufmann, E.; Hartmann, C.; Juergens, G.; Knoechel, W.; Jaeckle, H.

EMBO J. 14, 5306-5317, 1995

A;Title: The Drosophila fork head domain protein crocodile is required for the establish

A;Reference number: S59870; MUID:96080166; PMID:7489720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Hacker, U.; Grossniklaus, U.; Gehring, W.J.; Jackle, H.
Proc. Natl. Acad. Sci. U.S.A. 89, 8754-8758, 1992
A;Title: Developmentally regulated Drosophila gene family encoding the fork head domain.
A;Reference number: A46178; MUID:92409595; PMID:1356269
A;Accession: A46178
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A;Note: sequence extracted from NCBI backbone (NCBIP:114222)
C;Genetics:
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F;70-161/Domain: fork head DNA-binding domain homology <FHD>
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Pred. No.
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449 ASVAAASAAAAA 461
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Best Local Similarity 69.2
Best Local 9; Conservative
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Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-329 «GLA»
A;Cross-references: UNIPROT:Q8Y586; UNIPARC:UPI00005571F; GB:NC_003210; PIDN:CAD00261.1
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo2183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-407 <WIL>
A;Cross-references: UNIPROT:Q17877; UNIPARC:UPI00000754B2; EMBL:Z54235; PIDN:CAA90977.1;
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A;Residues: 1-407 <WI2>
A;Cross-references: UNIPARC:UP100000754B2; EMBL:Z54236; PIDN:CAA90986.1; GSPDB:GN00022;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein C09G9.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19155; T19510
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A,Introns: 13/2; 69/2; 146/2; 195/3; 273/1
C,Superfamily: Caenorhabditis elegans hypothetical protein ZC513.6
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Pred. No. 1.1e+02;
4; Mismatches 1; Indels
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A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AG1347
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                   Score 36; DB 2
Pred. No. 92;
3; Mismatches
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61.5%;
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347 SSLNAASAAAAA 359
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Best Local Similarity 61...
Rest Local Similarity 61...
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169 SSQSASSAASLA 180
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A;Accession: T19510
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Best Local Similarity
8; Conserve
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ferrichrome ABC transporter (permease) homolog lmo2183 [imported] - Listeria monocytogen
ferrichrome ABC transporter (permease) homolog lmo2183 [imported] - Listeria monocytogens
C;Species: 1.3teria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AG1347
C;Accession: AG1347
C; Dominguez-Bernal, G; Duchaud, E; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.D.; Jones, L.M.; Karst, U.
D.; Jones, L.M.; Karst, U.
Science 294 49-985, 2001
A;Authors: Kreft, J; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
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C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AC1718
C;Accession: AC1718
C;Accession: AC1718
C;Accession: A.; Bardence, F.; Bloecker
C;Accession: A.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
C;Accession: Farst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
A;Authors: Kreft, J.; Kuhn, M.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
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                                R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monke, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell, Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
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A;Cross-references: UNIPROT:08UIU3; UNIPARC:UP100000D177D; GB:AE008688; PIDN:AAL41324.1;
A;Experimental source: strain C58 (Dupont)
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A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577; MUID:21608550; PMID:11743193
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66.7%; Pred. No. 92;
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C,Superfamily: methyltransferase, YraL type
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nes 9; Conserv
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A; Residues: 1-329 <GLA>
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                 C; Accession: AF2613
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A,Gene: lin2287
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C,Accession: A55929
R;Cheah, P.Y.; Meng, Y.B.; Yang, X.; Kimbrell, D.; Ashburner, M.; Chia, W.
Rol. Cell. Biol. 14, 1487-1499, 1994
A;Title: The Drosophila 1(2)35Ba/nocA gene encodes a putative Zn finger protein involved A;Reference number: A55929; MUID:94119100; PMID:8289824
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R;Locke, M.E.H.; Guida, A.D.; Falco, S.C.
submitted to the EMBL Data Library, June 1997
A;Description: Deregulation of the methionine biosynthetic pathway in corn seeds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Introns: 129/1; 163/3; 188/2; 244/3; 264/3; 332/3; 361/3; 397/3; 429/3; 469/2
C; Superfamily: cystathionine gamma-synthase
C; Keywords: carbon-oxygen lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                  N;Alternate names: cystathionine gamma-synthase
C;Species: Zea mays (maize)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 05-Oct-2004
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C;Species: Drosophila melanogaster
C;Date: 08-Sep-1995 #sequence_revision 08-Sep-1995 #text_change 09-Jul-2004
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                                                                                     Score 36; DB 2; Length 509
Pred. No. 1.4e+02;
2; Mismatches 2; Indels
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Pred. No. 1.4e+02;
4; Mismatches 1; Indels
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     C;Superfamily: cystathionine gamma-synthase C;Keywords: carbon-oxygen lyase
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A;Experimental source: strain Missouri 17
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A,Accession: T02942
A,Status: translated from GB/EMBL/DDBJ
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69.28;
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Best Local Similarity 61.5%;
Matches 8; Conservative
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232 SSMAAAAAAAA 244
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Best Local Similarity 69.2
Matches 9; Conservative
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A; Residues: 1-509 <LOC>
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A;Residues: 1-537 <CHE>
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-474 «RES>
A;Cross-references: UNIPROT:Q06945; UNIPARC:UPI0000047FA0; EMBL:X70683; NID:g36552; PIDN
B;Cross-references: UNIPROT:Q06945; UNIPARC:UPI0000047FA0; EMBL:X70683; NID:g36552; PIDN
Nucleic Aids Res. 20, 2897, 1992
A;Title: A conserved family of genes related to the testis determining gene, SRY.
A;Reference number: S22935; MUID:92310993; PMID:1614875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 70,'P',72-123 <DEN>
A;Cross-references: UNIPARC:UPI000016B04E; EMBL:X65661; NID:936551; PIDN:CAA46612.1; PIQ
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A;Cross-references: UNIPROT:004981; UNIPARC:UPI00000A35C3; EMBL:AF007785; NID:g2198850;
A;Experimental source: strain H99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N'Alternate names: sex-determining region Y box 4 protein
C'Species: Homo sapiens (man)
C'Date: 06-Sep-1996 #sequence revision 06-Sep-1996 #text_change 05-Oct-2004
C'Accession: 138240; S22938; S21479; S31724
R'Farr, C.J.; Easty, D.J.; Ragoussis, J.; Collignon, J.; Lovell-Badge, R.; Goodfellow,
A'Fitle: Characterization and mapping of the human SOX4 gene.
A'Ritle: Characterization and mapping of the PMID:8268656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O-succinylhomoserine (thiol) -lyase (EC 4.2.99.9) 1 - maize
O-succinylhomoserine (thiol) -lyase (EC 4.2.99.9) 1 - maize
O-succinylhomoserine (thiol) -lyase (EC 4.2.99.9) 1 - maize
NyAlternate names: cystathionine gamma-synthase
C;Species: Zea mays (maize)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 05-Oct-2004
C;Accession: T02940
R;Locke, M.E.H.; Guida, A.D.; Falco, S.C.
submitted to the EMBL Data Library, June 1997
A;Description: Deregulation of the methionine biosynthetic pathway in corn seeds.
A;Reference number: Z14785
A;Accession: T02940
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Similarity 69.2%; Pred. No. 1.1e+02;
9; Conservative 2; Mismarches
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Pred. No. 1.3e+02;
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A;Molecule type: mRNA
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C;Keywords: DNA binding; transcription regulation
F;56-131/Domain: HMG box homology <HMG1>
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A; Experimental source: strain A3(2)
C;Genetics:
A;Genetics:
C;Superfamily: tetracycline 6-hydroxylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                            transcription factor SOX4 - human
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69.2%;
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327 ASVSAAAAASAPA 339
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Matches 9; Conserva
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nes 9; Conserv
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RESULT 19

Genetics:

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A, Cross-references: FlyBase: FBgn0000581
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Best Local Similarity 72.7
Matches 8; Conservative
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Best Local Similarity 61.5
Matches 8; Conservative
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Best Local Similarity
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315478

S15479

Glycoprotein H - suid herpesvirus 1

CjSpecies: anid herpesvirus 1

CjSpecies: anid herpesvirus 1

CjSpecies: anid herpesvirus 1

CjSpecies: o9-Jun-1994 #sequence_revision 12-May-1995 #text_change 09-Jul-2004

CjAccession: S15478

R,Meyer, A.L.; Petrovskis, E.A.; Thomsen, D.R.; Post, L.E.

Submitted to the EMBL Data Library, April 1991

A,Description: Cloning and sequence of a pseudorabies virus gene homologous to glycoprod A,Reference number: S15478

A,Accession: S15478

A,Accession: S15478

A,Accession: Specialminary

A,Holecule type: DNA

A,Residues: 1-686 <MEY>
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A, Molecule type: DNA
A, Residues: 1-68 < KLUJ.
A, Foreston: MIDPROT: P27416; UNIPARC: UPI000013870F; GB: M61196; NID: G334058; PIDN: A; Cross-references: UNIPROT: P27416; UNIPARC: UPI000013870F; GB: M61196; NID: G334058; PIDN: C; Superfamily: herpesvirus glycoprotein H
C; Keywords: glycoprotein; transmembrane protein
F;1-30/Domain: signal sequence #status predicted < SIG>F;47-66/Pomain: transmembrane #status predicted < GPH>F;647-67/Domain: transmembrane #status predicted < TMN>F;647-67/Domain: transmembrane #status carbohydrate (Asn) (covalent) #status predicted
                                                                               C,Accession: A42000; S16737 — R.; Gielkens, A.; Moormann, R. R.; Peeters, B.; de Wind, N.; Broer, R.; Gielkens, A.; Moormann, R. J. Virol. 66, 3888-3892, 1992, 1992, A.; A; Title: Glycoprotein H of pseudorabies virus is essential for entry and cell-to-cell A; Reference number: A42000; MUID:92260665; PMID:1316488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein H precursor - suid herpesvirus 1 (strain Ka)
C;Species: suid herpesvirus 1
C;Accession: A39990
R;Klupp, B.G.; Mettenleiter, T.C.
Virology 182, 732-741, 1991
A;Title: Sequence and expression of the glycoprotein gH gene of pseudorabies virus.
A;Reference number: A39990; MUID:91220723; PMID:1850925
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glycoprotein H precursor - suid herpesvirus 1 (strain NIA-3)
C;Species: suid herpesvirus 1
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66.7%; Score 36; DB 1; Length 686;
llarity 61.5%; Pred. No. 1.8e+02;
Conservative 3; Mismatches 2; Indels
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245 AQLSAAHAAALAA 257
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tes 8; Conserv
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Matches 8; Conserv
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Matches 8
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A;Cross-references: UNIPROT:P27593; UNIPARC:UPI0000138711; EMBL:X58868; NID:g59965; PIDN A;Note: the source is given as pseudorables virus C;Superfamily: herpesvirus glycoprotein H C;Keywords: glycoprotein; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #text_change 09-Jul-2004
C;Date: 11-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Date: 11-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
R;Stankunas, K; Berger, J; Ruse, C; Sinclair, D.A.; Randazzo, F.; Brock, H.W.
Development 125, 4055-4066, 1998
Development 125, 4055-4066, 1998
A;Title: The enhancer of polycomb gene of Drosophila encodes a chromatin protein conserv
A;Reference number: 217611; MUID:98407961; PMID:9735366
A;Accession: T13154
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A;Cross-references: UNIPROT:052789; UNIPARC:UPI000055B02; EMBL:AJ223012; NID:e1227119;
A;Experimental source: strain LBG A3136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-2023 <STA>
A;Cross-references: UNIPROT:096542; UNIPARC:UPI0000083EF3; EMBL:AF079764; NID:g3757889;
A;Experimental source: imaginal disc
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C,Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004
C,Accession: T17464
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Pred. No. 1.1e+03;
3; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polycomb protein enhancer - fruit fly (Drosophila melanogaster)
                                                                                                                                                                              Length 686;
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Pred. No. 4.88+02;
                                                                                                                                                   Score 36; DB 2; Length 600
Pred. No. 1.8e+02;
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;1631-1702/Domain: acyl carrier protein homology <ACP1>;3238-3309/Domain: acyl carrier protein homology <ACP2>;4399-5010/Domain: acyl carrier protein homology <ACP3>
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-339 <WIL>
A;Cross-references: UNIPARC:UPI000017BC34; EMBL:Z79758; NID:e1062260; PIDN:CAB02131.1;
A;Experimental source: clone W10D5
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39. A;Reference number: A81500; MUID:20150255; PMID:10684935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:Q9PJG1; UNIPARC:UPI0000057ABA; GB:AE002353; GB:AE002160; NI
A;Experimental source: strain Nigg (MOPn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ristophens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tran A;Reference number: A71570; MUID:99000809; PMID:9784136
A;Accession: E71497
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A,Residues: 1-439 <ARN>
A,Cross-references: UNIPROT:084583; UNIPARC:UPI0000139ACF; GB:AE001328; GB:AE001273; NI
A,Experimental source: serotype D, strain UW-3/Cx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      conserved hypothetical protein TC0868 [imported] - Chlamydia muridarum (strain Nigg)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: G81655
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C, Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
C, Accession: E71497
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Pred. No. 1.7e+02;
1; Mismatches 3; Indels
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64.8%; Score 35; DB 2; 1
Best Local Similarity 61.5%; Pred. No. 1.4e+02;
Matches 8; Conservative 4; Mismatches 1;
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A,Gene: CT579
C,Superfamily: conserved hypothetical protein TC0868
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A;Introns: 18/3; 56/2; 195/2; 269/1
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69.2%;
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|131 ASAASASAAAVAA 143
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268 AASGAASAASSAA 280
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Matches 9; Conservative
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A;Molecule type: DNA
A;Residues: 1-436 <TET>
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                                                                       ABC transporter (permease) BH2113 [imported] - Bacillus halodurans (strain C-125) C.Species: Bacillus halodurans C.Date: 01-De-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004 C.Accession: A83914 R.Takahi, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira R.Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000 A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A8350; MUD:20512582; PMID:11058132 A;Accession: A83914 A;Reference number: A8350; MUD:20512582; PMID:11058132 A;References: DNA A;Residues: 1-308 <STO>A;Residues: 1-308 <STO>A;Residues: UNIPROT:Q9XB22; UNIPARC:UPI00000D7427; GB:AP001514; GB:BA000004; NID A;Resperimental source: strain C-125 G;Genetics: A;Gene: BH2113 C;Superfamily: maltose transport protein malG
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A.Molecule type: mRNA
A.Residues: 1.314 **NOMA-
A.Coss-references: UNIPRCT:O61425; UNIPARC:UPI0000171F45; DDBJ:D29639
A.Experimental source: embryonal carcinoma F9 cells
C.Comment: This enzyme plays a role in the mitochondrial beta-oxidation of short chain f
C.Comment: This enzyme plays a role in the mitochondrial beta-oxidation of short chain f
C.Superfamily: 3-hydroxyacyl-CoA dehydrogenase; 3-hydroxyacyl-CoA dehydrogenase homology
C.Keywords: fatty acid beta-oxidation; homodimer; mitochondrion; NAD; oxidoreductase
F1-12/Domain: transit peptide (mitochondrion) #status predicted <TPP>
F13-314/Product: 3-hydroxyacyl-CoA dehydrogenase, short chain-specific #status predicte
F;27-314/Domain: 3-hydroxyacyl-CoA dehydrogenase homology <ACD>
F;29-57/Region: beta-alpha-beta NAD nucleotide-binding fold
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C;Species: Mus musculus (house mouse)
C;Dacte: 04-0ct-1995 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C;Accession: JC4210
R;Nomura, M; Takihara, Y; Shimada, K.
Gene 160, 309-310, 1995
A;Fitle: Isolation of a cDNA clone encoding mouse 3-hydroxyacyl CoA dehydrogenase.
A;Reference number: JC4210; MUID:95369712; PMID:7642117
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hypothetical protein W10D5.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Sacession: T26328
R;Kershaw, J.
submitted to the EMBL Data Library, September 1996
A;Reference number: Z20200
A;Reference number: Z20200
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64.8%; Score 35; DB 2; Length 308;
Local Similarity 69.2%; Pred. No. 1.3e+02;
les 9; Conservative 1; Mismatches 3; Indels
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Best Local Similarity 66.7%;
Matches 8; Conservative
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247 ASMSSGSAASAFA 259
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11 SMSSSSSASAAA 22
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Length 646 3; Indels

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R;Haller, J.; Cote, S.; Broenner, G.; Jaeckle, H.
Genes Dev. 1, 862-867, 1987
A;Title: Dorsal and neural expression of a tyrosine kinase-related Drosophila gene durin
A;Reference number: A27041; MJID:88112827; PMID:3428600
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A,Introns: 453/1; 497/1
A,Introns: 453/1; 497/1
A,Entrons: 453/1; 497/1
A,Entrons: 453/1; 497/1
B,55/187,223,224,250,611,660/Binding site: carbohydrate (Asn) (covalent) #status predi
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A;Residues: 1-771 <MIY>
A;Cross-references: UNIPROT:Q08122; UNIPARC:UPI0000027DAA; EMBL:X73360; NID:g313235; PI
A;Reference number: 222137; MUID:98094274; PMID:9434185
A;Accession: T42296
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-646 < ALO>
A;Cross-references: UNIPROT:048456; UNIPARC:UPI000009B4CA; EMBL:X97918; PIDN:CAA66557.1
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C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Oct-2004
C;Accession: S35681; S34162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tyrosine kinase-related protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C;Accession: A27041
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Pred. No. 2.8e+02;
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61.5%; Pred. No. 2.9e+02;
ive 3; Mismatches 2; Indels
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A;Residues: 1-753 <HAL>
A;Cross-references: UNIPROT:P14083; UNIPARC:UPI0000136FEA
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A;Title: Molecular cloning and expression of mouse and PA;Reference number: $35678; MUID:93373944; PMID:8365415
                                                                                                                                                                                                           Score 35; DB 2; 1
Pred. No. 2.5e+02;
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F;613-646/Domain: WD repeat homology «WD3»
F;695-728/Domain: WD repeat homology «WD4»
F;736-769/Domain: WD repeat homology «WD5»
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A, Cross-references: FlyBase: FBgn0003715
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61.5%;
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Best Local Similarity 61.5%;
Matches 8; Conservative
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Best Local Similarity 61.5
Matches 8; Conservative
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A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 32
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C;Species: phage SPP1
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
R;Alonso, J.C.; Luder, G.; Stiege, A.C.; Chai, S.; Weise, F.; Trautner, T.A.
Gene 204, 201-212, 1997
A;Title: The complete nucleotide sequence and functional organization of Bacillus subtil
                                                                                                                                                                                                                                                                                                               C;Accession: Ĥ83324
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, I., Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, I., Coulter, S.S., Olson, M.V.
I. Los, Olson, M.V.
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathod. A;Reference number: A62950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:Q910R3; UNIPARC:UP100000C5747; GB:AE004685; GB:AE004091; NID A;Experimental source: strain PAO1 C;Genetics: A;Gene: PA2573
                                                                                                                                                                                                                       probable chemotaxis transducer PA2573 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transcription factor btd - fruit fly (Drosophila sp.)

c;Species: Drosophila sp.
c;Species: Drosophila sp.
C;Date: 18-Feb-1994 #sequence_revision 01-Dec-1995 #text_change 07-May-1999
C;Accession: S39356
R;Wimmer, E.A.; Jaeckle, H.; Pfeifle, C.; Cohen, S.M.
Nature 366, 690-694, 1993
A;Title: A Drosophila homologue of human Sp1 is a head-specific segmentation gene.
A;Reference number: S39356, WUID:94081952; PMID:8259212
A;Reterence number: S39356, WUID:94081952; PMID:8259212
A;Reterence number: S39356
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-644 <WIM>A;Residues: 1-644 <WIM>A;Residues: DAA
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                                                                                                                                                                                                                                                          C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
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Pred. No. 2.1e+02;
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                                                                                  271 ATSGAASAASSAA 283
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Best Local Similarity 75.0
Matches 9; Conservative
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Matches 9; Conservative
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                             1 ASMSAASAASMAA
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A; Status: preliminary
A; Molecule type: DNA
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Length 753;

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Length 771;

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hypothetical protein AGR_L_2329 [imported] - Agrobacterium tumefaciens (strain C58, Cerr
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                               C;Accession: G98275
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B. Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tu
A,Reference number: A97359, MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-1520 «KUR»
A;Cross-references: UNIPROT:Q8U9Q4; UNIPARC:UPI00000D22BA; GB:AE007870; PIDN:AAK89729.1
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A;Cross-references: UNIPROT:O61845; UNIPARC:UPI000007A573; EMBL:AF067617; PIDN:AAC17559
A;Experimental source: strain Bristol N2; clone T04D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hexon-associated protein (IX) - human adenovirus 12 (Species: Mastadenovirus h12 (human adenovirus 12) (c;Species: Mastadenovirus h12 (human adenovirus 12) (c;Date: 02-Apr-1982 #sequence revision 02-Apr-1982 #text_change 09-Jul-2004 (c;Accession: A90814; A93745; S33931; A03855 (R;Bos, J.L.; Polder, L.J.; Bernards, R.; Schrier, P.I.; van den Elsen, P.J.; van der Eb (A;Title: The 2.2 kb Elb mRNA of human Ad12 and Ad5 codes for two tumor antigens starting A;Reference number: A90814; MUID:82115327; PMID:7326748
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C.Species: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C.Accession: T33152
R.Davidson, S.; Wohldmann, P.
submitted to the EMBL Data Library, May 1998
A.Description: The sequence of C. elegans cosmid T04D1.
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Pred. No. 9.8e+02;
3; Mismatches 2; Indels
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Pred. No. 5.3e+02;
2; Mismatches 1;
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A;Molecule type: DNA
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61.5%;
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Best Local Similarity 72...
Similarity 72...
Conservative
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484 LSARSAASLAA 494
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484 LSARSAASLAA 494
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A; Molecule type: DNA
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SXAD12
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DNA Res. 3, 363-377, 1996
A,Title: A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the A,Title: A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the A,Reference number: 216603; MUID:97251357; PMID:9037039
A,Returns: preliminary; translated from GB/EMBL/DDBJ
A,Rolecule type: DNA
A,Rolecule type: DNA
A,Residues: 3-1122 <AIB>
A,Residues: 3-1122 <AIB>
A,Cross-references: UNIPARC:UPI00001360ED; GB:AE000234; GB:U00096; NID:g1787633; PIDN:AP
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polyketide synthase Atu3672 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
[C.Species: Agrobacterium tumefaciens
[C.Species: Agrobacterium tumefaciens
[C.Species: Agrobacterium tumefaciens
[C.Bate: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
[C.Bacesion: AF3008
[C.Bacesion: AF303]
[C.Bacesion: AF303]
[C.Bacesion: AF303]
[C.Bacesion: Agrobacterium tumefaciens
[C.Bacesion: Agrob
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A;Molecule type: DNA
A;Residues: 1-1122 <BLAT>
A;Cross-references: UNIPROT:P76072; UNIPARC:UPI0000168098; GB:AE000234; GB:U00096; NID:9
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A;Molecule type: DNA
A;Residues: 1-150 «KUR»
A;Cross-references: UNIPROT:Q8U9Q4; UNIPARC:UPI0000D22BA; GB:AE008689; PIDN:AAL4484.1;
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Experimental source: strain K-12, substrain MG1655
R, Aiba, H.; Baba, T.; Fujita, K.; Hayashi, K.; Inada, T.; Isono, K.; Itoh, T.; Kasai, H
.; Motomura, K.; Nakade, S.; Nakamura, Y.; Nashimoto, H.; Nishio, Y.; Oshima, T.; Saito
                                                                                                                                                                                                                                                                                                                 probable tail fiber protein GP37 - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Species: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
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A;Reference number: AB2577; WUID:21608550; PMID:11743193
A;Accession: AF3008
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Pred. No. 5.3e+02;
2; Mismatches 1; Indels
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72.7%;
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1 ASMSAASAASMA 12

Conservative

Query Match Best Local Similarity

C,Genetics: A,Gene: Atu3672

3 MSAASAASMAA 13

Best Local Similarity 75.0 Matches 9; Conservative

Query Match

Gaps

; 0

Length 211; 4; Indels

Score 34; DB 2; I Pred. No. 1.3e+02; ); Mismatches 4;

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A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-211 <AAA>
A;Cross-references: UNIPROT:Q9NTF4; UNIPARC:UPI00006CFFC; EMBL:AL137304
A;Experimental source: adult testis; clone DKFZp434H247
C;Genetics:
A;Note: DKFZp434H247.1
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69.2%;
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A; Reference number: Z23037
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                         A; Accession: T46497
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C; Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C; Accession: T0303 #sequence acquisition after mitochondrial gene transfer to the nucl A; Reference number: 21829; MUID:97133294; PMID:8978691
                                                                           A,Cross-references: UNIPROT: P03284; UNIPARC: UPI000004007E
R;Kimura, T.; Sawada, Y.; Shinawawa, M.; Shimizu, Y.; Shiroki, K.; Shimojo, H.; Sugisaki
Nucleic Acida Res. 9, 6571-6589; 1981
A;Title: Nucleotide sequence of the transforming early region Elb of adenovirus type 12
A;Reference number: A93745; MUID: 82105565; PMID: 6275367
                                                                                                                                                                                                                     A;Accession: A93745
A;Molecule type: DNA
A;Residues: 1-144 <KIM>
A;Residues: 1-144 <KIM>
A;Cross-references: UNIPARC:UPI000004007E; GB:X73487; NID:g313361; PIDN:CAA51880.1; PID: R;Sprengel, J.
submitted to the EMBL Data Library, June 1993
A;Reference number: S33928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPARC:UPI00004007E; EMBL:X73487; NID:g313361; PIDN:CAA51880.1; PIC;Genetics:
A;Map position: 9.4-10.7
C;Superfamily: adenovirus hexon-associated protein (IX)
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hypothetical protein DKFZp434H247.1 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004

C;Accession: T46497

R;Koehrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, January 2000
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Pred. No. 1e+02;
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A;Introns: 55/1, 81/3, 98/3; 121/1; 147/3
C;Superfamily: mammalian cytochrome-c oxidase chain Vb
C;Keywords: mitochondrion; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
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16 ASASASAASGAA 28
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Best Local Similarity 69.2
Matches 9; Conservative
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A; Residues: 1-169 < KAD>
A; Accession: A90814
A; Molecule type: mRNA
A; Residues: 1-144 <BOS>
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A,Status: preliminary
A,Molecule type: DNA
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Q2N052_DSTRA
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Q9VJXS_DROME
Q9DYL7_STRAG
Q3DF29_STRAG
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Q6CLD7_YARLI
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argiope aur azoarcus sp candida alb phytophthor frankia sp. rhodobacter oryza sativ oryza sativ burkholderi oryza sativ yersinia ps yersinia pe oryza sativ burkholderi burkholderi burkholderi burkholderi methanospha myxococcus burkholderi drosophila arthrobacte arthrobacte bradyrhizob aspergillus burkholderi gallus gall burkholderi nilaparvata aspergillus cryptococcu thiomicrosp dechloromon drosophila burkholderi cryptococcu ajellomyces leishmania 007m3m8 002mgf6 002dki7 002dki7 002dki7 002xy89 002xy89 002xy89 002xy89 002xy89 002xy89 002xy89 002xy81 004efn1 0061dl0 0061dl 03.335 02.03b6 06.2ba7 07.xbr2 09.1ba2 06.1492 06.1492 06.1492 06.1492 06.1492 07.022 07.022 06.3yw2 06.3yw 09vtw5 02sum3 06my65 04ws26 02swb0 02swb0 055pk0 030pt0 09kwr3 04qgr7 042720 CAS\_DROME

Q2UQE0\_ASPOR

Q2UG1\_QRSA

Q2UK1\_QRSA

Q2UK1\_LISMO

Q4EPUT

Q4EFUT

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ALIGNMENTS

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NUCLEOTIDE SEQUENCE.
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=67593;
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Local Sim.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN-CBS 2359 / IFO 1267 / NRRL Y-1140 / WM37;

PubMed=1522592; DDI=10.1038/nature02579;

Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,

Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,

Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,

Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,

Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,

Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,

Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,

Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,

Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,

Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,

Romnen D., Tekaia F., Wesclowski-Louvel M., Westhof E., Wirth B.,

Zeniou-Meyer M., Zivanovic Y., Bolotin-Pukuhara M., Thierry A.,

Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,

Wincker P., Souciet J.-L.;

Nature 430:35-44(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP clade,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                              KLUYVCETOMYCEB 120T18 (18615).
Bukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
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07-FEB-2006, entry version 7.
Hypothetical protein OSJNBa0018M09.16 (Hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Length 272;
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to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 272 AA; 25696 MW; BC0464D2994066D1 CRC64;
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                                                                                                                                                  integrated into UniProtKB/TrEMBL
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                                                                                           272 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; CR382122; CAH02414.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
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Sasaki T., Matsumoto T., Yamamoto K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Katayose Y.
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                                                                                           PRT;
                                                                                                                                                                                            sequence version 1.
                                                                                                                                                                                                                                                                             OrderedLocusNames=KLLA0B11055g;
                                                                                                                                                                                                                         07-FEB-2006, entry version 11
                                                                                                                                                                                                                                                                                                                    Kluyveromyces lactis (Yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                           PRELIMINARY;
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Submitted (JUL-2002)
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nes 10; Conserv
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                                                                                       QECVLB_KLULA
QECVLB;
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Qekat3;
                                                                                                                                                        16-AUG-2004,
16-AUG-2004,
                                                                                                                                                                                                                                                       Similarity.
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1006K473 OR
1006K473 OR
1007 OS-4
1007 OS-4
1007 OS-4
1007 OS-6
100
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QGCVL8 KA

DD QGCV

AC QGCV

DD 16-A

DT 16-A

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                                            Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jiang R.H., Tyler B.M., Whisson S.C., Hardham A.R., Govers F.; "Ancient Origin of Blicitin Gene Clusters in Phytophthora Genomes."; Mol. Biol. Evol. 23:338-351(2006).
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Jiang R.H.Y., Tyler B.M., Whisson S.C., Hardham A.R., Govers F.;
Submitted (SEP-2005) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                   Length 285;
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Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
NCBI_TaxID=1642;
[1]
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                                                                                                                                                                                                                                                                                                                     Indels
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                         Gramene, Q6K4T3; -.
Hypothetical protein.
SEQUENCE 285 AA; 30341 MW; E955D01FD443ED22 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; DQ229265; ABB56018.1; -; Genomic DNA.
SEQUENCE 207 AA; 19497 MW; F467E939F266199A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 42; DB 2;
Pred. No. 62;
2; Mismatches
                                                                                                                                                                                                                                                                 Score 43; DB 2;
Pred. No. 59;
0; Mismatches
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01-DEC-2001, sequence version 1.
07-FBB-2006, entry version 14.
07-FBP-2005, protein.
OrderedLocusNames=lin2792;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-FEB-2006, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          207 AA
                                                                                                                       EMBL; AP005533; BAD22199.1; -; Genomic_DNA.
EMBL; AP004001; BAD21485.1; -; Genomic_DNA.
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84.6%;
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76.9%;
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Q927J6;
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                                                                                                                                                                                                                                                                                                                                                                                                                    173 ASRCAASAASMAA 185
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nes 10; Conservative
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Query Match
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     Adams M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides D.G., Scherer S.E., Li P.W., Hookins K.A., Galle R.F.,
Amanatides D.G., Scherer S.E., Li P.W., Hookins R.A., Galle R.F.,
A George R.A., Lewis S.E., Kichards S., Ashburner M., Henderson S.N.,
B. Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
A Bardon R.C., Rogers Y.-H.C., Blazel R.G., Nelson C.R., Miklos G.L.G.,
M. Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
B. Ballew R.M., Basu A., Baxendale J., Bardakfaroglu L., Beasley B.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
A Burtis K.C., Busam D.A., Buller H., Cadieu B., Center A., Chandra I.,
A Barlos B., Delcher A., Dang Z., Mays A.D., Dew I., Dietz S.M.,
A Doson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
A Godson K.J., Royngelista C.C., Ferrac C., Ferriera S., Fleischmann W.,
A Godson K.J., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
A Godek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris N.L., Harvey D.A., Heiman T.J., Wei M.-H., Ibegwam C.,
A Harris N.L., Harvey D.A., Heiman T.J., Wei M.-H., Ibegwam C.,
Alalii M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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             STRAIN=CIIP 11262 / Serovar 6a,
MEDLINE=21537279; PubMed=11679669; DOI=10.1126/science.1063447;
Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve B., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
Entian K.-D., Fshih H., Gazcia-del Portillo F., Garrido P.,
Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
Madueno E., Maltournam A., Mata Vicente J., Ng E., Nedjari H.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
Fermel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
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Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Budopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77.8%; Score 42; DB 2; Length 328; 76.9%; Pred. No. 98; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                   Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A. Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.; "Comparative genomics of Listeria species.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            328 AA; 36670 MW; F2E1A0F2C6D98622 CRC64;
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
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01-MAY-2000, sequence version 1.
07-FEB-2006, entry version 19.
CG16850-PA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AL596173; CAC98018.1; -; Genomic_DNA.
PIR; AB1781; AB1781.
ListiList; LIN2792; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BioCyc; LINN1642:LIN2792-MONOMER; -.
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                                                                                                                                                                                                                                                                                                                                                                               Science 294:849-852(2001).
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313 AAMSAAAAASAAA 325
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Matches 10; Conservative
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Q9VJX5 DR
Q9VJX5 DR
DD O1-M
DT O1-M
DT O1-E
DE CG16
GN ORFN
OC BURB
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Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liang Y., Lin X., Mattei B.E., McIntosh T.C., McLeod M.P., McPherson D., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Markilov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Musskern D.R., Pacleon D.L., Melson D.R., Nelson K.A., Nixon K., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T., Shue B.C., Stapleton M., Skupski M.P., Smith T., Shiesen B.C., Stapleton M., Skupski M.P., Smith T., Shiesen B.C., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Yeb R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zhong K.M., Zhong K.M., Wenter J.C., Shu X., Smith H.O., Gibbs R.A., Myers B.W., Rubin G.M., Venter J.C.;
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MEDIJNE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
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Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Sylraksa R., Tabor P.E., Wan K., Stapleron M., Sutron G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; Finishing a whole-genome shotgun: release 3 of the Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whiffield B.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D. N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Berkeley Drosophila Genome Project,
Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
Yu C., Rubin G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Drosophila melanogaster release 4 sequence.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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FlyBase; FB9n0032527; CG16850.
SEQUENCE 417 AA; 44286 MW; 42EA717B5604565F CRC64;
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Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             melanogaster euchromatic genome sequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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77.8%; Score 42; DB 2; Length 417;

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                                       STRAIN=2603 V/R / ATCC BAA-611 / Serctype V;
MEDLINE=2222988; PubMed=12200547; DOI=10.1073/pnas.182380799;
MEDLINE=22222988; PubMed=12200547; DOI=10.1073/pnas.182380799;
Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,
Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
Radune D., Fedorova N.B., Scanlan D., Khouri H.M., Mulligan S.,
Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D.,
Frasser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pubmed=1617279; DOI=10.1073/pnas.0506758102;
Pubmed=1617279; DOI=10.1073/pnas.0506758102;
Tettelin H., Masignani V., Cieslewicz M.J., Joneti C., Medini D.,
Ward N.L., Angiuoli S.V., Crabtree J., Jones A.L., Durkin A.S.,
DeBOY R.T., Davideen T.M., Mora M., Scarselli M., Margarit Y Ros I.,
Peterson J.D., Hauser C.R., Sundaram J.P., Nelson W.C., Madupu R.,
Brinkac L.M., Dodson R.J., Rosovitz M.J., Sullivan S.A.,
Daugherty S.C., Haft D.H., Selengut J., Gwinn M.L., Zhou L., Zafar N.
Khouri H., Radune D., Dimitrov G., Watkins K., O'Connor K.J.,
Smith S., Utterback T.R., White O., Rubens C.E., Grandi G.,
Madoff L.C., Kasper D.L., Telford J.L., Wessels M.R., Rappuoli R.,
Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genome analysis of multiple pathogenic isolates of Streptococcus agalactiae: implications for the microbial 'par-genome'."; Proc. Natl. Acad. Sci. U. S.A. 102:13950-13955 (2005).
-!-CUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                             "Complete genome sequence and comparative genomic analysis of ar
emerging human pathogen, serotype V Streptococcus agalactiae.";
Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77.8%; Score 42; DB 2; Length 970 69.2%; Pred. No. 2.9e+02; Winnerches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGN, 30.0109986; C:cell surface; IEA.

GO; GO:0005618; C:cell wall; IEA.

InterPro; IPR00189; Gram pos anchor.

Pfam; PF00746; Gram pos anchor; 1.

TIGRFAMS; TIGR01167; LEXIG_anchor; 1.

PROSITE; PS50847; GRAM POS_ANCHORRING; 1.

Cell wall; Complete protecome; Peptidoglycan-anchor.

SEQUENCE 970 AA; 99433 MW; 0E817044FGEE9CE6 CRC64;
                        NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-NOV-2005, integrated into UniProtKB/TrEMBL. 22-NOV-2005, sequence version 1. 07-FBB-2006, entry version 5. Cell wall surface anchor family protein. Name=c1fB, ORFNames=SAM_1428, Streptococcus agalactiae CMB111.
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QBDFZ9;
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881 ASMSASTSASMSA 893
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Matches 9; Conservative
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NCBI_TaxID=342617;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome analysis of multiple pathogenic isolates of Streptococcus agalactiae: implications for the microbial 'pan-genome'."; Proc. Natl. Acad. Sci. U.S.A. 102:13950-13955 (2005).
-:- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus.
NCBI_TaxID=216466;
                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     910 AA; 94148 MW; C7F57665B2C99CFC CRC64;
    Pred. No. 1.2e+02;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, AAJO01000001; EAO63494.1; -; Genomic_DNA.
GO; GO:0009986; C:cell surface; IEA.
GO; GO:0005618; C:cell wall; IEA.
Cell wall; Peptidoglycan_anchor.
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                                                                                                                                                                                                                                                                                            22-NOV-2005, integrated into UniProtKB/TrEMBL. 22-NOV-2005, sequence version 1. 27-NOV-2005, esquence version 5. Cell wall surface anchor family protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=18RS21;
PubMed=16172379; DOI=10.1073/pnas.0506758102;
                                                                                                                                                                                                                                                  910 AA.
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                                                                                                                                                                                                                                               PRELIMINARY; PRT;
                                                                                                                                                                                                                                                                                                                                                                                                ORFNames=SAJ 1458;
Streptococcus agalactiae 18RS21
76.9%;
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821 ASMSASTSASMSA 833
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225 ASTSAAAAAAAA 237
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                                                                          1 ASMSAASAASMAA 13
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nes 9; Conservative
                           10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
  Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI TaxID=342613;
                                                                                                                                                                                                                                               Q3DVC9_STRAG
Q3DVC9;
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Matches

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Q8DYL7
ID Q8
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Gaps

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Length 970;

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PRT; 1310 AA.

PRELIMINARY;

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                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=NRW316 / Serotype III;
BUDLINE-SZ242508; PubWed=12354221;
Glaser P., Rusniok C., Buchrieser C., Chevalier F., Frangeul L.,
Msadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genome sequence of Streptococcus agalactiae, a pathogen causing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BIOCYC; SAGAZIIII0:GBS1529-MONOMER; -.
BIOCYC; SAGAZIIII0:GBS1529-MONOMER; -.
GO; GO:000986; C:cell surface; IEA.
GO; GO:0005618; C:cell wall; IEA.
InterPro; IPRO01899; Gram pos anchor; 1.
FIGREAMS; TIGR01167; LPXTG anchor; 1.
PROSITE; PS50847; GRAM POS_ANCHORING; 1.
Cell wall; Complete protecome; Peptidoglycan-anchor.
SEQUENCE 1310 AA; 129398 MW; 9FB7ABBE89B8F155 CRC64;
                                                                                                                                                                                                                                              Streptococcus agalactiae serotype III.
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                    01-MAR-2003, integrated into UniProtKB/TrEMBL. 01-MAR-2003, sequence version 1. 07-FBB-2006, entry version 17. Prothetical protein gbs1529. OrderedLocusNames=gbs1529.
                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AL766851; CAD47188.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mol. Microbiol. 45:1499-1513(2002).
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781 ASMSASTSASMSA 793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invasive neonatal disease.
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                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=216495;
                                                        QBE473_STRA3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                 STRA3
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                         Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-A909 / ATCC 27551 / Serotype Ia;
PubMed=16172379; DOI=10.1073/pnas.0506758102;
PubMed=16172379; DOI=10.1073/pnas.0506758102;
Tettelin H., Masignani V., Cieslewicz M.J., Donati C., Medini D., Ward N.L., Angiuoli S.V., Crabtree J., Jones A.L., Durkin A.S., DeBoy R.T., Davidsen T.M., Mora M., Scarselli M., Margarit y Ros Peterson J.D., Hauser C.R., Sundaram J.P., Nelson W.C., Madupu R., Brinkac L.M., Dodson R.J., Rosovitz M.J., Sullivan S.A., Daugherty S.C., Haft D.H., Selengut J., Gwinn M.L., Zhou L., Zafar N., Smith S., Utterback T.R., White O., Rubens C.E., Grandi G., Madélin M.C., Kasper D.L., Telford J.L., Wessels M.R., Rappuoli R.,
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                                                                                                                                                                                                                                                                    Score 42; DB 2; Length 1130;
Pred. No. 3.4e+02;
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GO; GO:0009986; C:cell surface; IEA.

GO; GO:0005618; C:cell wall; IEA.

InterPro; IPR001899; Gram_pos_anchor.

Fram; PP00746; Gram_pos_anchor; 1.

TIGRFAMS; TIGR01167; LFXTG_anchor; 1.

PROSITE: PSSO847; GRAM POS_ANCHORING; 1.

Cell wall; Complete protecome; Peptidoglycan-anchor.

SEQUENCE 1258 AA; 124927 MW; AF0CC314FFBAB9BE CRC64;
                                                                                               EMBL; AAJQ01000008; EA073831.1; -; Genomic_DNA.
GO; GO:0009986; C:cell surface; IEA.
GO; GO:0005618; C:cell wall; IEA.
Cell wall; Peptidoglycan-anchor.
SEQUENCE 1130 AA; 113624 MW; 264E398D72562EGE CRC64;
                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-NOV-2005, sequence version 1.
07-FEB-2006, entry version 5.
Cell wall surface anchor family protein.
OrderedLocusNames=SAL 1493, ORFNames=SAK 1493;
Streptcococus agalactiae serotype Ia.
Bacteria; Firmicutes; Lactobacillales; Streptcoccaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-NOV-2005, integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1258 AA.
                                                                                                                                                                                                                                                                                                                          4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; CP000114; ABA45159.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                       77.8%;
69.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                           945 ASMSASTSASMSA 957
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Best Local Similarity 69.2.
Pest Local 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q3K052_STRA1
Q3K052;
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03K052 ST
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DT 08-N

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Gaps

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77.8%; Score 42; DB 2; Length 1310;

Pred. No. 3.9e+02; 4; Mismatches 0; Indels

69.2%;

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PubMed=16172379; DOI=10.1073/pnas.0506758102;
Tettellin H., Masignani V., Cieelewicz M.J., Donati C., Medini D.,
Ward N.L., Angiquoli S.V., Crabtree J., Jones A.L., Durkin A.S.,
DeBOY R.T., Davidsen T.M., Mora M., Scarselli M., Margarit y Ros I.,
Peterson J.D., Hauser C.R., Sundaram J.P., Nelson W.C., Madupu R.,
Brinkac L.M., Dodson R.J., Rosovitz M.J., Sullivan S.A.,
Bugherty S.C., Haft D.H., Selengut J., Gwinn M.L., Zhou L., Zafar N.,
Khouri H., Radune D., Dimitrov G., Watkins K., O'Connor K.J.,
Smith S., Utterback T.R., White O., Rubens C.E., Grandi G.,
                                                                                                                                       Name=sdrE; ORFNames=SAI 1566;
Streptococcus agalactiae H36B.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                         22-NOV-2005, integrated into UniProtKB/TrEMBL. 22-NOV-2005, sequence version 1. 07-FEB-2006, entry version 5.
                      PRT; 1326 AA.
                                                                                                                     Cell wall surface anchor family protein.
                    Q3D424 STRAG PRELIMINARY;
Q3D424;
                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                         NCBI TaxID=342615;
                                                                                                                                                                                                       Streptococcus
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STRAIN=CLIB 122 / E 150;

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                                                                                                                                                                                                                                                                                                                                                                                                    Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, AAJS01000004; EA078954.1; -; Genomic_DNA.
GO, GO:0009986. C:cell surface; IEA.
GO; GO:0005618; C:cell wall; IEA.
Cell wall; Peptidoglycan-anchor.
SEQUENCE 1326 AA; 131101 MW; 2866221DCFBD528E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
Madoff L.C., Kasper D.L., Telford J.L., Wessels M.R., Rappuoli R.,
Fraser C.M.;
                                                                                             Genome analysis of multiple pathogenic isolates of Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yarrowia lipolytica (Candida lipolytica).
Eukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Yarrowia.
                                                                                                                                          agalactiae: implications for the microbial 'pan-genome'.";
proc. Natl. Acad. Sci. U.S.A. 102:13950-13955 (2005).
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-AUG-2004, integrated into UniProtKB/TrEMBL.
16-AUG-2004, sequence version 1.
07-FBB-2006, entry version 12.
Similar to tr/Q9C228 Neurospora crassa Related to CSI2 protein.
OrderedLocusNames=YALI0F17204g;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77.8%; Score 42; DB 2; Length 1326; 69.2%; Pred. No. 4e+02; tive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75.9%; Score 41; DB 2; Length 324; 83.3%; Pred. No. 1.4e+02; rive 0; Mismatches 2; Indels
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QGCID7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [||||:::|||:|
685 ASMSASTSASMSA 697
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Best Local Similarity 83.3
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                             preliminary data.
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Les 9; Conserv
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SEQUENCE 324 AA:
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Ry STRANN=231.

Ry Ait—Sahra M., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,

Ait—Zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,

Arachini H.W., Armbruster J., Bachantsang P., Baldwin J., Barry A.,

Ry Bayul T., Blitshstern B., Brunache A., Butler J., Callixce N.,

Ry Calvosky M., Boukhagalter B., Brunache A., Butler J., Callixce N.,

Ry Calvo S.E., Camarata J., Campo M., Chang J., Cheshatsang Y.,

Ry Citroen M., Collymore A., Considine T., Cook A., Cooke P., Corum B.,

Ry Corum C., Davoe T., Dayoe T., Degray S., Dodges R., Dooley K.,

Ry Berickson J., Farina A., Farch S., Fischer H.,

Ry Erickson J., Farina A., Farch S., Fischer H.,

Ry Fitzgerald M., Poley K., Gage D., Galagan J.E., Gearin G., Gnerre S.,

Ry Fitzgerald M., Foley K., Gage D., Galagan J.E., Gearin G.,

Ry Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Ilter I.,

Ry Jaffe D., Jones C., Kamal M., Kamat A., Kamysoelis M., Karlsson E.,

Ry Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,

Andiblad-Took K., Liu X., Lokytsang T., Lokytseang Y., Lucien O.,

Ry Mcarthy M., McDonough S., McGhee T., Meldrim J., Meneus L.,

Ry Mcarthy M., McDonough S., Mihova T., Mikkelsen T., Mlenga V., Moru K.,

Ry Mcarthy M., McDonough S., Mihova T., Mikkelsen T., Mlenga V., Moru K.,

Ry Mcarthy M., Nguyen T., Minoon G., Naylor J., Newse C., Mayyen N.,

Ry Mchall K., Osman S., Parker S., Perrin D., Phunkhang P., Rogov P.,

Retten R., Stolker S., Perrin D., Phunkhang P., Roger D.,

Retten R., Stolker S., Perrin D., Sertipalli S., Sharpe T.,

Ry Person S., Stalker J., Samaen C., Settipalli S., Sharpe T.,

Ry Person S., Stalker C., Willeen C., Scone S., Sunner C., Settipalli S., Wangchuk T.,

Ry Person S., Stalker C., Willeman N., Tohang S., Wangchuk T.,

Ry Person S., Yang S., Yee 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i. - CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Fungi, Basidiomycota, Ustilaginomycetes,
Ustilaginomycetidae, Ustilaginales, Ustilaginaceae, Ustilago.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The genome sequence of Ustilago maydis.";
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
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GO; GO:0044449; P:cellular biosynthesis; IEA.
GNPERPC; IPR000649; IF-2B_related.
PANTHER; PTHR10233; IF-2B, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                19-JUL-2005, integrated into UniProtKB/TrEMBL
                                                                                                                                                                             805 AA.
                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                             19-JUL-2005, sequence version 1.
07-FEB-2006, entry version 4.
                                                                                                                                                                                                                                                                                                                           07-FEB-2006, entry version 4. Hypothetical protein.
                                                                                                                                                                                PRELIMINARY;
179 SMSKAQAASMAA 190
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RESULT 14 Q7S1A6\_NEU

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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
A manatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.E.,
A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
A Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Banos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Buller H., Caddeu E., Center A., Chandra I.,
A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MUCLEOTIDE SEQUENCE [GENOMIC DNA].
MEDLINE=89249328; PubMed=2566386; DOI=10.1016/0092-8674(89)90133-5;
Weigel D., Juergens G., Kuettner F., Seifert E., Jaeckle H.;
"The homeotic gene fork head encodes a nuclear protein and is
expressed in the terminal regions of the Drosophila embryo.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).

Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                      Rhodopseudomonas palustris.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74.1%; Score 40; DB 2; Length 210; 83.3%; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome, Hypothetical protein.
SEQUENCE 210 AA; 21813 MW, 07F77C8SCCABFFES CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PKH DROME STANDARD; PRT; 510 AA. 014734; Q9VAV0; D1.4734: Q9VAV0; O1.4 PR-1990, integrated into UniProtKB/Swiss-Prot. 01.4 PR-1990, sequence version 1. 07-FBB-2006, entry version 57. Fork bad protein. Name=fkh; ORFNames=CG10002;
                                                                                                                                                                          NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=CGA009 / ATCC BAA-98;
PubMed=14704707; DOI=10.1038/nbt923;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; BX572594; CAE25971.1; -; Genomic_DNA.
BioCyc; RPAL258594:RPA0527-MONOMER; -;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                    Bradyrhizobiaceae; Rhodopseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                       Nat. Biotechnol. 22:55-61(2004).
                            OrderedLocusNames=RPA0527;
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       protein
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Best Local Similarity
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                                                                                                                              NCBI_TaxID=1076;
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WEDINES-2258913-15; PubMed=12712197; DOI=10.1038/nature01554;

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I'm egenome sequence of the filamentous fungus Neurospora crassa.";

Nature 422:859-868(2003).

EMBLIGGHBBANKDDBJ whole genome shotgun (WGS) entry which is
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Sordariomycetidae, Sordariales, Sordariaceae, Neurospora.
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Pred. No. 5.6e+02;
0; Mismatches 2; Indels
                                              Score 41; DB 2; Length 805;
Pred. No. 3.5e+02;
1; Mismatches 2; Indels
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PROSITE; PS00014; ER TARGET; UNKNOWN 1.
SEQUENCE 1293 AA; 136804 MW; C85AF94F062EB449 CRC64;
86248 MW; 5A4CC28D1060ACD6 CRC64;
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InterPro; IPR000886; ER target S.
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15-DEC-2003, sequence version 1.
07-FBB-2006, entry version 10.
ORFOIcted protein.
ORFNames=NCU07514.1;
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                                                Query Match
Best Local Similarity 76.9%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                          Q7S1A6 NEUCR PRELIMINARY;
Q7S1A6;
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Matches 11; Conservative
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805 AA;
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QENCES;
SEQUENCE
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Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann M.,

Rosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,

A Jalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Liu X., Mattei B., McIntosh T.C., Morris J., Mosherson D.,

Merkulov G., Milshina N.V., Mobarry C., Morris J., Mosherson D.L.,

Merkulov G., Milshina N.V., Mobarry C., Morris J., Mosherson D.L.,

Melson D.K., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

Spier B., Spradling A.C., Stapleton M., Strong R., Sun E.,

Spier B., Spradling A.C., Stapleton M., Strong R., Sun E.,

Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

Walliams S.M., Woodage T., Weinsterok G.M., Weissenbach J.,

Wang Z.-Y., Wassarman D.A., Weinsterok G.M., Weissenbach J.,

Reiner K., Spradling A.C., Stapleton M., Strong R., Zho Q., Zheng L.,

And J., Xeh R.-F., Zaveri J.S., Zhan M., Zhou K., Zhu X., Smith H.O.,

Zheng X.H., Zhong F.N., Rubin G.M., Venter J.C.,

The Genome sequence of Drosophila melanogaster.",

Science 287:2185-2195(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          systematic review.";
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
-!- FUNCTION: Fkh promotes terminal as opposed to segmental
- ethorograment. In the absence of £kh, this developmental switch does not occur. The nuclear localization of the £kh protein suggest that £kh regulates the transcription of other, subordinate, genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P., Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lewis S.E.; a. Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:000515; F: protein binding; IPI.
GO; GO:0006916; P:anti-apoptosis; IMP.
GO; GO:0007439; P:ectodermal gut development; TAS.
GO; GO:0001743; P:endoderm formation; TAS.
GO; GO:000122; P:endoderm formation; TAS.
GO; GO:000122; P:negative regulation of transcription from R.
GO; GO:0007435; P:salivary gland morphogenesis; IMP.
InterPro; IPR001766; TF Fork head.
InterPro; IPR011991; Wing hix DNA_bd.
PF00250; Fork head: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9V860:CG6459; NbExp=1; IntAct=EBI-124027, EBI-151216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Nucleus.
SIMILARITY: Contains 1 fork-head DNA-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BioCyc; DMEL-XXX-02:DMEL-XXX-02-013832-MONOMER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE003766; AAF56798.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSFAC, T01054, -.
Ensembl, CG10002, Drosophila melanogaster.
FlyBase, FBgn0000659; fkh.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; J03177; AAA28535.1; -; Genomic_DNA
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SMART; SM00339; FH; 1.
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ProDom; PD000425; TF_Fork_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A32380; A32380.
HSSP; Q99958; 1D5V.
SMR; P14734; 210-300.
IntAct; P14734; -.
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GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DNA-binding; Nuclear protein.
SEQUENCE 510 AA; 54242 MW; 3089574C2BE7981B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endoptazoygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
PROSITE; PS00657; FORK HEAD_1; 1.
PROSITE; PS00658; FORK HEAD_2; 1.
PROSITE; PS50039; FORK HEAD_3; 1.
Complete proteome; Developmental protein; DNA-binding;
Nuclear protein; Transcription; Transcription regulation.

| 510 | Fork head protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stapleton M., Carlson J., Chavez C., Frise E., George R., Park S., Wan K., Yu C., Celniker S., Submitted (OCT-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 510;
                                                                                                                                                                             Length 510;
                                                                                                                                                                                1; Indels
                                                                                                                                                    2B86E807CBF7881B CRC64;
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69.2%; Pred. No. 3.2e+02;
tive 3; Mismatches 1;
                                                                                                                                                                              Score 40; DB 1;
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13-SEP-2005, sequence version 1.
07-FEB-2006, entry version 2.
Hypothetical protein.
Brymanes=Becpl808DRAFT 7796;
Burkholderia vietnamiensis G4.
                                                                                                                                                                                                                                                                                                                            510 AA.
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                                                                                                           Fork-head.
                                                                                                                          Gly-rich.
His-rich.
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                                                                                                                                                      54286 MW;
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69.2%;
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101 ASMSASMSASMSA 113
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Q4B6Z4;
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COMPBIAS
COMPBIAS
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9; Conservative
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NUCLEOTIDE SEQUENCE.
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Q6Z461_ORYSA
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                                                                                                                                                                                                                                                                                      STRAIN=G4;
US DOE Joint Genome Institute (JGI-ORNL);
Larimer F., Land M.;
"Annotation of the draft genome assembly of Burkholderia vietnamiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP clade,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-DEC-2004, integrated into UniProtKB/TrEMBL.
07-DEC-2004, sequence version 1.
21-FEB-2006, entry version 7.
Hypothetical protein P0679C08.7-2 (Hypothetical protein P0493C11.25-
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                                                                                                         US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome and assembly of Burkholderia vietnamiensis G4.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina Hammon N., Israni S., Pitluck S., Richardson P.;
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74.1%; Score 40; DB 2; Length 1839; 76.9%; Pred. No. 1.2e+03; ive 1; Mismatches 2; Indels
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"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6,
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                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                         Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases
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InterPro; IPR003006; Ig MHC.
PROSITE; PS00290; IG MHC; UNKNOWN_1.
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QSVRP3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
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Sasaki T., Matsumoto T., Yamamoto K.
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                           NCBI_TaxID=269482;
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OGSVRP3 ORY
DGSVRP3 ORY
DG C5VRP
DT 07-DE
DT 07-DE
DT 21-FE
DE Hypot
DE 23--
DG OC Sperm
OC Bukar
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US DOE Joint Genome Institute (JGI-ORNL);
Larimer F., Land M.;
"Annotation of the draft genome assembly of Rhodopseudomonas palustris
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome and assembly of Rhodopseudomonas paluetris BisBl8.";
Submitted (OCT-2005) to the EMBL/GenBank/DDBJ databases.
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07-FEB-2006, entry version 3.
Cell wall surface anchor family protein (Fragment).
ORFNames-RPCDRAFT 0879;
Rhodopseudomonas palustris BisB18
Bacteria, Proteobacteria, Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Rhodopseudomonas.
                                                                                                                                                                                                                                                                                                                                                                         72.2%; Score 39; DB 2; Length 181; 69.2%; Pred. No. 1.7e+02; ive 3; Mismatches 1; Indels
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clone:P0493C11.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BisB18.";
Submitted (NOV-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                              Hypothetical protein.`
SEQUENCE 181 AA; 18397 MW; A5CAB7C54081C7D0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-DEC-2005, integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                   EMBL; AP002542; BAD67872.1; -; Genomic_DNA.
EMBL; AP000559; BAD67675.1; -; Genomic_DNA.
Gramene; QSVRP3; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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50 AAMSASSAAAAA 62
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preliminary data.
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Best Local Similarity
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                                                                                                                                                                                                                                                             Q4IBZ8_GIBZE
Q4IBZ8;
                                                                                                                 Query Match
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STRAIN-CLIB 122 / E 150;
Nubmed-12295952; DOI=10.1038/nature02579;
Nubmed-12295952; DOI=10.1038/nature02579;
Nubmed-1229592; DOI=10.1038/nature02579;
Nubmed-1229592; DOI=10.1038/nature02579;
Nubmed-1229592; Doi=10.1038/nature02579;
Nubmed-12.10 Marck C., Neuveglise C., Talla E.,
A Goffard N., Frangell L., Aigle M., Anthourd V., Babour A., Barbe V.,
A Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., Geopura R.,
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A Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Suleau A.,
A Swennen D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
A Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
A Mincker P., Souciet J.-L.;
A Wincker P., Souciet J.-L.;
                                                                                                                                                                                                                                               Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                    Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP clade;
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OrderedLocusNames=YALIOA18524g;
Yarrowia lipolytica (Candida lipolytica).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Yarrowia.
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                                                                                                                                                                                   Sasaki T., Maľsumoto T., Katayose Y.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, PAC
                                                                                                                                                                                                                                                                                                                                                                                           72.2%; Score 39; DB 2; Length 216;
69.2%; Pred. No. 2e+02;
ive 3; Mismatches 1; Indels
                                                                                                                                                                                                                        Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                       INCEPTO; IPR004333; SDr.
Pfam; PF03110; SBP; 1.
PF01TRNCE 216 AA; 22044 MW; AF74A6B47B498B60 CRC64;
             Q62461;
05-JUL-2004, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-AUG-2004, integrated into UniProtKB/TrEMBL
 216 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          298 AA
                                                               Putative squamosa-promoter binding protein.
                                                                                                                                                                                                                                                                                        EMBL; AP005186; BAC84006.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                                 GO, GO:0005634, C:nucleus, IEA.
GO, GO:0003677, F:DNA binding, IEA.
InterPro; IPR004333; SBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
 PRT;
                                     05-JUL-2004, sequence version 1.
07-FEB-2006, entry version 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-AUG-2004, sequence version 1. 07-FEB-2006, entry version 12.
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Nature 430:35-44(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 69.2 nes 9; Conservative
                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
                                                                            Name=P0430F03.47;
                                                                                                                                            NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                      Gramene; Q6Z461;
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                                                                                                                                                                                                            clone: P0430F03.
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QGCGK6 YARLI
QGCGK6;
Q6Z461_ORYSA
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Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Bukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,

Hypocreomycetidae, Hypocreales, Nectriaceae, Gibberella.
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81.8%; Pred. No. 2.7e+02;
ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   Length 298;
                                                                                                                                                                                                                                                                                                                                                                  Score 39; DB 2; Length 2>0.
Pred. No. 2.7e+02;
2; Indels
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Complete proteome; Hypothetical protein.
SEQUENCE 301 AA; 32281 MW; E5838FC4C947BA3B CRC64;
                                                                                                                                                                                                                                                                                                                298 AA; 29325 MW; 50660B6CAC94A883 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-AUG-2005, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 AA
                                                                                                                       EMBL; CR382127; CAG84139.1; -; Genomic_DNA.
InterPro; IPR001778; PoA allergen_C.
PRINTS; PR00833; POAALLERGEN.
Complete proteome.
SEQUENCE 298 AA; 29325 MW; 50660B6CAC94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-AUG-2005, sequence version 1.
07-FEB-2006, entry version 4.
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                                                                                                                                                                                                                                                                                                                                                                                                            72.2%;
76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   222 AASSAASAASSAA 234
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es 10; Conservative
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clone: P0679C08
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Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-ATCC 23344;

PubMed=15377793; DOI=10.1073/pnas.0403306101;

Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,

Reldblyum T.V., Ulrich R.L., Ronning C.M., Brinkac L.M.,

Daugherty S.C., Davideen T.D., DeBoy R.T., Dimitrov G., Dodson R.J.,

Durkin A.S., Gwinn M.L., Haft D.H., Rhouri H.M., Kolonay J.F.,

Madupu R., Mohammoud Y., Nelson W.C., Radune D., Romero C.M.,

Sarria S., Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y.,

Zafazn N., Zhou L., Praser C.M.,

"Structural flexibility in the Burkholderia mallei genome.",

Proc. Natl. Acad. Sci. U.S.A. 101:14246-14251(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=15377794; DOI=10.1073/pnas.0403302101; PubMed=15377794; DOI=10.1073/pnas.0403302101; Ploden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.-M., Atkins T., Crosenter C., Mungall K.L., Bentley S.D., Sebaiha M., Thomson N.R., Bason N., Baccham I.R., Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                        OrderedLocusNames=BMA2157;
Burkholderia mallei (Pseudomonas mallei).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Burkholderia pseudomallei (Pseudomonas pseudomallei).
Bacteria: Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia; pseudomallei group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72.2%; Score 39; DB 2; Length 378; 69.2%; Pred. No. 3.4e+02; ive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR004455; NADPoxred F420.

Pfam; PF03807; F420 oxidored; I.

Complete proteome; Hypothetical protein.

SEQUENCE 378 AA; 38312 MW; E714B642803AD906 CRC64;
                                                                                                                                                                                                                                                                                        25-OCT-2004, integrated into UniProtKB/TrEMBL. 25-OCT-2004, sequence version 1. 25-EB-2006, entry version 8. Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
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GO; GO:0006118; P:electron transport; IEA.
                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ASMSAASAASMAA 13
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3 MSAASAASMAA 13
                                                            LSAASAASMVA 56
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Best Local Similarity
9; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=13373;
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                                                                                                                                                                                                                           Q62HU5_BURMA
Q62HU5;
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106 24163
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DT 25-
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063RM7 BURN
AC 063RM
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DT 25-0C
DT 07-FE
DE HYPOT
GN BURKH
OC BURKH
CI II
RR HUDGH
RR PUDMCIE
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RR PUDMI
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©58NM6 OB4Z21;
01-MAY-2000, integrated into UniProtKB/TrEMBL.
01-MAY-2000, sequence version 1.
21-FEB-2006, entry version 20.
Putative OSNAC7 protein (Putative NAM (No apical meristem) protein).
Name=P0493C11.25-1; Synonyme=134P10.2, P0679C08.7-1;
Oryza sativa (japonica cultivar-group).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; BEP Clade;
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Chillingworth T., Cronin A., Crossett B., Davis P., DeShazer D., Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K. Keith K.E., Maddison M., Moule S., Price C., Quail M.A., Rabbinowitesh E., Rutherford K., Sanders M., Simmonds M., Songsivilai S., Stevens K., Tumapa S., Vesaratchavest M., Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.; "Genomic plasticity of the causative agent of maljoidosis, Burkholderia pseudomallei.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72.2%; Score 39; DB 2; Length 378; 69.2%; Pred. No. 3.4e+02;
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Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome, Hypothetical protein.
SEQUENCE 378 AA; 38429 MW; 846216FB210C015E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sasaki T., Marsumoto T., Yamamoto K.; In' nipponbare (GA3) genomic DNA, chromosome
                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004)
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GO; GO:0045449; P:regulation of transcription; IEA.
InterPro; IPR003441; NAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, BX571965; CAH36643.1; -; Genomic DNA.
GO; GO:0006118; P:electron transport; TEA.
Interpro; IPR004455; NADPoxred F420.
Pfam; PF03807; F420_oxidored; T.
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EMBL; AP002542; BAB19365.1; -; Genomic_DNA.
EMBL; AP48413; AA033144.1; -; Genomic_DNA.
HSSP; Q9C932; 1UT7.
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Matches 9; Conservative
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                            NUCLEOTIDE SEQUENCE.
STRAIN=H12424;
US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucias S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome assembly of Burkholderia cenocepacia
                                                                                                                                                                                                                                                                                                     STRAIN=H12424;
US DOD Joint Genome Institute (JGI-ORNL);
Larimer F., Land M.;
"Annotation of the draft genome assembly of Burkholderia cenocepacia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Bristol N2;
MEDLINE-99069613; PubMed=9851916; DOI=10.1126/science.282.5396.2012;
                                                                                                                                                                                                                                                                                                                                                                                                                        -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales,
Burkholderiaceae, Burkholderia, Burkholderia cepacia complex.
NCBI_TaxID=331272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence of the nematode C. elegans: a platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72.2%; Score 39; DB 2; Length 441; 76.9%; Pred. No. 4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                    Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          441 AA; 46730 MW; 81765FDA8EF6B8D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AAHL01000098; EAM15573.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1999, integrated into UniProtKB/TrEMBL. 01-NOV-1999, sequence version 1. 07-FBB-2006, entry version 27. 07-PPD-tional protein. 0RPNOMMES=F56G4.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MormBase; WBGene00010159; F56G4.4.
WormBase; WBGene00010159; F56G4.4.
WormPep; F56G4.4; CE18758.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005476; F:nucleic acid binding; IEA.
GO; GO:0008270; F:zinc ion binding; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         investigating biology.";
Science 282:2012-2018(1998)
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=AU 1054;
US DOB Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome assembly of Burkholderia cenocepacia
                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AU 1054.";
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Burkholderiaceae, Burkholderia, Burkholderia cepacia complex.
NCBI_TaxID=331271;
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                                                                                                  Length 395;
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                                                                                                                                        1; Indels
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Hypochetical protein.
SEQUENCE 441 Aa, 46730 MW; 81765FDA8EF6B8D5 CRC64;
                  Pfam; PF02365; NAM; 1.
PROSITE; PS51005; NAC; 1.
SEQUENCE 395 AA; 42027 MW; 907916BE379EE14C CRC64;
                                                                                                72.2%; Score 39; DB 2; L
69.2%; Pred. No. 3.6e+02;
tive 3; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                  13-SEP-2005, sequence version 1.
07-FEB-2006, entry version 2.
Hypothetical protein.
ORFNames=BcenDRAFT 5768;
Burkholderia cenocepacia AU 1054.
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Burkholderia cenocepacia HI2424.
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264 AAMSASSAAAAA 276
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Best Local Similarity 76.3.
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                                                                                                                                            Conservative
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nes 9; Conserv
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Q4LHN7;
                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Frager C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A., Lathigra R., White O., Ketchum R.A., Palmer N., Dodgon R., Hickey E.K., Gwinn M., Dougherty B., Fleischmann R.D., Richardson D., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M., van-Vugt R., Adams M.D., Gocayne J.D., Weidman J., Utterback T., Watthey L., McDonald L., Artiach P., Bowman C., Garland S., Fujii C., Cotton M.D., Horst K., Tomb J.-F., Roberts K., Hatch B., Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Saccharomycetales, Saccharomycopsidaceae, Saccharomycopsis.
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Burkholderiaceae, Burkholderia, pseudomallei group.
                                                                                                                                                                                                                                  72.2%; Score 39; DB 2; Length 470; 75.0%; Pred. No. 4.3e+02; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72.2%; Score 39; DB 2; Length 629; 76.9%; Pred. No. 5.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                           470 AA; 53845 MW; 91F3A5A0A433E37A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               629 AA; 65145 MW; 305D2666A67EC6EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-JAN-2006, integrated into UniProtKB/TrEMBL.
24-JAN-2006, sequence version 1.
07-FEB-2006, entry version 2.
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GO; GQ:0016740; F:transferase activity; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
InterPro; IPR003604; Znf_U1.
InterPro; IPR013085; Znf_U1-C.
Pfam; PF06220; zf-U1; 1.
SMART; SM0451; ZnF_U1; 1.
Complete proteome; Hypothetical protein.
SEQUENCE 470 AA; 53845 WW; 91F7AREANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomycopsis fibuligera (Yeast).
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07-FEB-2006, entry version 15.
Acetolactate synthase (EC 4.1.3.18)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gamma-glutamyltransferase.
ORFNames=BTH_10389;
Burkholderia_thailandensis E264.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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Matches 10; Conservative
                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                          66 AKMEAAAAAMA 77
                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QZT1K2_BURTH
Q2T1K2;
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Q8NJ49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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080149 SAC
1D QBNJ4
AC QBNJ4
AC QBNJ4
DT 01-OC
DT 07-FB
DE Acetc
GN Names
OS Sacct
OC Sacct
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11K2

12G2

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GO; GO:0016829; F:lyase activity; IEA.
GO; GO:0016829; F:lyase activity; IEA.
GO; GO:0019076; F:thiamin pyrophosphate binding; IEA.
GO; GO:0009082; P:hanched chain family amino acid biosynthesis; IEA.
InterPro; IPR012846; Acetolac syn lg.
InterPro; IPR004407; Acolac syn lg.
InterPro; IPR012001; TPP_bd enzyme N.
InterPro; IPR012001; TPP_bd enzyme N.
InterPro; IPR012001; PPP_enzyme M.
InterPro; IPR012000; PPP_enzyme M.
PANTHER; PTHR1868:SF61; Acolac_synthlrg; 1.
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ight]^{-} NUCLEOTIDE SEQUENCE, FUNCTION, TISSUE SPECIFICITY, AND DEVELOPMENTAL
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24-MAY-2004, integrated into UniprotKB/Swiss-Prot.
24-MAY-2004, integrated into UniprotKB/Swiss-Prot.
24-MAY-2004, sequence version 2.
17-MAY-2004, equence version 2.
17-MAY-2004, equence version 2.
17-MAY-2004, entry version 2.
17-MAY-2004, entry version 2.
17-MAY-2004, entry version 2.
17-MAY-2004, main and accordance of the control of the contro
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PubMed=1418995; DOI=10.1016/0896-6273(92)90234-5;
Mellerick D.M., Kassis J.A., Zhang S.-D., Odenwald W.F.;
"Castor encodes a novel zinc finger protein required for the development of a subset of CNS neurons in Drosophila.";
Neuron 9:789-803(1992).
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76.9%; Pred. No. 6.6e+02; Indels
NUCLEOTIDE SEQUENCE.
STRAIN-8014;
NG L.L.H., Nga B., Tan K.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    724 AA; 77781 MW; 678EC6021FC874DF CRC64;
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NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
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                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AJ491151; CAD36014.1; -; Genomic_DNA.
HSSP; P07342; 1N0H.
SMR; Q8NJ49; 117-724.
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Pfam; PF02705; TPP enzyme M; 1.
Pfam; PF02776; TPP enzyme M; 1.
PIRSF; PIRSF500108; Acetolac syn lg; 1.
PIRSF; PIRSF001370; ThDP depend aci; 1.
TIGRFAMS; TIGR00118; acolac lg; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00187; TPP ENZYMES;
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87 ASASSAASAAA 99
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MEDLINE=22426066; PubMed=12537569;
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"The role of the coll cycle and cytokinesis in regulating neuroblast
sublineage gene expression in the Drosophila CNS.";
Development 121:3233-3243(1995).
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Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
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Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Annotation of the Drosophila melanogaster euchromatic genome: a systematic review.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE OF 281-660, FUNCTION, AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=1339340;
Cui X., Doe C.O.;
"ming is expressed in neuroblast sublineages and regulates gene
expression in the Drosophila central nervous system.";
Development 116:943-952(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION AS REPRESSOR, DNA-BINDING, AND SUBCELLULAR LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
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PubMed=9436984;

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Blocyc,
GO:0003700; F.
GO:0003700; F.
GO:0003700; F.
GO:0003700; F.
GO:0003700; F.
GO:000417; P:Centr.

A GO:000417; P:Centr.

B InterPro; IPR000637; AT hook DNA_L.

DR Pfan; PF00178; AT hook; I

DR SMAR; SM0035; ZDR CZH2; J.

DR SMAR; SM0035; ZDR CZH2; J.

DR SMAR; ZM0028; ZINC FINGER CZH2 1; 3.

DR SMAR; ZM0028; ZINC FINGER CZH2 2; 2.

DR PROSITE; PS00028; ZINC FINGER CZH2 2; 2.

DR PROSITE; PS00028; ZINC FINGER CZH2 2; 2.

DR PROSITE; PS0105; AT PACH CANCER CANCER
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Under, Dev. 103:3-11(2001).

Hech. Dev. 103:3-11(2001).

Hech. Dev. 103:3-11(2001).

Hech. Dev. 103:3-11(2001).

Hech. Dev. 103:3-11(2001).

Heapes in developing central nervous system (CNS). Essential for many, if not all, late developing neuroblastcoma (NB) sublineages.

Ends to the 5'-(GG[C[CT][CT]AAAAA[AT]-3' DNA sequence, like hb, suggesting that cas and ha act as a late regulators in early and late CNS NB sublineage, respectively. Acts by repressing expression of nub/pdm-1 and pdm2/pdm-2 POU genes, and restrict this pattern of expression in appropriate cells. Required for a full expression of vvl/drifter and acj6/1-POU; it is however unknown whether it directly activates these genes. Controls unknown whether it directly activates these denes. Controls

Hospital (en) expression in the ventral nerve chord.

Hospital SpECIFICITY: Expressed in a specific subset of neuroblasts in the ventral nerve chord and the procephalic region in the embryo. Expressed in many, if not all, late delaminating NBs, and in early NBs, but only after they have undergone several rounds of marily NBs, but only after they have undergone several rounds of sugalion mother cell-producing divisions.

Hospital SpECIFICITY: Expressed in embryos. Expressed from blarcoerm embryos. Not expressed in first and second instar larvae. May be weakly
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                                 Odenwald W.F.; "Regulation of POU genes by castor and hunchback establishes layered compartments in the Drosophila CNS."; Genes Dev. 12:246-260(1998).
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                                                                                                                                                                                                                                                                                  Pubhed=11335107; DOI=10.1016/S0925-4773(01)00312-4;
Hitler R., Chaminade M., Preat T.;
"The Drosophila castor gene is involved in postembryonic brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Contains 1 A.T hook DNA-binding domain.
-!- SIMILARITY: Contains 4 C2H2-type zinc fingers.
-!- CAUTION: Ref.1 sequence differs from that shown due to a frameshift in position 782.
Kambadur R., Koizumi K., Stivers C., Nagle J., Poole S.J.,
Odenwald W.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L04487; ; NOT ANNOTATED CDS; MRNA.
EMBL; AE002602; AAF51966.1; -; Genomic_DNA.
EMBL; AY051865; AAK93289.1; -; MRNA.
EMBL; 215091; -; NOT ANNOTATED_CDS; MRNA.
PIR; A49129; A49129.
PIR; JH0797; JH0797.
Ensembl; CG2102; Drosophila melanogaster.
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                                                                                                                                                                                                                                                         TISSUE SPECIFICITY
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Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
                                                                                Burkholderia pseudomallei (Pseudomonas pseudomallei).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia; pseudomallei group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72.2%; Score 39; DB 2; Length 4574; 76.9%; Pred. No. 4.2e+03; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4574 AA; 484884 MW; F8FA0909D2D9C75F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; BX571966; CAH38467.1; -; Genomic DNA.
GO; GO:0048037; F:cofactor binding; IEĀ.
GO; GO:0016829; F:lyase activity; IEĀ.
GO; GO:0016829; F:lyase activity; IEĀ.
GO; GO:000620; P:amino acid metabolism; IEĀ.
GO; GO:000633; P:fatty acid biosynthesis; IEĀ.
GO; GO:0008152; P:metabolism; IEĀ.
InterPro; IPR0019981; ACP like.
InterPro; IPR001597; Beta_elim_lyase.
InterPro; IPR001597; Beta_elim_lyase.
InterPro; IPR001597; Beta_elim_lyase.
InterPro; IPR00163; Phsphopanteth_bd.
InterPro; IPR002198; SDR.
PANTHER; PFRR11712; Receacyl_synth; 8.
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Pfam; PP01212; Beta_elim_lyase; 2.
Pfam; PF00109; Ketoacyl-synt; 3.
Pfam; PF02801; Ketoacyl-synt c; 3.
Pfam; PF0550; PP-binding; 2.
Probem; PS05052; Beta_elim_lyase; 1.
PROSITE; PS050606; ACP_DOMAIN; 2.
PROSITE; PS06066; B KETOACYL SYMTHASE; 1.
PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_2.
                                                                                                                                                                                           NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
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                                                                                                                                                                                                              STRAIN-K96243;
PubMed=15377794; DOI=10.1073/pnas.0403302101;
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    25-OCT-2004, sequence version 1. 07-FEB-2006, entry version 10. Putative polyketide synthase.
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Q2QLR1;
                                                                 OrderedLocusNames=BPSS1006;
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Matches 10; Conservative
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A Kusumoto K., Arima T., Akita O., Kashiwagi Y., Abe K., Gomi K.,
Kusumoto K., Arima T., Akita O., Kashiwagi Y., Abe K., Gomi K.,
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Burotiales, Trichocomaceae, mitosporic Trichocomaceae, Aspergillus.
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                                                                                                                                                                                                                                                     72.2%; Score 39; DB 1; Length 793; 69.2%; Pred. No. 7.2e+02;
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SEQUENCE 1014 AA; 109950 WW; 29FB09A9CAB2F5EA CRC64;
                                                          0 -> E (in Ref. 1).

R -> A (in Ref. 1).

A -> G (in Ref. 1).

G -> R (in Ref. 1).

S -> T (in Ref. 1).

A -> R (in Ref. 1).

A -> R (in Ref. 1).

B35DE18DD3C37671 CRC64;
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24-JAN-2006, sequence version 1.
07-MAR-2006, entry version 3.
MRNA cleavage and polyadenylation factor II complex.
ORFNames=A6099005501277;
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25-OCT-2004, integrated into UniProtKB/TrEMBL.
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                                                                                                                                                                                                                                                                                               3; Mismatches
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                       Poly-Ala.
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| 758 AALSAASAAAAA 770
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793 AA;
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Matches 9; Conserv
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AC Q63LK9;
DT 25-OCT-20
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Q2UKI7 ASE
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                              Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=OSJNBD0096M04.140; Synonyms=OSJNBD0043P23.4;
Oryza sativa (japonica cultivar-group).
Bukaryota; Viridipantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Duell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M., Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S., Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M.;

"Oryza sativa chromosome 3 BAC OSJNBD0096M04 genomic sequence.", Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2003, sequence version 1.
21-FRB-2006, entry version 13.
Hypothetical protein OSJNBb0096M04.140 (Hypothetical protein
OSJNBD0043P23.4)
                                                                                                                                                                                                                                                                                                                                                                                                                   70.4%; Score 38; DB 2; Length 129; 75.0%; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Buell R.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                          Buell C.R., Wing R.A., McCombie W.A., Ouyang S.;
Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Buell R.; Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
SEQUENCE 129 Aa; 13507 MW; 61F89A3E8FF8AA49 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2003, integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                                                                                                                                                       EMBL; DP000011; ABA99936.1; -; Genomic_DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 75.0
Matches 9; Conservative
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                                                                                               NCBI_TaxID=39947;
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Q84JT2_ORYSA
ID Q84JT2_ORYSA
ID O1-JUN-21
DT O1-JUN-21
DT O1-JUN-21
DT O1-JUN-21
DE HYPOCHETE
DE GSJUBBDOO,
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X PubMed=16772010; DOI=10.1038/nature04300;

A machida M., Asai K., Sano M., Tanaka T., Kumagai T., Terai G.,

A Kusumoto K., Arima T., Akita O., Kashiwagi Y., Abe K., Gomi K.,

A Galagan J.B., Nierman W.C., Yu J., Archer D.B., Bennett J.W.,

Bhatnagar D., Cleveland T.B., Pedorova N.D., Gotoh O., Horikawa H.,

Hosoyama A., Ichinomiya M., Igarashi R., Iwashita K., Juvvadi P.R.,

Kato M., Kato Y., Kin T., Kokubun A., Maeda H., Maeyama N.,

Kato M., Sawano T., Takahashi M., Takase K., Terabayashi Y.,

Wortman J.R., Yamada O., Yamagata Y., Anazawa H., Hata Y., Koide Y.,

Komori T., Koyama Y., Minecoki T., Suharnan S., Tanaka A., Isono K.,

Kuhara S., Ogasawara N., Kikuchi H.; Suharnan S., Tanaka A., Isono K.,

Mature 438:1157-1161(2005).
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Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
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                                                                                                                                                                                                                                                 Length 166;
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SEQUENCE 169 AA; 17228 NW; 3A2A8F472B04F675 CRC64;
                                                                                                                                                                                          166 AA; 17181 MW; 6EC080E8429A16DB CRC64;
                                                                                                                                                                                                                                                 70.4%; Score 38; DB 2; I 75.0%; Pred. No. 2.2e+02; iive 2; Mismatches 1;
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20-DEC-2005, sequence version 1.
20-EBB-2006, entry version 3.
CG13448 (Fragment).
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EMBL; AC092559; AAO37944.1; -; Genomic_DNA.
EMBL; AC099324; AAO73278.1; -; Genomic_DNA.
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                                                      Gramene; Q84JT2; -.
InterPro; IPR000095; PAK_box_Rho_bd
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Q2XY88;
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Q2UKI7;
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                                                                                                       Pfam, PF00786; PBD; 1.
PROSITE; PS50108; CRIB; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Predicted protein.
ORFNames=A0090003000790;
                                                                                                                                                                   Hypothetical protein. SEQUENCE 166 AA; 1
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Matches 9; Conserv
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51 SYSAATAAAMAA 62
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                                                 CG13448 (Fragment
                                                                                                              NCBI_TaxID=7220;
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                                                                                                           Comeron J.M., Guthrie T.B.;
"Intragenic Hill-Robertson Interference Influences Selection Intensity
on Synonymous Mutations in Drosophila.";
Mol. Biol. Evol. 22:2519-2530(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=16120803; DOI=10.1093/molbev/msi246;
Comeron J.M., Guthrie T.B.;
"Intragenic Hill-Robertson Interference Influences Selection Intensity
on Synonymous Mutations in Drosophila.";
Mol. Biol. Evol. 22:2519-2530(2005).
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           Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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NCBI_TaxID=7245;
                                                                                                                                                                                                                                                                          70.4%; Score 38; DB 2; Length 172; 75.0%; Pred. No. 2.3e+02; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 38; DB 2; Length 172;
Pred. No. 2.3e+02;
2; Mismatches 1; Indels
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20-DEC-2005, sequence version 1.
07-FEB-2006, entry version 3.
                                                                                    STRAIN=T33;
PubMed=16120803; DOI=10.1093/molbev/msi246;
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Drosophila yakuba (Fruit fly).
Drosophila yakuba (Fruit fly)
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QZXY89 DROYA PRELIMINARY;
Q2XY89;
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SYSAATAAAMAA 62
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                                                                       NUCLEOTIDE SEQUENCE.
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                                              NCBI_TaxID=7245;
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Q2XY87 DRO
ID Q2XY8
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174 AA

PRT;

QZXY87\_DROER PRELIMINARY;

DROER

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                                                                                                                                                                                                                                                                                                      PubMed=16120803; DOI=10.1093/molbev/msi246;
Comeron J.M., Guthrie T.B.;
"Intragenic Hill-Robertson Interference Influences Selection Intensity
on Synonymous Mutations in Drosophila.";
Mol. Biol. Evol. 22:2519-2530(2005).
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                                                                                                       Drosophila erecta (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 38; DB 2; Length 174;
Pred. No. 2.3e+02;
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20-DEC-2005, integrated into UniProtKB/TrEMBL. 20-DEC-2005, sequence version 1. 07-FEB-2006, entry version 3.
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Best Local Similarity 75...
6 9; Conservative
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Search completed: September 9, 2006, 23:00:14 Job time: 125.139 secs

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GenCore version 5 Copyright (c) 1993 - 2006 Bi	OM protein - protein search, using sw model	Run on: September 9, 2006, 22:37:17; (wit) (wit) (41.0	Title: US-10-617-568-36 Perfect score: 44 Sequence: 1 AXXAAAAAXAA 13	Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	Searched: 2589679 segs, 457216429 residue	Total number of hits satisfying chosen parameters	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 100 summaries	A_Geneseq_8:* :geneseq_1980	2: generary1990s:* 3: generary1990s:* 4: generary2000s:* 4: denesery2001g:*	geneseqp200	** ** **	0: geneseqp2006	Pred. No. is the number of results predict score greater than or equal to the score of	derived by analysis of the total	SUMMARIES . Result Query	Score Match Length DB	44 100.0 13 9 44 100.0 13 10	44 100.0 14 9	44 100.0 15 6	44 100.0 15 6 44 100.0 15 6	44 100.0 15 6 44 100.0 15 6	44 100.0 15 6	44 100.0 15 8 44 100.0 15 9	44 100.0 15 10 44 100.0 15 10	44 100.0 16 2	44 100.0 16 9	44 100.0 17 2 44 100.0 18 7	44 100.0 18 8 44 100.0 18 10	222

Adb59489 Synthetic Adh58955 Silk prot Adh58955 Silk prot Adj21560 Human lun Adv5895 Silk prot Adf21560 Human lun Adv78618 Cell atta Adf40072 Cell atta Adf81312 Self-asse Adv78590 Cell atta Adv78600 Cell

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Composition useful for producing fibers or films, comprises hybrid multiblock copolymer derived from Nephila clavipes or Bombyx mori silks.
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84.6%; Pred. No. 1.8;
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AED86538 standard; peptide; 13 AA.
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                                                                                                                    Silk peptide linker, SEQ ID 10
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Best Local Similarity
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Synthetic.

ADV78640;

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Gaps

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Query Match Best Local Matches

6 g RESULT 2 AED86538

Length 13; Indels

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ABR38361;
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                                                                    Cell attachable polypeptide useful for culturing cell, comprises auxiliary amino acid sequence having specific amount of Gly and A chemically bonded to cell attachable minimal amino acid sequence,
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                                                                                                                            Disclosure; SEQ ID NO 105; 20pp; Japanese
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13-MAY-2003; 2003US-00436611.
21-MAY-2003; 2003JP-00144125.
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The present invention relates to novel human cancer-related genes and proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and proteins are useful for eliciting a humoral or cellular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic agents. The proteins and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The present
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                                                         The present invention relates to a novel composition (CI) comprising a hybrid multiblock copolymer. The multiblock copolymer comprise peptide linkers, which are derived from peptide sequences found in native silk biomacromolecules or the crystalline domains of Nephila clavipes or Bombyx mori silks. The present sequence is one such peptide linker. (CI is useful for producing films or fibers utilized in tissue-engineering scaffolds, cell culture substrates, biocompatible coatings, sutures, membranes, grafts and drug delivery systems. (CI) enables to produce fibers or films having increased stiffness and tensile strength.
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Pred. No. 1.9;
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Disclosure; SEQ ID NO 11; 27pp; English.
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10-APR-2001; 2001US-0283112P.
25-APR-2001; 2001US-0286630P.
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human leukocyte antigen.
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Best Local Similarity
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New composition comprising a substance that modulates the structure of proteins and polynucleotides, useful for therapeutic, prognostic and diagnostic reagents for eliciting cellular or humoral immune response in
                                                                                                                                                                                                                                       Human; cytostatic; vaccine; cancer; immune response; HLA; human leukocyte antigen.
                                                                                                                                                                                                         Human cancer-related protein 187P3F2 HLA peptide #1491.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Raitano AB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 13; Page 618; 1021pp; English.
                                                                                                      ABR38360 standard; peptide; 15 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Challita-Eid PM,
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10-APR-2001; 2001US-0283112P.
25-APR-2001; 2001US-0286630P.
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Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                 Homo sapiens.
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                                                                                                                                        ABR38360;
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                                                                      RESULT 7
                                                                                    ABR38360
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sequence is a human leukocyte antigen (HLA) peptide, used in an example from the invention
                                                                                                                            Gaps
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human leukocyte antigen.
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Pred. No. 2;
0; Mismatches
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                                                                                         Score 44;
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Morrison K, Morrison RK, Raitano AB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 13; Page 618; 1021pp; English.
                                                                                                                                                                                                                                                                                    ABR38363 standard; peptide; 15 AA.
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1 Similarity 84.6%; 1
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10-APR-2001; 2001US-0283112P.
25-APR-2001; 2001US-0286630P.
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Best Local Similarity
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                                                       Sequence 15 AA;
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The present invention relates to novel human cancer-related genes and proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and proteins are useful for eliciting a humoral or cellular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, as therapeutic agents. The proteins and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example
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Pred. No. 2;
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The present invention relates to novel human cancer-related genes and proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and proteins are useful for eliciting a humoral or cellular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic agents. The proteins and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example from the invention
                                                                                                                                                                                                                                                                                                       New composition comprising a substance that modulates the structure of proteins and polynucleotides, useful for therapeutic, prognostic and diagnostic reagents for eliciting cellular or humoral immune response in cancer patients.
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Morrison K, Morrison RK, Raitano AB;
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10-APR-2001; 2001US-0283112P.
25-APR-2001; 2001US-0286630P.
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human leukocyte antigen.
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                                    Human cancer-related protein 187P3F2 HLA peptide #1495.
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0; Mismatches
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25-APR-2001; 2001US-0286630P
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Morrison K, N
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19-MAY-2003
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Disclosure; SEQ ID NO 3; 23pp; English.

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The present invention relates to novel human cancer-related genes and proteins are useful ABZ78150-ABZ01861. The genes and proteins are useful for eliciting a humoral or cellular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic agents. The proteins and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example
                                                                                                                                                                    New composition comprising a substance that modulates the structure of proteins and polynucleotides, useful for therapeutic, prognostic and diagnostic reagents for eliciting cellular or humoral immune response in cancer patients.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                           Hubert RS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 44; DB 6; Length 15;
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0; Mismatches
                           Challita-Eid PM, Faris M,
                       Jakobovits A, Challita-Eid PM, Farıs
Morrison K, Morrison RK, Raitano AB;
                                                                                                                                                                                                                                                                                                                                                                 Claim 13; Page 618; 1021pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADO58104 standard; peptide; 15 AA
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                                                                                                                              WPI; 2003-075555/07.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15 AA;
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ID ADOS

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Multiblock copolymer useful for producing fibers and films having high tensile strength, comprising linkers and peptide blocks derived from peptide sequences found in native silk biomacromolecules of Nephila clavipes.

(CORR ) CORNELL RES FOUND INC.

Rathore O, Sogah DY; WPI; 2004-447966/42.

13-MAY-2002; 2002US-0380502P. 13-MAY-2003; 2003US-00436611

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The invention relates to a novel cell attachable polypeptide comprising an auxiliary amino acid sequence (Y) chemically bonded to a cell attachable minimal amino acid sequence (X), where (Y) contenins 1-50 amino acids and the sum total content of Gly and Ala in (Y) is 42-100% with respect to the total number of amino acids in (Y). The polypeptide of the invention may be utilized during culturing of cells for use in various experiments, including toxicity studies, gene transfer and production of useful substances such as cytokines, thrombolytic agents, vaccines, hormones and antibiotics. Furthermore, the polypeptide may be useful for culturing cells for transplantation, particularly, transplantation of skin, cranial bones, musciles, skin tissue, bone marrow and retina The polypeptide exhibits extremely potent cell adhesion properties and can attach cells, such as NHDF and VERO cells, more efficiently onto a base material, relative to conventional methods. The polypeptide also exhibits
                                                                                                                                                                                                                                                                                                                                                                     ö
                          The present invention relates to synthetic multiblock copolymers comprising linkers and peptide blocks derived from peptide sequences found in native silk biomacromolecules such as the crystalline domain of the spider, Nephila clavipes, or the silkworm, Bombyx mori. The synthetic multiblock copolymers are produced by replacing the amorphous peptide domain of a structural biopolymer such as silk with a nonpeptide segment while maintaining the beta-sheet forming crystalline segments. The
                                                                                                                                                            multiblock copolymers have solid-state structures and mechanical properties similar to the naturally occurring structural biopolymers. The copolymers are useful for producing films or fibres with high tensile strength. The present sequence represents a spider beta-sheet crystalline segment found in the silk biopolymer.
                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cell attachment; cell culture; transplantation; vaccine; antibiotic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cell attachment-related auxillary peptide - SEQ ID 106.
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                                                                                                                                                                                                                                                                                                                                  Score 44;
Pred. No. 2
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84.6%; I
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                                                                                                                                                                                                                                                                                            Sequence 15 AA;
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ADV78642
ID ADV78
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Determining, monitoring and/or controlling the quality of a sample comprising at least one peptide and/or protein comprises determining the level of proteolytic cleavage and/or modification, and/or peptide loss of
                                                          Arg-C proteinase digest peptide SEQ ID NO:4.
                                                                                 Protein degradation; protein detection.
                                                                                                                                                                                                                                                                                                                                                            Example 6; SEQ ID NO 4; 54pp; English.
                                                                                                                                                                         14-JUL-2005; 2005WO-EP007684.
                                                                                                                                                                                                15-JUL-2004; 2004EP-00016696
                                    23-MAR-2006 (first entry)
                                                                                                                                                                                                                                                       Kellmann M, Menzel C,
                                                                                                                                                                                                                      (BIOV-) BIOVISION AG
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                                                                                                                           WO2006005622-A1
                                                                                                                                                                                                                                                                                                                                     the standard.
                                                                                                                                                   19-JAN-2006.
                                                                                                       Synthetic.
                                                                                                                                                                                                                                             Tammen H,
               AEF42853
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high heat stability, thus sterilization in autoclaves can be performed conveniently. The current sequence is that of a cell attachment-related auxillary peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Composition useful for producing fibers or films, comprises hybrid multiblock copolymer derived from Nephila clavipes or Bombyx mori silks.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a novel composition (CI) comprising a hybrid multiblock copolymer. The multiblock copolymer comprise peptide linkers, which are derived from peptide sequences found in native silk biomacromolecules or the crystalline domains of Nephila clavipes or Bombyx mori silks. The present sequence is one such peptide linker. (Cl is useful for producing films or fibers utilized in tissue-engineering scaffolds, cell culture substrates, biocompatible coatings, sutures, membranes, grafts and drug delivery systems. (CI) enables to produce fibers or films having increased stiffness and tensile strength.
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                                                                                                                                                                                            AED86540 standard; peptide; 15
                                                                                                                                                                                                                                                                Silk peptide linker, SEQ ID 12
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84.6%; I
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                                                                                                                1 AAXAAAAAAAAA 13
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                                                                                         11; Conservative
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Best Local Similarity
Local 11; Conserve
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                                                                               Similarity
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                                               Sequence 15 AA
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                                                                   Query Match
Best Local 3
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                                                                                                                                                                        RESULT 13
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Zucht H, Hess

Lamping N,

<u>م</u>

Schulz-Knappe

Schulte I;

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The invention relates to determining, monitoring and/or controlling the quality of a sample comprising at least one peptide and/or protein, comprising providing at least one protease-sensitive standard and/or at least one modification-sensitive standard and/or at least one modification-sensitive standard and/or at least one standard and/or protein, and determining the level of proteolytic cleavage and/or modification and/or peptide loss of the standard. The proteolytic cleavage is due to the presence of at least one protease selected from cleavage is due to the presence of at least one proteases selected from the proteases, oxperine proteases, metallo proteases, metallo proteases, metallo proteases, cycleans proteases, metallo proteases, complement cascade. The protease sinvolved in the clotting cascade and protease sansitive standard is at least one protease complement cascade. The protease sensitive standard is at least one protease complement cascade. The protease sensitive standard is at least one protease complement cascade. The protease sensitive standard is at least one protein, capacitic comprising at least one cleavage site for at least one protein, capacitic proteins and/or appetide loss of the standard with time. The present sequence is an Arg-C digest peptide from a hypothetical standard peptide (containing an Asp-N endoproteinase site and an Arg-C proteinase containing and trypsin) site) useful in the method of the invention.
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); Mismatches
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Pred. No. 2;
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Best Local Similarity
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Conservative

AEF42853 standard; peptide; 15 AA.

RESULT 14

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AEF42853 ID AEF4

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This sequence represents a specific example of a polypeptide, which forms a beta sheet in an aqueous environment and has the general formula can beta sheet in an aqueous environment and has the general formula can Jahmixkuhmüün-NHiž, in which A = D- or L-alainine amino caid; ml.m2 = 0.40; ml.m2 = 10.40; J = a charged amino acid; n = 1 or 2; cx = any amino acid except proline; u = 0 or 1; J1 lyaine, hydroxylysine, carboxyglutamic acid; Ac = an acylation modification to the amino carboxyglutamic acid; Ac = an acylation modification to the carboxylic acid terminus; NH2 = an amidation modification to the carboxylic acid terminus; cramposition amidation modification to the carboxylic acid terminus; cramposition amidation acid; and XI = cysteine, threonine, tyrosine or serine. The peptides have thosphodiesterase activity and readily hydrolyse sugar phosphates. Further crampositions amine-catalysed decarboxylation (e.g. decarboxylation of they can cause amine-catalysed decarboxylation (e.g. decarboxylation of coxalacetate), and they can hydrolyse phospholipids. They can be used for screening drugs for the prevention or treatment of they can be used for screening drugs for the prevention or treatment of neurodegenerative diseases, e.g. Alzheimer's disease, which result in amiloid brotein deposition. They can also be used to screen for drugs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polypeptide(s) which form stable beta sheets in aq. environment - having phosphodiesterase and glycosidase activity and useful in bio:engineering.enzymatic and drug screening applications.
                                                 Beta sheet; circular dichroism spectroscopy; glycosidase activity; phosphodiesterase activity; drug screening; hydrolysis; neurodegenerative disease; Alzheimer's disease; amyloid deposition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 44; DB 2; Length 16;
Pred. No. 2.1;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                  'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                         /note= "C-terminal amide"
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                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 15; 35pp; English
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Beta-sheet forming peptide #2.
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Best Local Similarity 84.0
Best Local 11; Conservative
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                                                                                                                                                                                                                                Key
Modified-site
                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAY-1995;
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                                                                                                                                                                         Synthetic
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AC ADV7
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DT 24-M
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     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents a specific example of a polypeptide, which forms a beta sheet in an aqueous environment and has the general formula a beta sheet in an aqueous environment and has the general formula accorded to the control of the control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polypeptide(s) which form stable beta sheets in aq. environment - having phosphodiesterase and glycosidase activity and useful in bio:engineering.enzymatic and drug screening applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                    Beta sheet, circular dichroism spectroscopy, glycosidase activity, phosphodiesterase activity, drug screening, hydrolysis, neurodegenerative disease, Alzheimer's disease, amyloid deposition.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Forood B, Houghten RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TORR-) TORREY PINES INST MOLECULAR STUDIES.
                                                                                                                                                                                                                                                                                                                        'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                  "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                which inhibit or disrupt the beta sheet
                                                                                                                                                                                                                                                             Location/Qualifiers
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                                     Beta-sheet forming peptide #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96WO-US007564.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84.6%;
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                                                                                                                                                                                                                                                                      Key
Modified-site
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                                                                                                                                                                                                            Synthetic
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The invention relates to a novel cell attachable polypeptide comprising an auxiliary amino acid sequence (Y) chemically bonded to a cell attachable minimal amino acid sequence (X), where (Y) contains 1-50 amino acids and the sum total content of Gly and Ala in (Y) is 42-100$ with respect to the total number of amino acids in (Y). The polypeptide of the invention may be utilized during culturing of cells for use in various experiments, including toxicity studies, gene transfer and production of useful substances such as cytokines, thrombolytic agents, vaccines, hormones and antibiotics. Furthermore, the polypeptide may be useful for culturing cells for transplantation of skin, cranial bones, muscles, skin tissue, bone marrow and retina. The polypeptide exhibits extremely potent cell adhesion properties and can attach cells, such as NHDF and VERO cells, more efficiently onto a base material, relative to conventional methods. The polypeptide also exhibits high heat stability, thus sterilization in autoclaves can be performed conveniently. The current sequence is that of a cell attachment-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell attachable polypeptide useful for culturing cell, comprises auxiliary amino acid sequence having specific amount of Gly and Ala, chemically bonded to cell attachable minimal amino acid sequence,
                              cell attachment; cell culture; transplantation; vaccine; antibiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Beta sheet, circular dichroism spectroscopy, glycosidase activity, phosphodiesterase activity, drug screening, hydrolysis, neurodegenerative disease, Alzheimer's disease, amyloid deposition.
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Pred. No. 2.1;
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 107; 20pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.08;
                                                                                                                                                                                                                                                                                            20-MAY-2004; 2004JP-00150510.
                                                                                                                                                                                                                                                                                                                                                             21-MAY-2003; 2003JP-00144125.
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hes 11; Conserv
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This sequence represents a specific example of a polypeptide, which forms a beta sheet in an aqueous environment and has the general formula and under the analysis of the state of the sta
                                                                                                                                                                                                                                                                                                                                                                                           Polypeptide(s) which form stable beta sheets in aq. environment - having phosphodiesterase and glycosidase activity and useful in bio:engineering.enzymatic and drug screening applications.
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Pred. No. 2.2;
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                                                                                                                                                                                                                                                                                              Houghten RA;
                                                                                                                                                                                                                                              (TORR-) TORREY PINES INST MOLECULAR STUDIES.
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/note= "C-terminal amide"
                                                                                                                                                                                                                                                                                              Forcod B,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Page 16; 35pp; English
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                                                                                                                                                                                                                                                                                              Perez-Paya E,
                                                                                                                                                                                                95US-00452043
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                                                                                                                                                                                                                                                                                              Blondelle SE,
                                                WO9637212-A1
                                                                                                                                               23-MAY-1996;
                                                                                                                                                                                                26-MAY-1995;
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AAO30390
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RESULT 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Silk; genetically modified; silk-like protein; polymer; silkworm fibroin; elastin; fibronectin; textile; food; industry; cosmetics; pET-SLP(n); pET-SLP(2; 4; 6); SLP6.
                                                                                                                                                         The invention relates to human orthologue of Aristaless homeobox gene, ARX. ARX gene is associated with infantile spasms (IS), non-specific X-linked mental retardation, X-linked myoclonic epilepsy and Partington syndrome. ARX gene is useful for diagnosing ARX-related disorders e.g., mild mental retardation, infantile spasms or dystonia. The present sequence is human ARX (GCG)10+7 mutant cDNA fragment encoded peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mass production of silk protein and silk-like protein having imparted function by employing genetically-modified Escherichia coli, useful in textiles, food industry and cosmetics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a method for producing silk or genetically-modified silk-like protein, comprising designing a silk or silk-like polymer containing e.g. domesticated silkworm fibroin and synthesizing
                                                                                                                                                                                                                                                                      Gaps
                                                                                                           New ARX gene, useful for diagnosing ARX-related disorders e.g., mild mental retardation, infantile spasms or dystonia.
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                                                                                                                                                                                                                                                   100.0%; Score 44; DB 7; Length 18;
                                                                                                                                                                                                                                                                       2; Indels
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                       Silk protein related peptide #SEQ ID 9.
                                        (WOME-) WOMEN'S & CHILDREN'S HOSPITAL.
                                                                                                                                         Disclosure; Fig 2a; 74pp; English.
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 26-NOV-2002; 2002WO-AU001599
                    26-NOV-2001; 2001AU-00009095
                                                                                                                                                                                                                                                              84.68;
                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                           1 AAXAAAAAAAAA 13
                                                                                                                                                                                                                                                                                                             AAAAAAAAAAA 13
                                                                                                                                                                                                                                                                       11; Conservative
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                                                                               WPI; 2003-505184/47.
                                                           Stromme P;
                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                         N-PSDB; AAL61167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2003100065-A1.
                                                                                                                                                                                                                                 Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                      25-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-DEC-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Asakura T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                  ADH58940;
                                                           Gecz J,
                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                             RESULT 20
                                                                                                                                                                                                                                                                                                                                                       ADH58940
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the minimum unit of the silk or the thus designed polymer for integration into expression vectors and transfer into Escherichia coli prior to growing in a medium. Also disclosed is a method for producing silk or capencically-modified silk-like protein, comprising designing a silk or silk-like polymer containing at least one protein selected from constitution, wild silkworm fibroin, elastin and comesticated silkworm fibroin, wild silkworm fibroin, elastin and fibroin and essentially comprising the domesticated from cfibroin. The produced silk and silk-like protein are useful in textiles, food industry and cosmetics. Using this method, expression efficiency is greatly improved, thus providing silk-like protein with designed functionalities easily in large quantities. The SLP gene, PUC-link and SLP(n) were constructed for producing expression vector pEr-SLP(n) with expression of pET-SLP(2,4,6). The target protein SLP6 was obtained after cleavage of the tag sequence with use of cyanogens bromide. The sequences given in records for ADHS8932-ADHS8971 represent silk-like protein crelated polypeptides and polymucleotides, and primers used in the creation of the vector of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides a method for mass production of silk protein and gene recombinant silk-like protein (SLP). The method involves integrating a silk like polymer selected from e.g. domestic silkworm fibroin, wild silkworm fibroin, elastin and fibronectin of the minimum unit into an expression vector selected from expression vectors containing Ty promoter. The method is useful for mass producing silk or silk-like proteins with improved cellular adhesiveness, elasticity or hardness and is also useful in clothing, food and cosmetic industries. The present sequence is a polyalanine peptide which is similar to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Producing silk or silk-like protein comprises integrating a silk like polymer comprising the minimum unit into an expression vector selected from expression vectors containing T7 promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein production; silk; food; cosmetics; polyalanine.
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 9; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AEF40057 standard; peptide; 18 AA.
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22-NOV-2004; 2004US-00515264.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US2006019348-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unidentified.
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cell attachment; cell culture; transplantation; vaccine; antibiotic.
                                                                                                                                                                                                                                                                                                                                                Cell attachable polypeptide useful for culturing cell, comprises auxiliary amino acid sequence having specific amount of Gly and Ala, chemically bonded to cell attachable minimal amino acid sequence,
                                                                           Cell attachment-related auxillary peptide - SEQ ID 51.
                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 51; 20pp; Japanese.
                                                                                                                                                                                                                                                         21-MAY-2003; 2003JP-00144125.
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                                                (first entry)
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                                                24-MAR-2005
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                                                                                                                                      Synthetic
                  ADV78587;
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polyalanine region in wild silk worm and is used in the formation of SLPA (Silk-like protein with polyalanine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARX. ARX gene is associated with infantile spasms (IS), non-specific X-linked mental retardation, X-linked myoclonic epilepsy and Partington syndrome. ARX gene is useful for diagnosing ARX-related disorders e.g., mild mental retardation, infantile spasms or dystonia. The present sequence is human ARX 428-451dup(24bp) mutant cDNA fragment encoded
                                                                                                                                                                                                                                                                                                                                                            Homeobox gene; ARX; ARX-related disorder; X-linked myoclonic epilepsy; infantile spasm; mental retardation; Partington syndrome; diagnosis; dystonia; human; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to human orthologue of Aristaless homeobox gene,
                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                Human ARX 428-451dup(24bp) mutant cDNA fragment encoded peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New ARX gene, useful for diagnosing ARX-related disorders e.g., mental retardation, infantile spasms or dystonia.
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0
                                                                          Score 44; DB 10; Length 18;
Pred. No. 2.3;
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Pred. No. 2.4;
                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                           Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (WOME-) WOMEN'S & CHILDREN'S HOSPITAL.
                                                                                                                                                                                                                                        AAO30392 standard; peptide; 19 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74pp; English
                                                                           100.08;
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                                                                                           84.6%;
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                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                         1 AAXAAAAAAAA 13
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                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2003-505184/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 2b;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stromme P;
                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                              Sequence 18 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                            sapiens
                                                                                                                                                                                                                                                                                                    22-SEP-2003
                                                                                                         11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                       AA030392;
                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptide
                                                                                         Best Loc
Matches
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The invention relates to a novel cell attachable polypeptide comprising an auxiliary amino acid sequence (Y) chemically bonded to a cell attachable minimal amino acid sequence (X), where (Y) contains 1-50 amino acids and the sum total content of Gly and Ala in (Y) is 42-100% with creapect to the total number of amino acids in (Y). The polypeptide of the invention may be utilized during culturing of cells for use in various compenients, including toxicity studies, gene transfer and production of useful substances such as cytokines, thrombolytic agents, vaccines, commones and antibiotics. Furthermore, the polypeptide may be useful for culturing cells for transplantation, particularly, transplantation of skin, cranial bones, muscles, skin tissue, bone marrow and retina. The colypeptide exhibits extremely potent cells, more efficiently onto a base attach cells, such as NHDF and VBRO cells, more efficiently onto a base commentation methods. The polypeptide also exhibits conveniently. Thus sterilization in autoclaves can be performed conveniently. The current sequence is that of a cell attachment-related conveniently.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ 63.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cell adhesion; cytokine; hormone; antibiotic; heat tolerance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 9; Length 19;
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AEB23102 standard; peptide; 19 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.6%;
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ADV78587 standard; peptide; 19 AA.

RESULT 23 ADV78587 ID ADV

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ADH47641;
                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                    The invention relates to a novel polypeptide having cell adhesion property. The polypeptide comprises a minimum amino acid sequence and an auxiliary amino acid sequence capable of expressing a cell adhesion property and having a molecular weight of 1500-15000. The invention turther comprises a cell adhesion property polypeptide base material. The cell adhesion property polypeptide base material is useful for producing a cell. The cell adhesion property polypeptide is useful for culturing and analyzing cells, screening assays, and producing bloactive culturing and analyzing cells, screening assays, and producing bloactive substances such as cytokines, hormones, antibiotics, etc. The cell adhesion property polypeptide has excellent cell adhesion property, heat stability and has low immunogenicity. This sequence used in the cell adhesion property polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis A virus, HAV; immunogen; immunostimulant; virucide; vaccine; antigen; major structural capsid polypeptide; HAV antibody detection.
                                                                                                                                                                         polypeptide having cell adhesion property, useful for culturing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 44; DB 9; Length 19;
Pred. No. 2.4;
0; Mismatches 2; Indels
                                                                                                                                                                                                                  Disclosure; SEQ ID NO 63; 26pp; Japanese.
                                                                                                                                                                                         cells and producing bioactive substances.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic HAV peptide, SEQ ID NO: 89.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB69489 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
84.6%; P
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                                                   09-DEC-2003; 2003JP-00409854.
                                                                           09-DEC-2003; 2003JP-00409854.
                                                                                                   (SANN ) SANYO CHEM IND LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAAAAAAAAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fields HA, Khudyakov YE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AAXAAAAAAAAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-112681/12.
                                                                                                                                                      WPI; 2005-514832/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis A virus
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 19 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200105824-A2
 JP2005170810-A.
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                           30-JUN-2005
                                                                                                                             Kurokawa Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB69489;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                             Novel
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AAB69489
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molecules at the carboxy end of the peptide. The peptides are used to detect the presence of antibodies against HAV in mammalian serum, to detect the presence of HAV in a human or animal through the binding of the peptide to an antibody, to detect acute phase infection by detecting IgM antibodies in mammalian serum and detecting convalescence in ammunal. The peptides are used to detect or quantify HAV antibodies in samples in clinical or research-based assays using immunoblotting, fluorescence in situ hybridisation analysis, gel-mobility shift assays,
                                                                                                                                                                                                                                                                                                                                           tracking of radioactive or bioluminescent markers, chromatography or electrophoresis. The peptides are used to induce an immune response to HAV when administered to a human or animal. Glutamine at the carboxy end of the peptides enhances the IGM antibody reactivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lung cancer; tumour; cytostatic; immunostimulant; vaccine; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to novel compositions and methods for the therapy and diagnosis of cancer, particularly lung cancer. The compositions
                                                                                                      The present sequence is one of a number of synthetic peptides which are immunoreactive with hepatitis A virus (HAV) antibodies. The peptides comprise antigenic epitopes of the major structural capsid polypeptides or non-structural polypeptides of HAV with one or more glutamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polypeptides and encoding polynucleotides, useful for diagnosing, preventing and/or treating lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
Synthetic peptides used as antigen sources for enzyme immunoassays detecting anti-hepatitis A virus and as vaccines.
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Fanger GR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 44; DB 4; Length 20;
Pred. No. 2.5;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human lung tumour clone peptide, SEQ ID No 2122.
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Durham M, Carter D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 2122; 258pp; English.
                                                                    Disclosure; Page 127; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADH47641 standard; peptide; 20 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-OCT-2001; 2001US-00017754.28-MAR-2002; 2002US-00113872.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 84.6
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Henderson RA, Wang T,
Johnson JC, Retter MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mcnabb A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-468346/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2003037267-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human; clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAR-2004
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The invention relates to a method for producing silk or genetically-
modified silk-like protein, comprising designing a silk or silk-like
polymer containing e.g. domesticated silkworm fibroin and synthesizing
the minimum unit of the silk or the thus designed polymer for integration
into expression vectors and transfer into Escherichia coli prior to
growing in a medium. Also disclosed is a method for producing silk or
growing in a medium. Also disclosed is a method for producing silk or
growing in a medium. Also disclosed is a method for producing silk or
silk-like polymer containing at least one protein selected from
domesticated silkworm fibroin, wild silkworm fibroin, elastin and
fibronectin and essentially comprising the domesticated or wild silkworm
cibroin. The produced silk and silk-like protein are useful in textiles,
food industry and cosmetics. Using this method, expression efficiency is
greatly improved, thus providing silk-like protein with designed
functionalities easily in large quantities. The SLP gene, PUC-link and
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comprise one or more lung turmour polypeptides, immunogenic portions therof, polymucleotides that encode such polypeptides, antigen presenting cells that express such polypeptides, and T cells that are specific for cells expressing such polypeptides. The novel compositions have cytostatic and immunostimulant activity. The lung turmour antigens can be used in the creation of a vaccine. The polymucleotides that encode the lung turmour polypeptides can be used in gene therapy to help in the treatment of lung turmours. This sequence represents a human lung turmour clone polypeptide of the invention. This sequence was not shown in the specification. It has been taken from a World Intellectual Property
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Silk; genetically modified; silk-like protein; polymer; silkworm fibroin; elastin; fibronectin; textile; food; industry; cosmetics; pET-SLP(n); pET-SLP(2; 4; 6); SLP6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mass production of silk protein and silk-like protein having imparted function by employing genetically-modified Escherichia coli, useful in textiles, food industry and cosmetics.
                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                  Length 20;
                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                            Organization CD ROM supplied with the specification
                                                                                                                                                                                                                                                                                                                                        2;
                                                                                                                                                                                                                                                                                             Score 44; DB 7;
Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Silk protein related peptide #SEQ ID 24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; SEQ ID NO 24; 56pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADH58955 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                             100.0%;
84.6%; F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYNI-) UNIV JAPAN TOKYO AGR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                            1 AAXAAAAAAAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                       AAAAAAAAAA 17
                                                                                                                                                                                                                                                                                                                                    11; Conservative
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                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                       Sequence 20 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADH58955;
                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 27
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SLP(n) were constructed for producing expression vector pET-SLP(n) with expression of pET-SLP(2,4,6). The target protein SLP6 was obtained after cleavage of the tag sequence with use of cyanogens bromide. The sequences given in records for ADH58932-ADH58971 represent silk-like protein related polypeptides and polynucleotides, and primers used in the creation of the vector of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a novel isolated polynucleotide comprising a
                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel polynuclectide encoding lung tumor polypeptides, useful for diagnosing, preventing and treating cancer e.g. lung cancer.
                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                   Human lung cancer-related L984P peptide fragment - SEQ ID 2122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sleath PR;
Fanger GR,
                                                                                                                8; Length 20;
                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                           lung tumour; cytostatic; lung cancer; human; 1984P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kalos MD,
Carter D,
                                                                                                                DB
                                                                                                                                         0; Mismatches
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                                                                                                                100.0%; Score 44;
                                                                                                                              Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Watanabe Y,
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                                                                                                                                                                                                                                                         ADJ21560 standard; peptide; 20 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-MAR-2000; 2000US-00546259.
10-ARR-2000; 2000US-00546259.
27-APR-2000; 2000US-00560406.
05-UJN-2000; 2000US-005614124.
11-JUL-2000; 2000US-00614124.
29-AUG-2000; 2000US-0065163.
08-SEP-2000; 2000US-0065824.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-00346492.
99US-00419356.
99US-00466867.
99US-00476300.
2000US-00519642.
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30-0CT-2000; 2000US-00702705.
13-DBC-2000; 2000US-00736705.
03-MAY-2001; 2001US-00849626.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-OCT-2002; 2002US-00283017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-JUL-2001; 2001US-00902941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-OCT-2001; 2001US-00017754
28-MAR-2002; 2002US-00113872
                                                                                                                           84.68;
                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                 1 AAXAAAAAAAA 13
                                                                                                                                                                                          3 AAAAAAAAAAA 15
                                                                                                                                         11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , Wang T,
Retter MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bangur CS, Mcnabb A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-167010/16.
                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                             US2003211510-A1.
                                                                                       Sequence 20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RA,
                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                          04-NOV-2004
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                                                                                                                                                                                                                                                                                  ADJ21560;
                                                                                                                Query Match
                                                                                                                                           Matches
                                                                                                                                                                                                                               RESULT 28
                                                                                                                                                                                                                                            ADJ21560
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The invention relates to a novel cell attachable polypeptide comprising an auxiliary amino acid sequence (Y) chemically bonded to a cell attachable minimal amino acid sequence (X), where (Y) contains 1-50 amino acids and the sum total content of Gly and Ala in (Y) is 42-100% with respect to the total number of amino acids in (Y). The polypeptide of the invention may be utilized during culturing of cells for use in various caperinents, including toxicity studies, gene transfer and production of useful substances such as cytokines, thrombolytic agents, vaccines, hormones and antibiotics. Furthermore, the polypeptide may be useful for culturing cells for transplantation, particularly, transplantation of skin, cranial bones, muscles, skin tissue, bone marrow and retina. The polypeptide exhibits extremely potent cell adhesion properties and can attach cells, such as NUPP and VERO cells, more efficiently onto a base material, relative to conventional methods. The polypeptide also exhibits has tability, thus sterillamethods. The polypeptide also exhibits conveniently. The current sequence is that of a cell attachment-related
sequence chosen from any one of 40 lung tumour polypeptides or its complements, fragments or degenerate variants. The method of the invention has cytostatic applications and may be useful for detecting and treating lung cancer in a patient, as well as for inhibiting the development of lung cancer in a patient via incubating CD4+ and/or CD8+ cells isolated from a patient with at least one component chosen from a polypeptide, polynucleotide or antigen presenting cell (ApC) of the invention and administering an effective amount of the proliferated T cells to the patient. The current sequence is that of the human lung cancer-related peptide of the invention. The current sequence is not shown in the specification per se but is available on the USPTO web-site http:seqdata.uspto.gov/sequence.html?DocID=20030211510.
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell attachable polypeptide useful for culturing cell, comprises auxiliary amino acid sequence having specific amount of Gly and Ala, chemically bonded to cell attachable minimal amino acid sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cell attachment; cell culture; transplantation; vaccine; antibiotic.
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                                                                                                                                                                                                                                                                                                                                       100.0%; Score 44; DB 8; Length 20;
                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cell attachment-related auxillary peptide - SEQ ID 52
                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 52; 20pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                               Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADV78588 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-MAY-2004; 2004JP-00150510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-MAY-2003; 2003JP-00144125.
                                                                                                                                                                                                                                                                                                                                                               84.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AAXAAAAAAAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 AAAAAAAAAAA 17
                                                                                                                                                                                                                                                                                                                                                                                      11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2005-053150/06.
                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                Sequence 20 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADV78588;
                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                   Domestic silkworm silk-like protein with polyalanine peptide SEQ ID: 24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Producing silk or silk-like protein comprises integrating a silk like polymer comprising the minimum unit into an expression vector selected from expression vectors containing T7 promoter.
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                                                                                    Gaps
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                                                                                   ;
                                                                                                                                                                                                                                                                                                                             Protein production; silk; food; cosmetics; silk-like protein;
polyalanine; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 44; DB 10; Length 20; 84.6%; Pred. No. 2.5; 2; Indels iive 0; Mismatches 2; Indels
                                                        Length 20;
                                                                                    2; Indels
                                                     Score 44; DB 9;
Pred. No. 2.5;
0; Mismatches 2.
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auxillary peptide of the invention.
                                                                                                                                                                                                                   AEF40072 standard; peptide; 20 AA.
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22-NOV-2004; 2004US-00515264.
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                                                          100.08;
                                                                        84.68;
                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                             4 AAAAAAAAAAA 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Conservative
                                                                                                                 1 AAXAAAAAAAAA 13
                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 11; Conserv
                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ASAK/) ASAKURA T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AEF40068.
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                               Sequence 20 AA;
                                                                                                                                                                                                                                                                                                                                                                               Bombyx mori.
Unidentified.
                                                                                                                                                                                                                                                                            23-MAR-2006
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Local Sim
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                                                                                                                                                                                                                                                 AEF40072;
                                                           Query Match
                                                                                       Matches
                                                                                                                                                                                          RESULT 30
                                                                                                                                                                                                         AEF40072
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AAY25436

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immunoreactive with hepatitis A virus (HAV) antibodies. The peptides comprise antigenic epitopes of the major structural capsid polypeptides or non-structural polypeptides of the major structural capsid polypeptides or non-structural polypeptides of HAV with one or more glutamine molecules at the carboxy end of the peptide. The peptides are used to detect the presence of antibodies against HAV in mammalian serum, to the peptide to an antibody, to a human or animal through the binding of the peptide to an antibody, to detect acute phase infection by detecting IgM antibodies in mammalian serum and detecting convalescence in a mammal. The peptides are used to detect or quantify HAV antibodies in samples in clinical or research-based assays using immunoblotting, fluorescence in situ hybridisation analysis, gel-mobility shift assays, tracking of radioactive or bioluminescent markers, chromatography or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAV when administered to a human or animal. Glutamine at the carboxy end of the peptides enhances the IgM antibody reactivity
                                                                                                                                                                                                                                                                                                                                                                                                      synthetic peptides which are antibodies. The peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            miniblock polymer; optical response; mid infrared wavelength range; long range ordered fluid; liquid crystals; nanolithography; IR-sensitive device; IR sensor; IR filter; night telescope; thermosensitive detector; non-linear chromophore; biomaterial; tissue engineering scaffold; ferroelectric material; artificial muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             electrophoresis. The peptides are used to induce an immune response to
                                                                                                                                                                                                                                                                                            Synthetic peptides used as antigen sources for enzyme immunoassays detecting anti-hepatitis A virus and as vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 44; DB 4; Length 21; Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      sequence is one of a number of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                  (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 127; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Self-assembling polymer peptide #67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ¥.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.08;
                                                                                  14-JUL-2000; 2000WO-US019267
                                                                                                                           99US-0144412P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-OCT-2002; 2002WO-US031375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-OCT-2001; 2001US-0326743P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84.68;
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                                                                                                                                                                                                              Khudyakov YE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11; Conservative
                                                                                                                                                                                                                                                     WPI; 2001-112681/12
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          device
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 21 AA;
WO200105824-A2.
                                                                                                                           15-JUL-1999;
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                                         25-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-JUL-2003,
                                                                                                                                                                                                              Fields HA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          switching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADJ81212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADJ81212
X4X4X8X8Y8Y8Y8X8X8X8X8X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes the production of a novel synthetic DNA (I), wells, encoding an antifreeze polypeptide, AFPWFBR modelled on the antifreeze peptide (AFP) found in winter flounder. The polypeptides encoded by (I) lower the freezing temperature of water and prevent ice formation, therefore are useful as antifreeze agents. The use of reminions produced synthetic peptides is less toxic than the use of chemicals (prior art). Naturally occurring antifreeze polypeptides are not available in large quantities, synthetic antifreeze polypeptides are more readily available. The antifreeze polypeptides are more readily available. Which is cheaper and less time consuming compared to direct chemical synthesis of synthetic peptides (prior art)
                                                                                                                                                                                                       Antifreeze peptide; AFP; wf8r; AFPWF8R; winter flounder; ice formation; water freezing temperature; antifreeze agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis A virus; HAV; immunogen; immunostimulant; virucide; vaccine; antigen; major structural capsid polypeptide; HAV antibody detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic antifreeze peptide and the gene coding its production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                              Synthetic antifreeze protein AFPWF8R insert fragment B2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (VIRG ) VIRGINIA TECH INTELLECTUAL PROPERTIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 44; Db 2
No. 2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 2.6;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic HAV peptide, SEQ ID NO: 90
                                  AAY25436 standard; protein; 21 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 8C; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB69490 standard; peptide; 21 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.08;
                                                                                                                                                                                                                                                                                                                                                                                                  91US-00814220.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAX88104, AAX88105.
                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Toth TE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-418272/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis A virus.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Szumanski MBW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 21 AA;
                                                                                                                                                                                                                                                                                                                                                                                                23-DEC-1991;
                                                                                                                       09-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                       20-JUL-1999
                                                                                                                                                                                                     Antifreeze
                                                                                                                                                                                                                                                                    Synthetic
                                                                            AAY25436;
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Matches

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AAB69490

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Gaps

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The invention relates to a miniblock polymer (I) comprising a self-
fabricating block and a solubilizing block, a block for triggering self-
can self-fabricate to form 3 - dimensional material and block for
incorporating turns in the polymer or for providing sites for chemical
modifications, has a molecular weight of 1000-300000 and, in solution,
can self-fabricate to form 3 - dimensional material and in solution,
controlled delivery of a drug which involves incorporating a drug
order, and where (I) has glycine content of at least 20%. (I) is useful
for controlled delivery of a drug which involves incorporating
the drug. The drug is incorporated within layers of the self-fabricating
material. (II) is useful for modifying the optical response of a device
in the near to mid infrared wavelength range which involves applying (II)
to the surface of the device (all claimed). (I) is useful for preparing
long range ordered fluids (i.e., liquid crystals) in a variety of phases
or forms, which can then undergo very specific structural transitions to
form rigid materials. (I) can be used as structural tissue implants, in
liquid crystal displays, and for producing high-performance composites.
(I) is useful for preparing chemically patterned templates with either
general features are specific features. (I) is also useful in
nanolithographic processes. A self-fabricated structure containing the
polymer (II) is useful for modifying and improving performance of IR-
sensitive devices, IR sensors, IR filters, inglet telescopes and
membranes or coatings that absorb specific perparing films,
membranes or coatings that absorb specific apple or parameters.
                                                                                                                                                                                      Miniblock polymer useful in nanolithographic processes, has self-fabricates fabricating block and solubilizing block, has glycine and self-fabricates to form 3-dimensional materials having long-range orders, in solution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     miniblock polymer, optical response; mid infrared wavelength range; long range ordered fluid; liquid crystals; nanolithography; IR-sensitive device; IR sensor; IR filter; night telescope; thermosensitive detector; non-linear chromophore; biomacerial; tissue engineering scaffold; ferroelectric material; artificial muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               radiation, and in optical applications e.g., as matrices to align non-
linear chromophores which are useful in creating materials for second
order non-linear orbits. (II) is useful in hydrogen catalysis, as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               coatings for biomaterials, scaffolds for tissue engineering, ferroelectric materials, artificial muscles, switching devices, et sequence represents a peptide used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 44; DB 7; Length 21; Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 2.6;
0; Mismatches
                                                                                                                                                                                                                                                                                        Claim 31; SEQ ID NO 67; 91pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Self-assembling polymer peptide #197.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADJ81342 standard; peptide; 21 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
04-JUN-2002; 2002US-0385809P
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Best Local Similarity 84.6'
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                                                                                                Valluzzi R, Kaplan DL;
                                              (TUFT ) TUFTS COLLEGE.
                                                                                                                                            WPI; 2003-671392/63.
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Gaps

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etc. This

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The invention relates to a minibility block, a block for triggering self-
cabricating block and a solubilizing block, a block for triggering self-
fabrication by external or environmental conditions, and a block for
fabrication by external or environmental conditions, and a block for
incorporating turns in the polymer or for providing sites for chemical
can self-fabricate to form 3-dimensional material having long-range
can self-fabricate to form 3-dimensional material having long-range
corder, and where (1) has glycine content of at least 20%. (1) is useful
corder, and administering the self-fabricating material incorporating
corder, and administering the self-fabricating material incorporating
corder, and administering the self-fabricating acting
the drug. The drug is incorporated within layers of the self-fabricating
corder to mid infrared wavelength range which involves applying (1)
corder to mid infrared wavelength range which involves applying (1)
corder to mid infrared wavelength range which involves applying (1)
corder surface of the device (all claimed). (1) is useful for preparing
corder fluids (i.e., liquid crystals) in a variety of phases
corder form rigid materials. (1) can be used as structural transitions to
corder range ordered fluids (i.e., liquid crystal displays, and for producing high-performance compositions
corder range ordered fluids (i.e., liquid crystal transitions
corder range ordered fluids (i.e., liquid crystal transitions
corder range ordered fluids.
cordered fluids.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Miniblock polymer useful in nanolithographic processes, has self-fabricates fabricating block and solubilizing block, has glycine and self-fabricates to form 3-dimensional materials having long-range orders, in solution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     radiation, and in optical applications e.g., as matrices to align non-
linear chromophores which are useful in creating materials for second
order non-linear orbits. (II) is useful in hydrogen catelysis, as
coatings for biomaterials, scaffolds for tissue engineering,
ferroelectric materials, artificial muscles, switching devices, etc. The
sequence represents a peptide used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention relates to a miniblock polymer (I) comprising a self-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 198; 91pp; English
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                                                                                                                                                                                                    02-OCT-2001; 2001US-0326743P.
04-JUN-2002; 2002US-0385809P.
                                                                                                                                                       02-OCT-2002; 2002WO-US031375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Conservative
                                                                                                                                                                                                                                                                                                                                      Valluzzi R, Kaplan DL;
                                                                                                                                                                                                                                                                                     (TUFT ) TUFTS COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-671392/63.
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                                                WO2003056297-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21 AA;
                                                                                                 10-JUL-2003
Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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The invention relates to a novel cell attachable polypeptide comprising an auxiliary amino acid sequence (Y) chemically bonded to a cell attachable minimal amino acid sequence (X), where (Y) contains 1-50 amino acids and the sum total content of Gly and Ala in (Y) is 42-100% with caids and the sum total content of Gly and Ala in (Y) is 42-100% with crespect to the total number of amino acids in (Y). The polypeptide of the invention may be utilized during culturing of cells for use in various experiments, including toxicity studies, gene transfer and production of useful substances such as cytokines, thrombolytic agents, vaccines, culturing cells for transplantation, particularly, transplantation of skin, cranial bones, muscles, skin tissue, bone marrow and retina. The cylypeptide exhibits extremely potent cell adhesion properties and can attach cells, such as NHDF and VERO cells, more efficiently onto a base catach relative to conventional methods. The polypeptide also exhibits conveniently. The current sequence is that of a cell attachment-related conveniently. The current sequence is that of a cell attachment-related auxillary peptide of the invention.
                                                                                                                                                                        Cell attachable polypeptide useful for culturing cell, comprises auxiliary amino acid sequence having specific amount of Gly and Ala, chemically bonded to cell attachable minimal amino acid sequence,
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Pred. No. 2.8;
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0; Mismatches
                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 54; 20pp; Japanese
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                                21-MAY-2003; 2003JP-00144125.
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                                                                             (SANN ) SANYO CHEM IND LTD.
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Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a novel cell attachable polypeptide comprising an auxiliary amino acid sequence (Y) chemically bonded to a cell attachable minimal amino acid sequence (X), where (Y) contains 1-50 amino acids and the sum total content of Gly and Ala in (Y) is 42-100% with respect to the total number of amino acids in (Y). The polypeptide of the invention may be utilized during culturing of cells for use in various experiments, including toxicity studies, gene transfer and production of useful substances such as cytokines, thrombolytic agents, vaccines, hormones and antibiotics. Furthermore, the polypeptide may be useful for culturing cells for transplantation, particularly, transplantation of skin, cranial bones, muscles, skin tissue, bone marrow and retina. The polypeptide exhibits extremely potent cell adhesion properties and can attach cells, such as NHDF and VERO cells, more efficiently onto a base material, relative to conventional methods. The polypeptide also exhibits high heat stability, thus sterilization in autoclaves can be performed conveniently. The current sequence is that of a cell attachment-related auxillary peptide of the invention.
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                                                  cell attachment; cell culture; transplantation; vaccine; antibiotic
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Cell attachment-related auxillary peptide - SEQ ID 53.
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0; Mismatches
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                                                                                                                                               JP2005002106-A.
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                                                                                                    Synthetic
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Best Local
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Gaps

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2; Indels

an auxiliary amino acid sequence (X) chemically bonded to a cell attachable minimal amino acid sequence (X), where (Y) contains 1-50 amino acids and the sum total content of Gly and Ala in (Y) is 42-100\$ with respect to the total number of amino acids in (Y) is 42-100\$ with respect to the total number of amino acids in (Y). The polypeptide of the invention may be utilized during culturing of cells for use in various experiments, including toxicity studies, gene transfer and production of useful substances such as cytokines, thrombolytic agents, vaccines, corners, rannial bones, muscles, such the polypeptide may be useful for culturing cells for transplantation, particularly, transplantation of skin, crannial bones, muscles, skin tissue, bone marrow and retina. The polypeptide exhibits extremely potent cells, more efficiently onto a base material, relative to conventional methods. The polypeptide also exhibits high heat stability, thus sterilization in autoclaves can be performed conveniently. The current sequence is that of a cell attachment-related auxillary peptide of the invention. The invention relates to a novel cell attachable polypeptide comprising Disclosure; SEQ ID NO 55; 20pp; Japanese. 

Sequence 23 AA;

Gaps ; 0 Score 44; DB 9; Length 23; Pred. No. 2.9; 2; Indels Pred. No. 2.9; 0; Mismatches 100.08; 11; Conservative Query Match Best Local Matches

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ADV78592 standard; peptide; 24 AA.

(first entry) 24-MAR-2005 Cell attachment-related auxillary peptide - SEQ ID 56.

cell attachment; cell culture; transplantation; vaccine; antibiotic.

Synthetic.

JP2005002106-A.

06-JAN-2005

20-MAY-2004; 2004JP-00150510.

21-MAY-2003; 2003JP-00144125.

(SANN ) SANYO CHEM IND

WPI; 2005-053150/06.

Cell attachable polypeptide useful for culturing cell, comprises auxiliary amino acid sequence having specific amount of Gly and Ala, chemically bonded to cell attachable minimal amino acid sequence, alternatively.

Disclosure; SEQ ID NO 56; 20pp; Japanese.

The invention relates to a novel cell attachable polypeptide comprising an auxiliary amino acid sequence (Y) chemically bonded to a cell stateachable minimal amino acid sequence (X), where (Y) contains 1-50 amino acids and the sum total content of Gly and Ala in (Y) is 42-100% with respect to the total number of amino acids in (Y). The polypeptide of the invention may be utilized during culturing of cells for use in various experiments, including toxicity studies, gene transfer and production of useful substances such as cytokines, thrombolytic agents, vaccines, 

hormones and antibiotics. Furthermore, the polypeptide may be useful for culturing cells for transplantation, particularly, transplantation of skin, cranial bones, muscles, skin tissue, bone marrow and retina. The polypeptide exhibits extremely potent cell adhesion properties and can attach cells, such as NHDF and VERO cells, more efficiently onto a base material, relative to conventional methods. The polypeptide also exhibits high heat stability, thus sterilization in autoclaves can be performed conveniently. The current sequence is that of a cell attachment-related auxillary peptide of the invention. 8888888888888

Sequence 24 AA;

Gaps .; 0 100.0%; Score 44; DB 9; Length 24; 2; Indels Pred. No. 3; 0; Mismatches 84.68; 11; Conservative Query Match Best Local Similarity Matches

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ð g RESULT 39

ABG95821 standard; peptide; 25 AA. ABG95821

ABG95821;

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(first entry) 09-DEC-2002

Transmembrane domain peptide #1.

Transmembrane domain; human; cow; papillomavirus; HIV; psoriasis; composite receptor; cell proliferative disorder; cystic fibrosis; T-cell lymphotropic virus; human immunodeficiency virus; cytostatic; antipsoriatic; respiratory.

Unidentified.

WO200262823-A2

15-AUG-2002.

01-FEB-2002; 2002WO-US002837.

02-FEB-2001; 2001US-0265624P

(UYYA ) UNIV YALE.

ď Bray-Ward Rabinovich P,

WPI; 2002-723154/78.

ö New isolated peptide and fusion peptide, useful for inserting proteins peptides and nucleic acids into the cell membrane in vivo or in vitro that may be useful in treating cancer or other proliferative disorders, e.g. psoriasis. 

Claim 5; Page 62; 111pp; English.

The invention relates to an isolated peptide used in compositions for expressing a composite receptor on the cell surface. The peptide is a fusion peptide comprising at least one cell penetrating domain which is linked to at least one transmembrane domain or to an adapter domain capable of binding to a molecule, where the orientation of the cell penetrating domain is independent of the orientation of the transmembrane or adapter domain. The peptides are useful for inserting proteins or peptides such as regulatory factors, enzymes, antibodies, drugs or toxins and nucleic acids such as DNA or RNA into the cell membrane either in vivo or in vitro, that may be useful in inhibiting or treating diseases or disorders, which could benefit from the addition of surface receptors to cells, such as cancer and other proliferative disorders like psoriaeis and cystic fibrosis. The methods are useful for identifying agents that modulate the activity of a receptor protein and for preparing the fusion

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The invention relates to a miniblock polymer (I) comprising a self-
fabricating block and a solubilizing block, a block for triggering self-
c fabrication by external or environmental conditions, and a block for
incorporating turns in the polymer or for providing sites for chemical
modifications, has a molecular weight of 1000-300000 and, in solution,
c an self-fabricate to form 3 dimensional material having long-range
corder, and where (I) has glycine content of at least 20%. (I) is useful
for controlled delivery of a drug which involves incorporating
within (I), and administering the self-fabricating material incorporating
material. (II) is useful for modifying the optical response of a device
in the near to mid infrared wavelength range which involves applying (II)
to the surface of the device (all claimed). (I) is useful for preparing
to the surface of the device (all claimed). (I) is useful for preparing
to forms which can then whom where the surface of the control of the surface of the device (all claimed).
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peptide. This sequence represents a transmembrane domain of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Miniblock polymer useful in nanolithographic processes, has self-fabricates fabricating block and solubilizing block, has glycine and self-fabricates to form 3-dimensional materials having long-range orders, in solution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        miniblock polymer; optical response; mid infrared wavelength range; long range ordered fluid; liquid crystals; nanolithography; IR sensor; IR sensor; IR felter; night telescope; thermosensitive detector; non-linear chromophore; biomaterial; tissue engineering scaffold; ferroelectric material; artificial muscle;
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No. 3.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Self-assembling polymer peptide #198.
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                                                                          ch 100.0%;
1 Similarity 84.6%;
11; Conservative · 0
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                                                                                                  Local Similarity
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                                       Sequence 25 AA;
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polymer (II) is useful for modifying and improving performance of IRsensitive devices, IR sensors, IR filters, night telescopes and thermosensitive detectors. (II) can be used for preparing films, membranes or coatings that absorb specific wavelengths of infrared radiation, and in optical applications e.g., as matrices to align nonlinear chromophores which are useful in creating materials for second order non-linear orbits. (II) is useful in hydrogen catalysis, as coatings for biomaterials, scaffolds for tissue engineering, ferroelectric materials, artificial muscles, switching devices, etc. The sequence represents a peptide used in the method of the invention.
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Pred. No. 3.2;
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Job time : 99.4177 secs
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e version 5.1.9 3 - 2006 Biocceleration Ltd. sw model 22:48:41 ; Search time 14.8101 Seconds (without alignments) 84.457 Million cell updates/sec 6.5 6.3 residues sen parameters: 283416 summaries	ults predicted by chance to have a the score of the result being printed, the total score distribution.	PERAC4 - human  FREAC4 - human  Mi-2 autoantigen 2  finger protein sob  SH3 domains-contai  abdominal segment  female sterile hom  hypothetical prote  hypothetical protein  probable MASH-2 pr  achaete scute prot  LMO protein - frui  homeocite protein H  genomic screen hom  paired type homeob  homeocite protein H  sinc-finger protein  probable homeobox  probable homeobox  probable homeobox  probable homeocom  homeotic protein H  sinc-finger protein  probable homeocom  homeotic protein H  ball DNA-binding p  transcription fact  homeotic protein H  ball DNA-binding p  transcription fact  homeotic protein e  zinc-finger protein  ball basic helix-loop-h
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ALIGNMENTS

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C;Species: Drosophila melanogaster
C;Date: 21-Sep-1993 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: A46221; S22026
R;Barker, D.D; Wang, C.; Moore, J.; Dickinson, L.K.; Lehmann, R.
Genes Dev. 6, 2312-2226, 1992
A;Title: Pumilio is essential for function but not for distribution of the Drosophila ak
A;Reference number: A46221; MUID:93093466; PMID:1459455
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R;Macdonald, P.M.
Bibmitted to the EMBL Data Library, October 1991
A;Reference number: $22026
A;Accession: $22026
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A;Molecule type: mRNA
A;Residues: 1-361,'A',363-1102,'R',1104-1405,'KN',1408-1495,'V',1497-1518,'S',1520-1533
A;Cross-references: UNIPARC:UPI00001329FD; EMBL:X62589; NID:98393; PID:98394
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C.Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
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                                                                      Length 577;
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R;Tapon, N.; Nagata, K.; Lamarche, N.; Hall, A.
EMBO J. 17, 1395-1404, 1998
A;Reference number: Z16552; MUID:98151363; PMID:9482736
A;Accession: T09071
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A;Molecule type: mRNA
A;Residues: 1-892 <TAP>
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Pred. No. 26;
0; Mismatches
                                                                  Score 47; DB 2;
Pred. No. 18;
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0; Mismatches
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Pred. No.
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A, Cross-references: FlyBase:FBgn0003165
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Conservative (
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Local Similarity 92.3%;
es 12; Conservative
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Matches 12, Conserv
C; Keywords: zinc finger
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A,Status: preliminary
A,Molecule type: mRNA
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Cispecies: Drosophila melanogaster
Cispecies: Drosophila melanogaster
Cispecies: Drosophila melanogaster
Cispace: O4-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
Ciscossion: S72227
R.Hart, M.C.; Wang, L.; Coulter, D.E.
Genetics 144, 171-182, 1996
A;Title: Comparison of the structure and expression of odd-skipped and two related genes
A;Reference number: S72227
A;Reference number: S72227
A;Reference number: S72227
A;Reference number: S7227
A;Residues: 1-57
A;Residues: 1-58
A;Residues: 1-58
A;Residues: 1-58
A;Residues: 1-58

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C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 05-Nov-1999
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 05-Nov-1999
C;Accession: I38558
B;Ge, O; Nilasena, D.S.; O'Brien, C.A.; Frank, M.B.; Targoff, I.N.
J. Clin. Invest. 96, 1730-1737, 1995
A;Title: Molecular analysis of a major antigenic region of the 240-kD protein of Mi-2 A;Reference number: I38558; MUID:96013633; PMID:7560064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: I38558
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule type: mRNN
A;Residues: 1-530 «RES»
A;Cross-references: UNIPARC:UPI000016A09A; EMBL:U08379; NID:g761717; PIDN:AAC50228.1;
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C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Oct-2004
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138558 Mi-2 autoantigen 240 kDa protein - human (fragment)

290 ALFAAAAAAAA 302

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1 AAFAAAAAAAA 13

DB 2; Length 465; 1; Indels

Score 49; DB 2; Pred. No. 8.4; 0; Mismatches

90.7%; illarity 92.3%; Conservative 0

Local Similarity nes 12; Conserv

Query Match Best Local \$ Matches

C,Genetics: A,Gene: FREAC-4 F,125-216/Domain: fork head DNA-binding domain homology <FHD>

submitted to the EMBL Data Library, June 1996
A,Reference number: H01646
A,Accession: G02738
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1-465 <ENE>

C, Accession: G02738 R; Enerback, S.

- human

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Score 47; DB 2; Length 530; Pred. No. 17; 0; Mismatches 1; Indels

Best Local Similarity 92.3%; Matches 12; Conservative

AAVAAAAAAAA 99 1 AAFAAAAAAAA 13

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1; Indels

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C;Species: Homo sapiens (man)
C;Date: 16-Uul-1999 #text_change 02-Sep-2000
C;Date: 16-Uul-1999 #sequence_revision 16-Uul-1999 #text_change 02-Sep-2000
C;Accession JC5954
R;Tanaka, M.; Tanaka, T.; Harata, M.; Suzuki, T.; Mitsui, Y.
Biochem. Biophys. Res. Commun. 243, 531-537, 1998
A;Title: Triplet repeat-containing ribosomal protein L14 gene in immortalized human endth A;Reference number: JC5954; MUID:98153799; PMID:9480843
A;Accession: JC5954
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPARC:UP1000004E622; DDBJ:D87735; NID:g1620021; PIDN:BAA13443.1; E
C;Superfamily: rat ribosomal protein L14
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Cispecies: Rattus norvegicus (Norway rat)
Cibate: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
CiAccession: 511563
RiJohnson, J.E.; Birren, S.J.; Anderson, D.J.
Nature 346, 858-861, 1990
A;Title: Two rat homologues of Drosophila achaete-scute specifically expressed in neuror A;Reference number: 511562; MUID:90363294; PMID:2392153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:P19359; UNIPARC:UP10000047567; EMBL:X53725; NID:956630; PIDN
C;Keywords: DNA binding
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C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 09-Jul-2004
C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 09-Jul-2004
C;Accession: A48279
R;Ball, D;M.; Azzoli, C.G.; Baylin, S.B.; Chi, D.; Dou, S.; Donis-Keller, H.; Cumaraswan Proc. Natl. Azzoli, C.G.; Baylin, S.B.; Chi, D.; Dou, S.; Donis-Keller, H.; Cumaraswan A;Title: Identification of a human achaete-scute homolog highly expressed in neuroendocz A;Reference number: A48279; MUID:93296195; PMID:8390674
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A;Molecule type: mRNA
A;Residues: 1-230 «RES»
A;Cross-references: UNIPROT:PS0553; UNIPARC:UP10000047566; GB:L08424; NID:g306459; PID:g
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                                                                                                                                                                                                                                                                                                                                                                                                                           Score 46; DB 2;
Pred. No. 11;
0; Mismatches
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Pred. No. 12;
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Pred. No. 12;
0; Mismatches
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92.3%;
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92.3%;
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150 AAAAAAAAAAA 162
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Best Local Similarity 92.3
Matches 12; Conservative
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                             ribosomal protein L14 - human
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Best Local Similarity
Matches 12; Conserv
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                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
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Matches
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A;Cross-references: UNIPROT:P13709; UNIPARC:UPI000012AC6C; EMBL:M23221; NID:g157452; PID
                                                                                                                                                                        female sterile homeotic protein, 205K - fruit fly (Drosophila melanogaster)
NyAlternate names: membrane protein fsh, 205K
NyContains: female sterile homeotic protein, 110K
C;Species: Drosophila melanogaster
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 31-Dec-2004
C;Accession: A43742; B43742
R;Haynes, S.R.; Mozer, B.A.; Bhatia-Dey, N.; Dawid, I.B.
Dev. Biol. 134, 246-257, 1989
A;Title: The Drosophila fsh locus, a maternal effect homeotic gene, encodes apparent rance number: A43742; MUID:89276730; PMID:2567251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Keywords: alternative splicing; transmembrane protein
F;1-2038/Product: female sterile homeotic protein, 205K #status predicted <MA2>
F;1-1106/Product: female sterile homeotic protein, 110K #status predicted <MA7>
F;59-116/Domain: bromodomain homology <BRO1>
F;59-150/Domain: bromodomain homology <BRO2>
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C;Species: Homo sapiens (man)
C;Date: 23-Jul-1999 #text_change 09-Jul-2004
C;Accession: T12547
R;Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, June 1999
A;Accession: T12547
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A;Molecule type: mRNA
A;Residues: 1-150 <OTT>
A;Cross-references: UNIPROT:Q9Y4M1; UNIPARC:UPI0000071DDD; EMBL:AL080235
A;Experimental source: adult uterus; clone DKFZp586E1621
C;Genetics:
A;Note: DKFZp586E1621.1
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Pred. No. 50;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-1106 <HA2>
A;Cross-references: UNIPARC:UPI000017A10F; EMBL:M23222
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Pred. No. 8.4;
0; Mismatches
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92.3%;
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Best Local Similarity 92.3
Matches 12; Conservative
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1 AAFAAAAAAAAA
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Best Local Similarity
Matches 12; Conserv
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A;Cross-references: UNIPARC:UPI0000024E69; GB:S79041; NID:g1042008; PIDN:AAB34947.1; PID
C;Genetics:
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R;Yokoyama, M.; Nishi, Y.; Yoshii, J.; Okubo, K.; Matsubara, K.
R;Yokoyama, M.; Nishi, Y.; Yoshii, J.; Okubo, K.; Matsubara, K.
A;Title: Jdentification and cloning of neuroblastoma-specific and nerve tissue-specific A;Reference number: JC5272; MUID:97191543; PMID:9039501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Molecule type: mRNA
A,Residues: 1-314 < YOK>
A,Residues: 1-314 < YOK>
A,Residues: 1-314 < YOK>
A,Cross-references: UNIPROT:Q99453; UNIPARC:UPI0000131D16; DDBJ:DBJ:DB2344; NID:g1841337; PI
C,Comment: This protein is a transcriptional repressor involved in regulating gene expre
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;99-155/Domain: homeobox homeology < HOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Accession: S16318
A, Molecule type: DNA
A, Residues: 1-323 <12P>
A, Cross-references: UNIPROT. P23813; UNIPARC: UPI0000029F10; EMBL: X60761; NID: 951420; PIDI
R, Gerard, M.; Duboule, D.; Zakany, J.
EMBO J. 12, 3539-3550, 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: UNIPARC:UPI0000029F10; EMBL:X71422; NID:g397508; PIDN:CAAS0553.1; A; Cross-references: UNIPARC:UPI0000029F10; EMBL:X71422; NID:g397508; PIDN:CAAS0553.1; R; Takada, S.; Cook, M.; Kramlauf, R.; McMahon, A.P. submitted to the EMBL Data Library, May 1991 A; Describtion: Genomic sequence of mouse Hox-4.6. A; Reference number: S57443
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Nyalternate names: homeotic protein Hoxd-11
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Oct-2004
C;Accession: S16318; S40403; S57443
R;Izplaua-Belmonte, J.C.; Falkenstein, H.; Dolle, P.; Renucci, A.; Duboule, D.
BMBO J. 10, 2279-2289, 1991
A;Title: Murine genes related to the Drosophila AbdB homeotic gene are sequentially A;Reference number: S16317; MUID: 91293104; PMID:1676674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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C;Species: Homo sapiens (man)
C;Date: 16-Apr-1997 #sequence_revision 09-May-1997 #text_change 05-Oct-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                              A;Gene: Gsh-2
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;204-260/Domain: homeobox homology <HOX>
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Pred. No. 15;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                               Length 305;
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Pred. No. 15;
0; Mismatches
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Best Local Similarity 92.3%;
Matches 12; Conservative
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A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-323 <GER>
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C;Species: Mus musculus (house mouse)
C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 09-Jul-2004
C;Accession: A43562
R;Izpisua-Belmonte, J.C.; Dolle, P.; Renucci, A.; Zappavigna, V.; Falkenstein, H.; Dubou Development 110, 733-745, 1990
A;Title: Primary structure and embryonic expression pattern of the mouse Hox-4.3 homeobc A;Reference number: A43562; MUID:91209232; PMID:1982431
A;Accession: A43562
A;Accession: A43562
A;Accession: A43562
A;Accession: A63562
A;A
                                                                                                                                                                                                                                                                                                                                                                   C;Species: Drosophila sp.
C;Species: Drosophila sp.
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 15-Mar-2004
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 15-Mar-2004
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 15-Mar-2004
R;Zhu, T.H.; Bodem, U.; Keppel, E.; Paro, R.; Royer-Pokora, B.
Oncogene 11, 1283-1290, 1995
A;Title: A single ancestral gene of the human LIM domain oncogene family LMO in Drosophi
A;Pitle: A single ancestral gene of the human LIM domain oncogene family LMO in Drosophi
A;Pitche: A single ancestral gene of the human LIM conceptual translation
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Molecule rype: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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C;Superfamily: homeotic protein Hox A7; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;196-252/Domain: homeobox homology <HOX>
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A;Molecule type: mRNA
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Pred. No.
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Best Local Similarity 92.3%;
Matches 12; Conservative
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homeotic protein Hox D8
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S61522
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-334 <KUR>
A;Residues: 1-334 <KUR>
A;Cross-references: UNIPARC:UPI000016A2D0; EMBL:U48250; NID:g1199656; PIDN:AAC72247.1;
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A,Modecule type: mRNA
A,Residues: 1-364 <-RES>
A,Cross-references: UNIPROT:Q60554; UNIPARC:UP100001301FA; EMBL:X81409; NID:g587466; PII
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Plant J. 7, 927-938, 1995
A;Title: Alternative RNA products from a rice homeobox gene.
A;Reference number: Z15126; MUID:95322999; PMID:7599652
A;Accession: T03875
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A;Cross-references: UNIPROT:P93423; UNIPARC:UPI0000AB610; EMBL:D49704; NID:g1805615; Pi
A;Experimental source: cv. Nipponbare
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C;Species: Mesocricetus auratus (golden hamster)
C;Daccession: 149188
B;Rudnick, A.; Ling, T.Y.; Odagiri, H.; Rutter, W.J.; German, M.S.
Proc. Natl. Acad. Sci. U.S.A. 91, 12203-12207, 1994
A;Title: Pancreatic beta cells express a diverse set of homeobox genes.
A;Reference number: 148185; MUID:95083670; PMID:7991607
                                                                                                                                                                                          C,Species: Homo sapiens (man)
C,Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999
C,Accession: G02409
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C.Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-Oct-2004
C.Accession: T03875
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A;Reference number: H01212
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Pred. No. 16;
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Pred. No. 17;
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92.3%;
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Best Local Similarity 92.3%;
Matches 12; Conservative
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Best Local Similarity 92.33
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C;Species: Mesocricetus auratus (golden hamster)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 05-Apr-1995
C;Accession: B47236
R;Kennedy, G.C.; Rutter, W.J.
Rycor. Natl. Acad. Sci. U.S.A. 89, 11498-11502, 1992
A;Title: Pur-1, a zinc-finger protein that binds to purine-rich sequences, transactivate
A;Reference number: A47236; MUID:93087555; PMID:1454839
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A;Accession: S57443
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Kossereferences: WNDFDECGPSAAS',1-323 <TAK>
A;Cross-references: UNIPARC:UP1000026A38; EMBL:X60395; NID:g871427; PIDN:CAA42943.1; I;Genetics: Hoxd-11
A;Genetics: Hoxd-11
A;Genetics: 2461
A;Introns: 2461
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;252-308/Domain: homeobox homology <HOX>
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A;Title: BVX2, a human homeobox gene homologous to the even-skipped segmentation gene, A;Reference number: A39065; MUID:91257849; PMID:1675198
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homeotic protein EVX2 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 31-Dec-2004
C;Accession: A39065
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C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;46-102/Domain: homeobox homology <HOX>
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Pred. No. 16;
0; Mismatches 1; Indels
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Pred. No. 15;
0; Mismatches 1; Indele
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16;
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A;Cross-references: UNIPARC:UPI000017C615
A;Experimental source: Insulinoma cell line T
A;Experimente extracted from NCBI backbone (NCBIP:119832)
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Pred. No. 16;
0; Mismatches
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92.3%;
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                                                                                                                                                                                                                                                                    ch 85.2%;
1 Similarity 92.3%;
12; Conservative
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Best Local Similarity 92.3
Matches 12; Conservative
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Best Local Similarity
Matches 12; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
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B47236
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Length 378, Indels

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sequence extracted from NCBI backbone (NCBIN:102964, NCBIP:102966)
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Pred. No. 18;
0; Mismatches
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A;Residues: 311-401 <JO2>
A;Cross-references: UNIPARC:UP1000017A2B0
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                                                                                                                        A; Cross-references: FlyBase: FBgn0013115
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                                                                                                                                                                                                                                                                                                                                                           1 AAFAAAAAAAA 13
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                                                                                                                                                                                                                                                                                 12; Conservative
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Best Local Similarity
Matches 12; Conserv
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Best Local Similarity
                                                                                             A,Gene: FlyBase:Dvir/h
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                       A;Note: sec
C;Genetics
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                                                                                                                                                                                                                                                                                    Matches
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A; Residues: 174/3; 215/1; 277/3; 321/3; 367/2
C; Residues: 174/3; 215/1; 277/3; 215/1; 277/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31/3; 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable homeobox protein OSH45, splice form OSH44 [similarity] - rice
N.Contains: probable homeobox protein OSH45, splice form OSH42
C;Species: Oryza sativa (rice)
C;Species: Oryza sativa (rice)
C;Date: 32.Apr-1999 #squence_revision 23.Apr-1999 #text_change 05-Oct-2004
C;Accession: T03874; T03876
R;Tamaoki, M.; Tsugawa, H.; Minami, E.; Kayano, T.; Yamamoto, N.; Kano-Murakami, Y.; Mat Plant J. 7, 927-938, 1995
A;Title: Alternative RNA products from a rice homeobox gene.
A;Reference number: Z19126; MUID:95322999; PMID:7599652
A;Accession: T03874
                                                                                                                                    A;Introns: 174/3; 215/1; 277/3; 321/3; 367/2
C;Keywords: alternative initiators; alternative splicing; DNA binding; homeobox; nucleus
F;291-352/Domain: homeobox homology <HOX>
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basic helix-loop-helix transcription repressor H - fruit fly (Drosophila virilis)
basic helix-loop-helix transcription repressor H - fruit fly (Drosophila virilis)
C;Species: Drosophila virilis
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 02-Jul-1998
C;Accession: A4443
K;Wainwright, S.1., 2475-2483, 192
Mol. Cell Biol. 12, 2475-2483, 192
A;Title: Point mutations in the Drosophila hairy gene demonstrate in vivo requirements A;Reference number: A4443; MUID:92269819; PMID:1588951
A;Accession: A4443
A;Accession: A4443
A;Accession: A4443
A;Accession: A4443
A;Accession: A4443
A;Accides: 11378 cWal>
A;Accession: A4443
A;Accides: 11378 cWal>
A;Accides: 11378 cWal>
A;Accides: 12378 cWal>
A;Accides: sequence inconsistent with the nucleotide translation
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A;Cross-references: UNIPROT:P93424; UNIPARC:UPI00000AA5D5; EMBL:D49704; NID:g1805615;
A;Experimental source: cv. Nipponbare; splice form OSH44
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Pred. No. 17;
                                                                                                                                                                                                                                                                                        Length 374
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                       C:Comment: For alternative splice forms, see PIR:T03874 C;Genetics:
                                                                                                                                                                                                                                                                                            DB 2;
17;
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                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                Score 46;
Pred. No.
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92.3%;
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92.3%;
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Best Local Similarity 92..
Best Local 2; Conservative
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                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 92.3
Matches 12; Conservative
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                                                                                                                 A;Gene: H45
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C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Date: 01-Dec-1993 Heaquence_revision 18-Nov-1994 #text_change 31-Dec-2004
C.Date: 01-Dec-1993 Haggan A.S6629; A.24778
C.Accession: A48423; S13009; A.S6629; A.24778
Exilogan, C.; Hanks, M.C.; Noble-Topham, S.; Nallainathan, D.; Provart, N.J.; Joyner, A.L Dev. Genet. 13, 345-358, 1992
A;Title: Cloning and sequence comparison of the mouse, human, and chicken engrailed gene A;Reference number: A48423; MUID:93185339; PMID:1363401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; not compared with conceptual translation
A;Status: preliminary; not compared with conceptual translation
A;Residues: 1-401 <LOG>
A;Reperimental source: CD-1, embryo
A;Experimental source: CD-1, embryo
A;Reperimental source: CD-1, embryo
A;Note: sequence extracted from NCBI backbone (NCBIP:126620)
B;Holland, P-W-H, Williams, N-A.
B;Holland, P-W-H, Wil
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A;Molecule type: nucleic acid
A;Cross-references: UNIPARC:UPI000017A2AF
B;Joyner, A.L.; Martin, G.R.
Genes Dev. 1, 29-38, 1987
A;Title: En-1 and En-2, two mouse genes with sequence homology to the Drosophila engrail
A;Reference number: A91620; MUID:88112776; PMID:2892757
A;Accession: A26629
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A;Residues: 278-401 <JOY>
A;Cross-references: UNIPARC:UPI000016CA7C; GB:Y00201; GB:M11987; NID:g49587; PIDN:CAA68:
R;JOYDER: A.L.; Kornberg, T.; Coleman, K.G.; Cox, D.R.; Martin, G.R.
Cell 43, 29-37, 1985
A;Title: Expression during embryogenesis of a mouse gene with sequence homology to the I
A;Reference number: A24778; MUID:86079501; PMID:2416459
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C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;313-369/Domain: homeobox homology <HOX>
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engrailed homeodomain-containing protein En-1 - mouse
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Pred. No. 18;
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A;Reaiduea: 1-443 <STE1>
A;Cross-references: UNIPROT:P41225; UNIPARC:UP1000003F546; EMBL:X71135; NID:g468790; PI
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Dev. Biol. 151, 273-287, 1992
A.fitle. Analysis of mouse Evx genes: Evx-1 displays graded expression in the primitive
A.Reference number: A43915; MUID:92249649; PMID:1349539
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A;Residues: 1-475 < AUS5.
A;Cross-references: UNIPROT:P49749; UNIPARC:UPI0000020BC6; GB:S34322; NID:G249137; PIDN
A;Note: sequence extracted from NCBI backbone (NCBIN:100478, NCBIN:100480, NCBIN:100482
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Proc. Natl. Acad. Sci. U.S.A. 89, 11498-11502, 1992
Proc. Natl. Acad. Sci. U.S.A. 89, 11498-11502, 1992
A;Title: Pur.1, a zinc-finger protein that binds to purine-rich sequences, transactivat. A;Reference number: A47236; MUID:93087555; PMID:1454839
A;Accession: A47236
                                      A,Accession: 138242
A,Status: preliminary: translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Molecule type: mRNA
A,Residues: 143-156, P, 160-218 <STE2>
A,Cross-references: UNIPARC:UP10000071C8C; EMBL:X71137; NID:g468793; PIDN:CAA50467.1;
C,Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Mus musculus (house mouse)
C;Date: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 31-Dec-2004
C;Accession: A43915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Mus musculus (house mouse)
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 05-Apr-1995
C;Accession: A47236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A43915
homeotic protein even-skipped homolog Evx-2 - mouse
N/Alternate names: mesodermal cell dorsoventral fates determinator Evx-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: evx-2
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;192-248/Domain: homeobox homology <HOX>
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 443;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 46; DB 2; Length 475;
Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
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A;Experimental source: islet cell line beta TC3
A;Note: sequence extracted from NCBI backbone (NCBIP:119831)
                                                                                                                                                                                                                                               A,Gene: GDB:SOX3; SOX-3; SOXB
A;Cross-references: GDB:250376; OMIM:313430
A;Map position: XG2-Kq27
C;Superfamily: human SOX3 protein; HMG box homology
F;136-211/Domain: HMG box homology < HMG>
                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 46; DB 1
Pred. No. 20;
0; Mismatches
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92.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  234 AAAAAAAAAAA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      359 AASAAAAAAAAA 371
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Best Local Similarity 92.3°
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Best Local Similarity
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DZIP DNA-binding protein - parsley
C;Species: Petroselinum crispum (parsley)
C;Species: Petroselinum crispum (parsley)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 31-Dec-2004
C;Accession: Ti4911
R;Kircher, S.; Ledger, S.; Hayashi, H.; Weisshaar, B.; Schafer, E.; Frohnmeyer, H. Mol. Gen. Genet. 257, 595-605, 1998
A;Kircher, S.; Ledger, S.; Hayashi, H.; Weisshaar, B.; Schafer, E.; Frohnmeyer, H. Mol. Title: CPRF4a, a novel plant bZIP protein of the CPRF family: comparative analysis of A;Reference number: Z18261; MUID:98265918; PMID:9604882
A;Accession: T14911
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-420 <KIR>A;Cross references: UNIPROT:082037; UNIPARC:UPI00000A12C8; EMBL:X10810; NID:93336904; PI
                   C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 31-Dec-2004
C;Accession: A53662
R;Harrison, K.A.; Druey, K.M.; Deguchi, Y.; Tuscano, J.M.; Kehrl, J.H.
J. Biol. Chem. 269, 19968-19975, 1994
A;Titles: A novel human homeobox gene distantly related to proboscipedia is expressed in A;Reference number: A53662; MUID:94327547; PMID:7914194
                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-403 <HAR>
A;Cross-references: UNIPARC:UPI000017A29E; GB:U07663
A;Note: the nucleotide sequence and conceptual translation as given are self-consistent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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A;Note: CPRF4b
C;Superfamily: BZIP G-box-binding protein; fos/jun DNA-binding domain homology
C;Keywords: DNA binding; leucine zipper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transcription factor SOX3 - human
NyAlternate names: SRY (sex determining region Y)-box 3
NyAlternate names: SRY (sex determining region Y)-box 3
NyAlternate names: SRY (sex determining region Y)-box 3
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: I38239; I38242; S67816
R;Stevanovic, M.; Lovell-Badge, R.; Collignon, J.; Goodfellow, P.N.
Hum. Mol. Genet. 2, 2013-2018, 1993
A;Title: SOX3 is an X-linked gene related to SRY.
A;Reference number: I38239; MUID: 94154672; PMID: 9111369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Map position: 1q41-1q42.1
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;244-300/Domain: homeobox homology <HOX>
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                                                                                                                                                                                                                                                                            A;Status: preliminary; not compared with conceptual translation A;Molecule type: DNA
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18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
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A,Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 85.2%; Score 46; DB Best Local Similarity 92.3%; Pred. No. 18; Matches 12; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GDB:136411; OMIM:142994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 AAAAAAAAAAA 133
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les 12; Conserv
   homeotic protein HB9
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Matches
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0; Mismatches

85.2%; 92.3%;

Query Match Best Local Similarity

Matches

JC7583 basic helix-loop-helix protein, DEC2 - human

96 AAAAAAAAAAA 108

a

1 AAFAAAAAAAA 13 12; Conservative

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R;Pyrc, J.J.; Moberg, K.H.; Hall, D.J.
Biochemistry 31, 4102-4110, 1992
A;Title: Isolation of a novel cDNA encoding a zinc-finger protein that binds to two site A;Reference number: A42170; MUID:92232709; PMID:1567856
A;Accession: A42170
                                                                                                                                                                                                                                                                                                                 A,Cross-references: UNIPROT:P56270; UNIPARC:UPI000017C427; GB:J05371
A;NOTE: it is uncertain whether Met-18 is the initiator or whether translation is initial R;Bossone, S.A.; Asselin, C.; Patel, A.J.; Marcu, K.B.
Proc. Natl. Acad. Sci. U.S.A. 89, 7452-7456, 1992
A;Title: MAZ, a zinc finger protein, binds to c-MYC and C2 gene sequences regulating tra A;Reference number: A46153; MUID:92366479; PMID:1502157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RHATCA, Y., Rovescalli, A.C.; Kim, Y.; Nirenberg, M. Proc. Natl. Acad. Sci. U.S.A. 89, 3280-3284, 1992
A;Title: Structure and evolution of four POU domain genes expressed in mouse brain. A;Reference number: S31223; MUID:92228768; PMID:1565620
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NyAlternate names: class III POU domain protein brain-1
C;Species: Mus musculus (house mouse)
C;Pate: 02-bec-1993 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C,Species: Homo sapiens (man)
C,Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 18-417,'L',419-494 <BOS>
A;Cross-references: UNIPARC:UPI000012ECF8; GB:M94046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 46; DB 2;
Pred. No. 22;
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Pred. No.
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F;267-291/Region: histidine/proline-rich
F;316-383/Domain: POU domain homology <POU>
F;402-458/Domain: homeobox homology <HOX>
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F;162-180/Region: histidine/proline-rich
F;186-201/Region: alanine-rich
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Local Similarity 92.3%;
es 12; Conservative
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F;207-230/Region: zinc finger
F;296-318/Region: zinc finger
F;354-346/Region: zinc finger
F;354-368/Region: zinc finger
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F,409-430/Region: zinc finger
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Best Local Similarity
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A; Residues: 1-494 < PYR>
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A;Status: preliminary
A;Molecule type: DNA
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Matches
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TO9084
phosphatidylinositol 3-kinase - Chlamydomonas reinhardtii (fragment)
CiSpecies: Chlamydomonas reinhardtii
CiSpecies: Chlamydomonas reinhardtii
CiSpecies: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
CiAccesaion: T09084
Rimolendii, A. July Irvine, R.F.
Rimolendii, A. July Irvine, R.F.
Rimolendii, Biol. 37, 53-66, 1998
A,Title: Inositide signalling in Chlamydomonas: Characterization of a phosphatidylinosit A; Reference number: Z16411; MUID:98281574; PMID:9620264
A; Reterence number: Z16411; MUID:98281574; PMID:9620264
A; A; Atatus: preliminary; translated from GB/EMBL/DDBJ
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A,Experimental source: strain cw-15
                                                                                                                                                                                                                                                                                                                                                                                                                                      C,Accession: UC7583
R;Fujimoto, K.; Shen, M.; Noshiro, M.; Matsubara, K.; Shingu, S.; Honda, K.; Yoshida, E. R;Fujimoto, K.; Shen, M.; Noshiro, M.; Matsubara, K.; Shingu, S.; Honda, K.; Yoshida, E. A;Title: Molecular cloning and characterization of DEC2, a new member of basic helix-lod A;Reference number: UC7583; MUID:21092582; PMID:11162494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        zinc finger protein MAZ – human (fragment)
N;Alternate names: MYC-associated zinc finger protein MAZ; zinc finger protein ZF87
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C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
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            Score 46; DB 2; Length 477;
Pred. No. 21;
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F:130-173/Domain: Orange #status predicted <ORA>
F:286-411/Region: alanine and glycine-rich #status predicted
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Score 46; DB 2; Pred. No. 21;

0; Mismatches

Query Match 85.2%; Best Local Similarity 92.3%; Matches 12; Conservative

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1 AAFAAAAAAAA 13

C; Keywords: transcription factor

A;Gene: dec2 A;Map position: 12p11.23-p12.1

A; Accession: JC7583

Pred. No. 22; 0; Mismatches

115 AATAAAAAAAAA 127

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RESULT 31

A42170

1 AAFAAAAAAAA 13

12, Conservative

Matches

Query Match Best Local Similarity

A; Introns: 265/3; 331/3; 370/3; 455/1; 481/3

A; Residues: 1-490 <MOL>

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homeotic protein engrailed - fruit fly (Drosophila melanogaster)

NyAlternate names: specific body pattern development protein

Sispeciaes: Drosophila melanogaster

C;Speciaes: Drosophila melanogaster

C;Date: 27-Nov-1985 #sequence revision 27-Nov-1985 #text change 09-Jul-2004

C;Accession: A90862; A93354; A03321; A03322; A25682; S03667

C;Accession: A90862; A93354; A03321; A03322; A25682; C33667

Cell 40, 37-43, 1985

A;Title: The engrailed locus of Drosophila: structural analysis of an embryonic transcraft analysic analysic of an embryonic transcraft analysic an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:P02836; UNIPARC:UPI000012CA13; GB:M10017; NID:g157363; PIDN R;Fjose, A.; McGinnis, W.J.; Gehring, W.J.
Rature 313, 284-289, 1985
A;Title: Isolation of a homoeo box-containing gene from the engrailed region of Drosoph A;Reference number: A93354; MUID:90114393; PMID:2481829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 447-485,'E',487-518,'WH' <FJO>
A;Cross-references: UNIPARC:UP100001145BF; GB:X01765; GB:K03059; NID:g8084; PIDN:CAA259
A;Note: the translation of the nucleotide sequence from Fig. 5 is shown, not the transl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBO J. 5, 3583-3589, 1986
A,Title: Sequence conservation in the protein coding and intron regions of the engraile A,Reference number: A91059; MUID:87161768; PMID:2881781
A,Contents: annotation; intron locations and sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R,Gay, N.J.; Poole, S.J.; Kornberg, T.B.

Nucleic Acids Res. 16, 6637-6647, 1988

A;Title: The Drosophila engrailed protein is phosphorylated by a serine-specific protein the Drosophila engrailed protein; PMID:2899884

A;Reference number: 803667; MUID:88289425; PMID:2899884

A;Contents: annotation; potential phosphorylation sites; homeobox domain

C;Comment: This protein specifies the body segmentation pattern.
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R;Kassis, J.A.; Poole, S.J.; Wright, D.K.; O'Farrell, P.H.
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Pred. No. 24;
0; Mismatches
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C.Keywords: DNA binding; embryo; homeobox;
F.26-53/Region: glutamine-rich
F.68-87/Region: alanine-rich
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A;Map position: 2R,62.0 (48A1-4)
A;Introns: 438/1; 470/3
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A;Status: translated from GB/EMBL/DDBJ
Moolecule type: DNA
A;Residues: 1-627 <ROU>
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92.3%;
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F;320-368/Region: serine-rich
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Best Local Similarity 92.3
Matches 12, Conservative
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A; Residues: 1-552 < POO>
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                                                                                                                                                                                                                                                                          DUSONOR AND ALGERIAGE ZINC-finger protein - human
NyAlternate names: MAZ protein
C,Spacias: Homo sapiens (man)
C;Spacies: Homo sapiens (man)
C;Bate: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 05-Nov-1999
C;Accession: JC5076
R;TSHIGHLI, H; Sakatamme, O.; Itakura, K; Yokoyama, K.K.
Biochem. Biophys. Res. Commun. 226, 801-809, 1996
A;Title: Members of the MAZ family: A novel cDNA clone for MAZ from human pancreatic isl
A;Reference number: JC5076; MUID:96428591; PMID:8831693
A;Accession: JC5076
A;Molecule type: mRNA
A;Residues: 1-497 cTSUS
A;Accession: JC5076
A;Molecule type: mRNA
A;Residues: UNIPARC:UPI0000163B39; DDBJ:DB5131; NID:g1752741; PIDN:BAA12728.1; F
A;Experimental source: pancreatic islet
C;Comment: This protein plays a role in the control of transcriptional initiation of gen and between the introns of the mouse gene for immunoglobulin M-D.
C;Keywords: phosphoprotein; zinc finger
F;146,204,480/Binding site: phosphate (Ser) (covalent) #status predicted
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A48233
polyomavirus enhancer-binding protein 2 alpha chain type 1 - mouse
polyomavirus enhancer-binding protein 2 alpha chain type 1 - mouse
NiAlternate names: PEA2 alpha chain type 1; PEA2 alpha chain type 2; PEBP2 alpha chain t
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: A48233 B48233
R;Ogawa, E.; Maruyama, M.; Kagoshima, H.; Inuzuka, M.; Lu, J.; Satake, M.; Shigesada, K.
Proc. Natl. Acad. Sci. US. A. 90, 68529-6863, 1993
A;Title: PEBPZ/PEA2 represents a family of transcription factors homologous to the produ
A;Reference number: A48233; MUID:93342088; PMID:8341710
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A;Molecule type: mRNA
A;Residues: 1-304,'L',306 <OG2>
A;Cross-references: UNIPARC:UPI000002B2F9; GB:D14637; NID:g391768; PIDN:BAA03486.1; PID
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C;Superfamily: transcription factor CBF alpha 2
C;Keywords: alternative splicing; DNA binding; T-cell; transcription factor;
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Pred. No. 22;
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Best Local Similarity 92.3%;
Matches 12; Conservative
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122 AAAAAAAAAAA 134
                1 AAFAAAAAAAA 13
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nes 12; Conserv
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A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-513 <OGA>
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A;Cross-references: UNIPROT:080983; UNIPARC:UPI000017885F; EMBL:AC004747; NID:g3413696;

RESULT 35

Gaps

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R;Rampazzo, A.; Pivotto, F.; Occhi, G.; Tiso, N.; Bortoluzzi, S.; Rowen, L.; Hood, L.; N
Biochem. Biophys. Res. Commun. 278, 766-774, 2000
A;Title: Characterization of C14orf4, a novel intronless human gene containing a polyglu
A;Reference number: JC7555; MUID: 20549026; PMID:11095982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:Q9H1B7; UNIPARC:UPI00000738BA; GB:AJ277365
C;Comment: This protein, a proline-rich nuclear protein, functions as a transcriptional
s and undergoes rapid degradation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C;Accession: T49385
R;Schulte, U; Aign, V; Hoheisel, J; Brandt, P; Fartmann, B; Holland, R; Nyakatura, submitted to the Protein Sequence Database, May 2000
A;Reference number: 225022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Molecule type: DNA
*Residues: 1-805 <SCH3-
A,Cross-references: UNIPROT:Q9P682; UNIPARC:UPI000017B46C; EMBL:AL355927; GSPDB:GN00116.
A,Experimental source: BAC clone B1D1; strain OR74A
A,Gene: FlyBase:Brp
A,Cross-references: FlyBase:FBgn0003507
C,Superfamily: box A-binding factor; GATA-type zinc finger homology
C,Keywords: DNA binding; nucleus; transcription factor; transcription regulation; zinc
F;316-369/Domain: GATA-type zinc finger homology <GZF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C14orf4 protein - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C;Accession: JC7555
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Pred. No. 32;
0; Mismatches
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32;
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Pred. No. 31;
0; Mismatches
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Pred. No.
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Best Local Similarity 92.3%;
Matches 12; Conservative
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Best Local Similarity 92.3
Matches 12; Conservative
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Best Local Similarity 92.3
Matches 12; Conservative
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A;Map position: 6
A;Introns: 54/3; 212/3
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NyAlternate names: ABF; transcription factor dGATAb
C;Species: Drosophila melanogaster
C;Date: 13-dan-1995 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C;Date: 13-dan-1995 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C;Accession: 840382
R;Abel, T.; Michelson, A.M.; Maniatis, T.
Development 119, 623-633, 1993
A;Accession: 840382; MUD:94244465; PMID:8187633
A;Accession: 840382
A;Accession: 840382
A;Accession: 840382
A;Accession: 840382
A;Accession: 840382
A;Accession: 840382
A;Accession: 1779
A;Accessio
                                   Rilin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, b.; Tallon, L. Neture 402, Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
A,Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A,Reference number: A84420; MUD: 20083487; PMID: 10617197
A,Scatus: preliminary
                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPARC:UPI000017885F; GB:AE002093; NID:g3413700; PIDN:AAC31223.1;
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transcription factor btd - fruit fly (Drosophila sp.)
C;Species: Drosophila sp.
C;Date: 18-Feb-1994 #sequence_revision 01-Dec-1995 #text_change 07-May-1999
C;Date: 18-Feb-1994 #sequence_revision 01-Dec-1995 #text_change 07-May-1999
C;Accession: S39356
B;Wimmer, E.A.; Jackle, H.; Pfeifle, C.; Cohen, S.M.
Nature 366, 690-694, 1993
A;Title: A Drosophila homologue of human Spl is a head-specific segmentation gene.
A;Reference number: S39356; MuID:94081952; PMID:8259212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: UNIPARC: UPI0000124C17; EMBL: Z29361; NID: 9441283; PID: 9441284
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A;Introns: 40/1; 119/1; 160/3; 319/3
C;Superfamily: FtsH/SEC18/CDC48-type ATP-binding domain homology
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Pred. No.
                 A; Experimental source: cultivar Columbia
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A;Cross-references: FlyBase:FBgn0000233
A;Introns: 245/2
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A;Molecule type: DNA
A;Residues: 1-644 <WIM>
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A; Residues: 1-627 <STO>
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Q6QDA4 HUMAN
Q9BX46 HUMAN
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Q8BR71 MOUSE
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                                                                 2006, 22:38:21
                                                                                                                                                                                                                                                             summaries
                                             protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                        Q7YTA3 9
Q9ARR7 0
Q8IMU7 1
                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
       GenCore
Copyright (c) 1993
                                                                                                                                                                                                                                                                               UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum Match 100%
Listing first 100 s
                                                                                                                       AAFAAAAAAAA 13
                                                                                                                                                                                                            length: 0
length: 2000000000
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                                                                                                   US-10-617-568-4
54
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3395
3395
4328
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458
506
512
                                                                 September
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Match
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                                                                                                     Title:
Perfect score:
                                                                                                                                          Scoring table:
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                                              protein
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Maximum |
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ОЭDDF6\_РЕТМА ОЭFLD1\_АRATH D6CNB7

ALIGNMENTS

macaca fasc anopheles g glomeris ma rattus norv oryza sativ

homo sapien homo sapien homo sapien

petromyzon arabidopsis kluyveromyc

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Q8IMU7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22767835; PubMed=12885558; DOI=10.1016/S0012-1606(03)00217-3; Prpic N.M., Tautz D.; Prpic n.M., Tautz 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001, integrated into UniProtKB/TrEMBL.
01-JUN-2001, sequence version 1.
21-FEB-2006, entry version 15.
23-FEB-2006, entry version 15.
05JNBa0004G10.7 protein (Hypothetical protein B1008C01.41).
Name=CSINBa0004G10.7; Synonyms=B1008C01.41;
Oryza sativa (japonica cultivar-group).
BNkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.
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MEDILINE=22337376; PubMed=12447438; DOI=10.1038/nature01184;
MEDILINE=22337376; PubMed=12447438; DOI=10.1038/nature01184;
Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
HosoKawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iljima M., Ikeda M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AJ551276; CAD82905.1; -; mRNA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR01356; Homeodow.
InterPro; IPR012287; Homeodomain-rel.
                                                                                                                                                                                                                                                                                                                        Glomeris marginata.
Eukaryota, Metazoa, Arthropoda, Myriapoda, Diplopoda, Pentazonia,
Glomerida, Glomeridae, Glomeris.
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100.0%; Pred. No. 27;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163 AA; 17588 MW; 87B8BCD9F5421697 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           head appendages.";
Dev. Biol. 260:97-112(2003).
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
                                                                                                                                                            01-OCT-2003, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            269 AA.
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PROSITE; PS50071; HOMEOBOX 2; 1.
DNA-binding; Homeobox; Nuclear protein.
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O9ARR7;
                                                                                                                                                                                                01-OCT-2003, sequence version 1. 07-FEB-2006, entry version 11.
                                                                                                                                                                                                                                                          Distal-less protein (Fragment).
Name=dll;
                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00046; Homeobox; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=62006;
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                                                                                                 Q7YTA3_9MYRI
Q7YTA3;
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SEQUENCE
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RN NUCLECTIDE SEQUENCE.

RA MUCLECTIDE SEQUENCE.

RA Admanstides P.G., Scherer S.E., Lip P.W., Hoskins R.A., Galle R.F.,

RA Admanstides P.G., Scherer S.E., Lip P.W., Hoskins R.A., Galle R.F.,

RA Admanstides P.G., Scherer S.E., Lip P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA George R.A., Lewis S.E., Richards J. Champe W., Henderson S.N.,

RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeifffer B.D.,

RA Barandon R.C., Rogers Y.-H.C., Barael M., Pelson C.R., Miklos G.L.G.,

RA Barlew R.M., Basu A., Baxendale J., Bayraktaroglu L., Basaley B.M.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Basaley B.M.,

RA Berman D.P., Brander J., Brottier P.,

Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Durbin K.J., Evangelista C.C., Ferriera S., Pleischmann W.,

Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Hauck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

Hostin D., Houston K.A., Howland T.J., Mei M.-H., Ibegwam C.,

RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntcosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
Karasawa W., Ito S., Ito T., Ito Y., Ito Y., Iwabuchi A., Kamiya K., Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I., Machita K., Maehara T., Mizubo H., Mizubayashi T., Mukai Y., Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M., Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M., Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K., Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.-I., Eun M.-Y., Mana M., Andrew M., Mana M., Shibata M., Shibata M., Shibata M., Shibata M., Shibata M., Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.-I., Eun M.-Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92.6%; Score 50; DB 2; Length 269; 100.0%; Pred. No. 39; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                         "The genome sequence and structure of rice chromosome 1."; Nature 420:312-316(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR009148; SibA.
PRINTS; PR01852; SIBAPROTEIN.
Hypothetical protein.
SEQUENCE 269 AA: 27747 MW; 861429FCDB1141DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003, integrated into UniProtKB/TrEMBL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AP003074; BAB40060.1; -; Genomic_DNA.
EMBL; AP003196; BAB93147.1; -; Genomic_DNA.
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271 AAFAAAAAALAA 283

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Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
A Syirskas R., Tector C., Turner R., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Milliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhao G.,
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
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                                                                                                                                                                                                                                                                                                                                                                                          Celliker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren B.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstrock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; Frishing a whole-genome shotgun: release 3 of the Drosophila melanogaster euchromatic genome sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MUCLEOTIDE SEQUENCE.
MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Berkeley Drosophila Genome Project;
Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.
Yu C., Rubin G.;
"Drosophila melanogaster release 4 sequence.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Annotation of the Drosophila melanogaster euchromatic genome: a systematic review.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JAN-2006) to the EMBL/GenBank/DDBJ databases.
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FlyBase; FBgn0051422; CG31422.
SEQUENCE 305 AA; 32565 MW; 472F8AA40CFF9953 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Biol. 3: RESEARCH0083.1-RESEARCH0083.22 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a genomics perspective.";
Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002)
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MEDLINE=22426065; PubMed=12537568;
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                                                                                                                                                                                                                 Labbe M., Pery P.;
"Characterization of ribosomal phosphoprotein P0 of Eimeria tenella.";
Submitted (FBB-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Ribosomal protein P0 is the functional equivalent of
E.coli protein L10.
-!- SUBUNIT: P0 forms a pentameric complex by interaction with dimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Galagan J.E., Calvo S.E., Cuomo C., Ma L.-J., Wortman J.R.,
Batzoglou S., Lee S.-I., Bastuerkmen M., Spevak C.C., Clutterbuck J.,
Kapitonov V., Jurka J., Scazzocchio C., Farman M., Butler J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                  Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60S acidic ribosomal protein PO. /FTId=PRO 0000154770. 13214EFI694BDAC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Fungi; Ascomycota; Pezizomycotina; Burotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
NCBI_TaxID=227321;
                                                                                                                                                                                                                                                                                                                                    -!- PTM: Phosphorylated (By similarity).
-!- SIMILARITY: Belongs to the ribosomal protein L10P family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.7%; Score 49; DB 1; Length 314; 92.3%; Pred. No. 60; 1; Indels ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00428; Ribosomal 608; I.
Pfam; PF00466; Ribosomal L10; 1.
PRINTS; PR00456; RIBOSOMĀLP2.
Phosphorylation; Ribonucleoprotein; Ribosomal protein.
                             20-JUN-2002, integrated into UniProtKB/Swiss-Prot. 01-DEC-2001, sequence version 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-APR-2005, integrated into UniProtKB/TrEMBL
 314 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=FGSC 4;
PubMed=16372000; DOI=10.1038/nature04341;
                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF353516; AAK38887.1; -; mRNA.
INICEPPO; INFO01813; Ribosomal 60S.
INICEPPO; IPRO01790; Ribosomal L10.
INICEPPO; IPRO01859; Ribosomal P2.
 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-APR-2005, sequence version 1.
O-MAR-2006, entry version 5. .
Hypothetical protein.
ORFNames=ANS133.2;
                                                                07-FEB-2006, entry version 21.
60S acidic ribosomal protein P0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           314 AA; 33272 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aspergillus nidulans FGSC A4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QSB2U7 EMENI PRELIMINARY;
QSB2U7;
                                                                                                                                                                                    NUCLEOTIDE SEQUENCE [MRNA].
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hes 12, Conservative
 STANDARD;
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                                                                                                                                                                                                                                                                                                                      of Pl and P2.
                                                                                                                                                 NCBI_TaxID=5802;
                                                                                                  Eimeria tenella
                                                                                                                                                                                                     STRAIN=PAPt38
RLAO EIMTE
Q967<u>Y</u>7;
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Local Similarity 92.3 nes 12; Conservative

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Gaps

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Indels

90.7%; Score 49; DB 2; Length 305; 92.3%; Pred. No. 59;

0; Mismatches

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Query Match
     Adams N.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adams N.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adams N.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adamstides P.G., Scherer S.E., Holt R.A., Evans C.A., Gocayne J.D., Adamstides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N., Sutron G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., A sutron R.C., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X., A strandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., A pril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Abril J.F., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Ballew R.M., Babu A., Baxendale W.P., Broketter P., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Bullew R.M., Butler H., Cadieu E., Center A., Chandra I., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cawley S., Dahlke C., Davenport L.B., Davies P., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Pleischmann W. Ducbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W. Broth M. J., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J., Harvey D.A., Heiman T.J., Wein M.-H., Ibegwam C., Alasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X., Mattei B., Kodira C.D., Kraft C., Kavitz S., Liang Y., Lin X., Mattei B., Molthoy B., Murphy L., Morntoo B., Moutt S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Robert D.R., Nelson D.R., Nelson D.R., Nelson D.R., Robert D.R., Nelson D.R., Nelson D.R., Nelson D.R., Nelson D.R., Nelso
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                                                                                                                                                                                                                                                    Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
Purcell S., Harris S., Braus G.H., Draht O., Busch S., D'Enfert C., Bouchier C., Goldman G.H., Bell-Pedersen D., Griffiths-Jones S., Doonan J.H., Yu J., Vienken K., Pain A., Freitag M., Selker B.U., Archer D.B., Penalva M.A., Oakley B.R., Momany M., Tanaka T., Kumagai T., Asai K., Machida M., Nierman W.C., Denning D.W., Caddick M., Hynes M., Paoletti M., Fischer R., Miller B.L., Dyer P.S., Sachs M.S., Osmani S.A., Birren B.W.;
"Sequencing of Appergillus nidulans and comparative analysis with A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                               -i- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Bukaryota; Metazoa; Arthropoda; Haxpoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                         Score 49; DB 2; Length 399;
Pred. No. 72;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
SEQUENCE 399 AA; 43735 MW; 8D25BD74EFA8AD24 CRC64;
                                                                                                                                                                                                                                                                                                          EMBL; AACD01000088; EAA62314.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UMAY-2000, integrated into UniProtKB/TrEMBL.
01-MAY-2000, sequence version 1.
07-FBB-2006, entry version 20.
07-G15465-PA (IPIJEp).
ORFNAmmes=CG15465, Dmel_CG15465;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9W4E5_DROME PRELIMINARY; PRT;
                                                                                                                                                                                                                                                                                                                                                                              90.7%;
                                                                                                                                                      fumigatus and A. oryzae.";
Nature 438:1105-1115(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AEFAAAAAAAA 138
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                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 92.3 les 12, Conservative
                                                                                                                                                                                                                     preliminary data.
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Distributed under the Creative Commons Attribution-NoDerivs License
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Sheeler K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhou K., Zhu S., Zhu S., Zhu S., Sheng L., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDINES-22456065; PubMed=12537568;
MEDINES-22456065; PubMed=12537568;
MEDINES-22456065; PubMed=12537568;
MEDINES-22456065; PubMed=12537568;
MEDINES-22456065; PubMed=12537568;
Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Pacleb J.M., Park S., Weiffer B.D., Richards S., Sodergren E.J., Weinscock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; Weinstong a whole-genome shotgum: release 3 of the Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22426700; PubMed=12537573; MEDLINE=22426700; PubMed=12537573; Medler B., Carlson J.W., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.; the Drosophila melanogaster euchromatin: "The transposable elements of the Drosophila melanogaster euchromatin:
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MEDLINE=22426065; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Misra S., Crosby M.A., Mungall C.J., Millburn G.H., Prochnik S.E.,
Fradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pacleb J.,
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Celniker S., Carlson J., Wan K., Pfeiffer B., Frise B., George R.,
Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith B.
Yu C., Rubin G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stapleton M., Carlson J., Chavez C., Frise E., George R., Park S., Wan K., Yu C., Celniker S.; Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JAN-2006) to the EMBL/GenBank/DDBJ databases.
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3DF7F9EAF6A3DD1E CRC64;
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Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a genomics perspective.";
Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          melanogaster euchromatic genome sequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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EMBL; BT022700; AAY55116.1; -; mRNA.
FlyBase; FBgn0029746; CG15465.
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SEQUENCE
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90.7%; Score 49; DB 2; Length 422;

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Levinson R.S., Batourina E., Choi C., Vorontchikhina M.,
Kitajewski J., Mendelsohn C.L.;
Kitajewski J., Mendelsohn C.L.;

"Foxd1-dependent signals control cellularity in the renal capsule, a structure required for normal renal development.";

Lovelopment 132:259-539(2005).

L. FUNCTION: Transcription factor required for formation of positional identity in the developing retina, regionalization of the pottic chiasm and morphogenesis of the kidney.

C. ISSUE SPECIFICITY: Predominantly expressed in the CNS and temporal half of the retina. Also expressed in the condensed head mesenchyme, metanephric blastema of the developing kidney, cortex of the adrenal gland, condensed mesenchyme at the base of the follicles of vibrassae and cartilage perichondrium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of the
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                                                                                                                                                                                                                                                                                                                                                                                   07-FEB-2006, entry version 39.
Forkhead box protein D1 (Forkhead-related protein FKHL8) (Forkhead-related transcription factor 4) (FREAC-4) (Brain factor-2) (HFH-BF-2) Name=Foxdl; Synonyms=FKHL8, Freac4, Hihbf2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         developing vertebrate.

Developing vertebrate.

Subvision of the neuroepithelium and also in the temporal half of the primary optic cup and the optic stalk. At Elo.5, seen in the hypothalamus, temporal half of the optic stalk, and temporal hemiretina. At Ell.5 and Ell.5 a high expression is seen in regions of condensed mesenchyme of the head, and as neuroepithelial cells begin to differentiate and migrate outward.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MISCELLANEOUS: Mice lacking Foxdl show disrupted cell identity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the ventrotemporal area of the retina and aberrant morphogenesis of the optic chiasm. Their kidneys remain fused, have a disorganised ureteric tree and fail to ascend to a lumbar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=BALB/c; TISSUE=Embryo;
MEDLINE=95114592; PubMed=7815060;
Hatini V., Tao W., Lai E.;
Expression of winged helix genes, BF-1 and BF-2, define adjacent domains within the developing forebrain and retina.";
J. Neurobiol. 25:1293-1309(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: Contains 1 fork-head DNA-binding domain. CAUTION: Was originally (Ref.1) assigned to be BF-2 (FOXGIA).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=15509772; DOI=10.1242/dev.01431;
Herrera E., Marcus R., Li S., Williams S.E., Erskine L., Lai
Mason C.;
                                    Indels
                                                                                                                                                                                                                                                                                                                                 15-JUL-1998, integrated into UniProtKB/Swiss-Prot
                                                                                                                                                                                                                                                                                 456 AA.
        red. No. 75;
Mismatches
                                                                                                                                                                                                                                                                              PRT;
        Pred.
                                                                                                                                                                                                                                                                                                                                                               sequence version 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Muroidea; Muridae; Murinae; Mus
NCBI_TaxID=10090;
        92.3%;
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                                                                                      1 AAFAAAAAAAAA 13
                                                                                                                                        AQFAAAAAAAA 77
                                 Conservative
                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
Best Local Similarity
Matches 12; Conserv
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Mammalia, Butheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=CS7BL/6J; TISSUE=Eyeball, and Head; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                     PROSITE; PS00657; FORK HEAD_1; 1.
PROSITE; PS00658; FORK HEAD_2; 1.
PROSITE; PS50039; FORK HEAD_3; 1.
Developmental protein; DNA-binding; Nuclear protein; Transcription; Transcription;
                                                                         H RISPIP (04345): 12HDC.

R RANSFAC; T02293; -.

R Ensembl; ENSWIGGO000050789; Mus musculus.

R MG1: MG1:1347463; Foxdl.

R G0; G0:0003677; F:DNA binding; IDA.

G0; G0:0007411; P:axon guidance; IMP.

G0; G0:0007411; P:axon guidance; IMP.

R G0; G0:0007411; P:axon guidance; IMP.

R G1; G0:0007411; P:axon guidance; IMP.

R InterPro; IPR011991; Wing_hlx_hna_d.

R InterPro; IPR011991; Wing_hlx_bna_d.

R PRINTS; PR00053; PORKHEAD.

R PPRODOM; PR000425; TF Fork head; 1.

R SMART; SM00339; FH; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-OCT-2005, integrated into UniProtKB/TrEMBL.
11-OCT-2005, sequence version 1.
07-FBB-2006, entry version 6.
12 days embryo eyeball cDNA, RIKEN full-length enriched library, clone:123009510 product:forkhead box D1, full insert sequence (in embryo head cDNA, RIKEN full-length enriched library, clone:122401E09 product:forkhead box D1, full insert sequence).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43D93F89BBDFCCC7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                            Forkhead box protein D1
                                                                                                                                                                                                                                                                                                                                                                                                              'FTIG=PRO_0000091812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Methods Enzymol. 303:19-44(1999).
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Poly-Gly.
Poly-Arg.
Poly-Asp.
Poly-Pro.
Poly-Ala.
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Poly-Gly.
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                                                EMBL; L38607; AAC42042.1; -; mRNA.
HSSP; Q63245; 2HDC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45430 MW;
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NUCLEOTIDE SEQUENCE.
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NUCLEOTIDE SEQUENCE
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33
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Q3UQW8;
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COMPBIAS
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RESTRAINSCYBLAGY TISSUESEPREABIL, and Head;

RACEATING TO A STANDARY TO THE CASE A GOUGH J. FITCH M.C., Meade N., AND CARTING TO A STANDARY THE CASE A CASE

Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Itoh M., Atawaw T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Rakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alazawa T., Hara A., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Asibura Y., Gojobori T., Bono H., Kasukawa T., Saito R., Adacta K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Andra R., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Andra R., Matsuda H., Resukawa T., Baito R., Matsuda H., Rochima H., Rabil P., Suzuki R., Tomita M., Wagner L., Washio T., Rasai R., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Brake J., Boffelli D., Bojunga N., Carninici P., de Bonaldo M.F., Ancotore P., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazarelli J., Mombaetts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Narsawi H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Wanshaw-Borits A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Havashizaki V. Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License NUCLEOTIDE SEQUENCE.

STRAIN=20530913; PUBMed=11076861; DOI=10.1101/gr.152600;

MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Alzawa K., Risunai T., Tashiro H., Itoh M., Asuman J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Aumin N., Ishii T., Nakamura S., Hazama M., Nishine T., Harda A., Yamamoto R., Matsunco H., Sakaguchi S., Ikegami T., Kashiwagi K., Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Hayashizaki Y., IRKEN integrated sequence R., Kira A., Hayashizaki Y.; RIKEN integrated sequence analysis (RISA) system-384-format genome Res. 10:1757-1771(2000). STRAIN=C57BL/67; TISSUE=Eyeball, and Head; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000). Birney E., Hayashizaki Y.; "Analysis of the mouse transcriptome based on functional annotation of "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(2002). ATRAIN-CSTBL/6J; TISSUE-Eyeball, and Head;
Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
Hori P., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
Shiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
Muramatsu M., Hayashizaki Y.;
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
-: SUBCELLULAR LOCATION: Nuclear (By similarity). "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001). Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Sato Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., STRAIN=C57BL/61; TISSUE=Eyeball, and Head; MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500; EMBL; AK142034; BAE24920.1; -; mRNA. EMBL; AK132390; BAE21140.1; -; mRNA. NUCLEOTIDE SEQUENCE. NUCLEOTIDE SEQUENCE. (5) NUCLEOTIDE SEQUENCE. Hayashizaki Y.; 

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R GO; GO:0007411; P:axon guidance; IMP.
R GO; GO:0006757; P:regulation of transcription from RNA polyme. . .; IDA.
R InterPro; IPR001766; TF Bork head.
R InterPro; IPR0010217; Tubulin.
R Pfam; PF00250; Fork head; 1.
R PRINTS; PR000053; FORKHEAD.
R PRODOM; PD000425; TF Fork head; 1.
R RMART; SM00339; FH; I.
R RNOSITE; PS00557; FORK HEAD 1; 1.
DR PROSITE; PS0059; FORK HEAD 1; 1.
DR PROSITE; PS0059; FORK HEAD 1; 1.
DR PROSITE; PS00227; TUBULIN; UNKNOWN 1.
KW DNA-binding; Nuclear protein; Transcription; Transcription regulation.
SG SEQUENCE 456 AA; 45371 MW; 3153172991DC99A4 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95043392; PubMed=7957066;
Pierrou S., Hellqvist M., Samuelsson L., Enerbaeck S., Carlsson P.;
Pierrou S., Hellqvist M., Samuelsson L., Enerbaeck S., Carlsson P.;
Pierrou S., Hellqvist M., Samuelsson L., Enerbaeck S., Carlsson P.;
Piconing and enaracterization of seven human forkhead proteins:
binding site specificity and DNA bending.";
EMBO J. 13:5002-5012(1994).
- FORCTION: Transcription factor required for formation of positional identity in the developing retina, regionalization of the optic chiasm and morphogenesis of the kidney (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FOXD1 HUMAN STANDARD, PRT, 465 AA. 016676; Q12949; O1-NOV-1997, integrated into UniProtKB/Swiss-Prot. 01-NOV-1997, sequence version 1. 07-FBB-2006, entry version 3. Forkhead box protein D1 (Forkhead-related protein FKHL8) (Forkhead-related transcription factor 4) (FRBAC-4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE [GENOMIC DNA / MRNA].
MEDLINE=96355467; PubMed=8702877; DOI=10.1074/jbc.271.35.21094;
Ernstsson S., Pierrou S., Hulander M., Cederberg A., Hellqvist M.,
Carlsson P., Enerbaeck S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Characterization of the human forkhead gene FREAC-4. Evidence for regulation by Wilms' tumor suppressor gene (WT-1) and p53."; J. Biol. Chem. 271;21094-21099(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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-!- SIMILARITY: Contains 1 fork-head DNA-binding domain.
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EMBL; U59832; AAC50661.1; -; mRNA.
EMBL; U13222; AAA92039.1; -; mRNA.
PIR; G02738; G02738.
PIR; S51627; S51627.
HSSP, Q63245; 2HC.
SNR; Q16676; 124-220.
TRANSFAC; T02472; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        80;
                                                                                                                                                                                                                                                                                                                                                                                                90.7%; Score 49; 92.3%; Pred. No. 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE [MRNA] OF 120-225.
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Best Local Similarity 92...
Best Local 2; Conservative
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HGNC; HGNC:3802; FOXD1
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Sasaki T., Matsumoto T., Yamamoto K.;
Submitted (FEB-2002) to the EMBL/Genbank/DDBJ databases.
-!- DOMAIN: The RING-type zinc finger domain is essential for ubiquitin ligase activity. It coordinates an additional third zinc ion (By similarity).
-!- SIMILARITY: Contains 1 RING-type zinc finger.
                                                                                                                                                                                                                                                 Transcription, Transcription regulation.
Porkhead box protein D1.
/FTIG=PRO_000091811.
Pork-head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
Enrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Octobross; Cincleus; IEA.
GO; GO:0001553; Ciubiquitin ligase complex; IEA.
GO; GO:000151; F:metal ion binding; IEA.
GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
GO; GO:0006492; F:zinc ion binding; IEA.
GO; GO:0006579; F:zinc ion binding; IEA.
GO; GO:0016567; P:protein ubiquitination; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
MIM, 601091; gene.

GO; GO: 0003700; F: transcription factor activity; TAS.
InterPro; IPR011991; Wing hix_bna_bd.
InterPro; IPR011991; Wing hix_bna_bd.
Pfam; PF00250; Fork_head; 1.
PRINTS; PR00053; FORKHEAD.
Probom, PD0004035; FF Fork_head; 1.
PROSITE; PS00657; FORK_HEAD_1; 1.
PROSITE; PS00658; FORK_HEAD_1; 1.
PROSITE; PS00658; FORK_HEAD_2; 1.
PROSITE; PS00658; FORK_HEAD_3; 1.
PROSITE; PS00639; FORK_HEAD_3; 1.
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Pred. No. 81;
0; Mismatches
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Poly-Arg.
Poly-Glu.
Poly-Asp.
Poly-Asp.
Poly-Ala.
Poly-Ala.
Poly-Ala.
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07-FBB-2006, entry version 14.
Zinc finger protein family-like.
Name=P0686H11.17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46140 MW;
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Q6Z8T9;
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Best Local Similarity
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COMPBIAS
SEQUENCE
                                                                                                                                                                                                                                                                                                                  DNA BIND
COMPBIAS
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Matches
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RATAIN=221;

RATAIN=221;

RATAIN=221;

RATAIN=221;

RATAIN=221;

RATAIN=221;

RA Arechchi H.M., Armbruster J., Bachantsang P., Baldwin J., Barry A., Ratechchi H.M., Armbruster J., Bachantsang P., Baldwin J., Barry A., Barchchi H.M., Armbruster J., Campor K., Chang J., Cheshatsang Y., Calixten M., Collymore A., Campor K., Chang J., Cheshatsang Y., Citrcen M., Collymore A., Campor K., Chang J., Cheshatsang Y., Corne C., David R., Davier I., Duffey N., Dupes A., Elkins T., R., Bricken J., Farrina A., Faro S., Ferreira P., Fischer H., R. Figgerald M., Foley K., Gage D., Galagan J.E., Gearin G., Garrina T., Ram A., Goyette A., Gryette A., Grandbois E., Garina F., Halme Y., Hafer N., Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H., Ander D., Onnes C., Kanner P., Kodira C., Kulbokas E., Labutti K., Lama D., Landers T., Legeral M., Kaner P., Kodira C., Kulbokas E., Labutti K., Lama D., Landers T., Legeral W., MacDonald J., Mactens E., Malting W., Huspe E., Hulme W., Huspy E., Linchlad-Toh K., Liu X., Lokyitsang T., Lokyitsang Y., Lowis E., Marina J., Marbella R., Markelsen T., Mactens C., Maucell E., Marina J., Marbella R., Markelsen T., Markelsen T., Markelsen C., Mayor N., Moru K., Markelsen T., Rogers J., Rogers J., Rogers J., Romera J., Rogers J., Romeral M., Sharpe T., Serinnou J., Sharpe T., Ruthan W., Schupbach R., Ramasamy U., Ramasamy U., Ramasamy C., Starpe T., Sharpe T., Sharpe T., Sharpe T., Ruthans M., Schupbach R., Ramasamy U., Ramasamy U., Ramasam V., Sharpe T., Ruthans M., Schupbach R., Starker S., Perrin D., Pinkelsen T., Marker S., Raker S., Parker S., Perrin D., Sharpe T., 
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0
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Ustilaginomycetidae, Ustilaginales, Ustilaginaceae, Ustilago.
                                                                                                                                                                                                                   Score 48; DB 2; Length 167;
Pred. No. 50;
0; Mismatches 1; Indels
                    INTECTO; IPRO01841; Znf. RING.
Pfam; PF00097; zf-C3HC4; 1.
SMART; SM00184; RING; 1.
SMART; SM00744; RINGv; 1.
PROSITE; PS50089; ZF_RING_2; 1.
Metal-binding; Nuclear protein; Zinc; Zinc-finger.
SEQUENCE 167 AA; 17664 MW; 4729ACE00A901AE9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-JUL-2005, integrated into UniProtKB/TrEMBL.
19-JUL-2005, sequence version 1.
07-FEB-2006, entry version 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 361 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zimmer A., Zody M., Lander E.S.;
"The genome sequence of Ustilago maydis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q4PEI8_USTMA PRELIMINARY;
Q4PEI8;
                                                                                                                                                                                                                           88.9%;
92.3%;
  InterPro; IPR011016; RINGV
                                                                                                                                                                                                                                                                                                                            1 AAFAAAAAAAA 13
                                                                                                                                                                                                                                                                                                                                                                          56 AAIAAAAAAAA 68
                                                                                                                                                                                                                                                                              12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
ORFNames=UM01475.1;
                                                                                                                                                                                                                                                       Best Local Similarity
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Q40 PEI 8 UST

Q40 PEI 9 UST

Q40 PEI 19 -JU

DT 19 -JU

DE Hypot

RA Natice

RA Arace

RA Linda

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STRAIN=FVB/N;

MEDLINE=2388257; Pubbmed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=2388257; Pubbmed=12477932; DOI=10.1073/pnas.242603899;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Alschul S.F., Zeeberg B., Buetow K.H.; Schaefer C.F., Bhar N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Mang J., Haieh P.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malk J.A., Gunarathe P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Raha S.S., Modan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

R Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerth A., Schein J.E., Jones S.J.M., Marra M.A.,

Schnerth D.M., Marra M.A.,

R Schnerth D.M., Schein J.E., Jones S.J.M., Marra M.A.,

Schnerth D.M., Marra M.A.,

Schnerth D.M.,

Schnerth D.M., Marra M.A.,

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Schnerth D.M.,

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                                                                                                                                                                                                                  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Pred. No. 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              11 protein.
361 AA; 39615 MW; 038F774408202041 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-APR-2004, integrated into UniProtKB/Swiss-Prot.
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                                                                                                                                                                                                                                                                                                                                                EMBL; AACP01000053; EAK82242.1; -; Genomic_DNA.
Hypothetical protein.
SEQUENCE 361 AA; 39615 MW; 038F774408202041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 484 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ensembl; ENSMUSGO0000048485; Mus musculus.
MGI; MGI:2387181; Zbtb8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; BC023839; AAH23839.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2003, sequence version 1. 07-MAR-2006, entry version 22.
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InterPro; IPR013069; BTB POZ.
InterPro; IPR007087; Znf_C2H2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88.9%;
92.3%;
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hes 12; Conservative
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                                                                                                                                          preliminary data.
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Q8CIIO;
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Nobmed=16141072; DOI=10.1126/science.1112014;

Rarainci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., Cyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Davis M.J., Wilming L.G., Addinis V., Allen J.E.,

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Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,

Crowe M.L., Dalla B., Dalrymple B.P., de Bono B., Della Gatta G.,

Adi Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,

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Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,

Gustincich S., Harbers M., Hayashi Y., Hansech T.K., Hirokawa T.,

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Aust M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,

Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-OCT-2005, integrated into UniProtkB/TrEMBL.
11-OCT-2005, sequence version 1.
21-FEB-2006, entry version 7.
16 days embryo head cDNA, RIKEN full-length enriched library, clone:C130068L16 product:Zinc finger and BTB domain containing 8, full insert sequence (0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:C230068H07 product:Zinc finger and BTB domain containing 8, full insert sequence) (14, 17 days embryo head cDNA, RIKEN full-length enriched library, clone:3222401B20 product:Zinc finger and BTB domain containing 8, full insert sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/6J; TISSUE=Cerebellum, and Head; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                  SWART; SWUUJDD; ....
PROSITE; PSSO097; BTB; 1.
PROSITE; PSSO0157; ZINC_FINGER_C2H2_1; 1.
PROSITE; PSSO157; ZINC_FINGER_C2H2_2; 2.
DNA-binding; Metal-binding; Nuclear protein; Repeat; Transcription; Transcription; Zinc_finger.
Transcription regulation; Zinc; Zinc_finger.

Transcription and BTB domain-containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 48; DB 1; Length 484;
Pred. No. 1.1e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1, Indels
                                                                                                                                                                                                                                                                                                                  24 92 BTB. —
331 353 C2H2-type 1.
359 382 C2H2-type 2.
132 149 Ala-rich.
484 AA; 53387 MW, B4FP082555BOCAIA CRC64;
                                                                                                                                                                                                                                                                     protein 8.
/FTId=PRO_0000047722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Methods Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
Pfam; PF00651; BTB; 1.
Pfam; PF00096; zf-C2H2; 2.
ProDom; PD000003; Znf_C2H2; 1.
SMART; SM00225; BTB; 1.
SMART; SM00355; ZnP_C2H2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            88.9%;
92.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AAFAAAAAAAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
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ID Q3US18 MOUSE
AC Q3US18;
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ZN_FING
ZN_FING
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MESCACHAIN, T. Garcan L.P. Inagrach D. Ligotoch L. Will J.
Liuni S. Mochillam S. Madah Babo M. Padera M. Warchiont L. M.
Rastaid H. Weisland S. Mishikawa S. Nori F. Ohara O. Marandi H. May Ps. J. Manishand S. Mishikawa S. Nori F. Ohara O. Manishand S. Mishikawa S. Nori F. Ohara O. Personal G. Pesole G. Percrowky M. P. Paza S. Reed J. Read J. F. Mishikawa G. Percrowky M. P. Paza S. Reed J. Read J. F. Mishikawa G. Percrowky M. P. Paza S. Manishand S. Nori F. Manishand M. Percrowky M. P. Paza S. Manishand S. Mishikawa S. Nori F. Ohara O. P. Paga S. Mishikawa S. Nori F. Manishand S. Manishand S. Mishikawa S. Nori F. Manishand S. Manishand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/6J; TISSUB=Cerebellum, and Head; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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Genome Res. 10:1757-1771(2000).
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EMBL; AK163910; BAE2741.1; -; mRNA.
EMBL; AK163915; BAE20999.1; -; mRNA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:00046872; F:mereal ion binding; IEA.
GO; GO:0003576; F:nucleic acid binding; IEA.
GO; GO:0005515; F:protein binding; IEA.
GO; GO:0008210; F:zinc ion binding; IEA.
INEAFPC; IPR013069; BTB_POZ.
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Burdon R.C., Rogers V.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,

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RADAMA R., Matchi B., McInton R., Danger P., Marry D. M., Nelson D.L.,

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RADAMA R., Tectro C., Truner R., Venter E., Wang A.,

RADAMA R., Reinert K., Zhong F.N., Zhon M., Zhong S., Zhon Q., Zhan W., Zhong S., Zhon G., Zhan M., Zhong S., Zhon G., Zh
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Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa, Arthropoda, Hexapoda; Insecta; Pterygota;
Neoptera; Endoptera; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
InterPro; IPR007087; Znf_C2H2.
Pfam; PF00651; BTB; 1.
Pfam; PF00096; zf-C7H2; 2.
Prodom; PD000003; Znf_C2H2; 1.
SMART; SM00255; BTB; 1.
SMART; SM00355; Znf_C2H2; 2.
PROSITE; PS50028; ZINC_FINER_C2H2; 1.
PROSITE; PS50028; ZINC_FINER_C2H2_1; 1.
PROSITE; PS00028; ZINC_FINER_C2H2_2; 2.
Metal-binding; Nuclear protein; Repeat; Zinc; Zinc-finger.
SEQUENCE 484 AA; 53414 WW; ACA81D5402A2E7F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 484;
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Pred. No. 1.1e+02;
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92.3%; Pred. No. ...
0; Mismatches
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                                                                                          MUCLEOTIDE SEQUENCE.
MEDINER=22456065; PubMed=12537568;
MEDINER=22456065; PubMed=12537568;
Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M., "Finishing a whole-genome shotgun: release 3 of the Drosophila melanogaster euchromatic genome sequence.";
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MEDLINE=224456069; PubMed=12537572;
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Celniker S., Carlson J., Wan K., Přeiffer B., Frise E., George R.,
Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.
Yu C., Rubin G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Annotation of the Drosophila melanogaster euchromatic genome: a
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-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
-!- SIMILARITY: Contains 2 LIM zinc-binding domains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a genomics perspective.";
Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
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Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
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EMBL; BT003467; AAO39470.1; -; mRNA.
HSSP; P50480; 1BW5.
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InterPro; IPR012287; Homeobox.
InterPro; IPR012287; Homeodomain-rel.
InterPro; IPR00107; LIM homeo.
InterPro; IPR001781; LIM Zn bd.
InterPro; IPR01965; Znf PHD.
Pf00046; Homeobox; 1.
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FlyBase; FBgn0052105; CG32105.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
Pooideae; Triticeae; Hordeum.
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GO; GO:0008883; F:glutamyl-tRNA reductase activity; IEA.
GO; GO:0008883; F:glutamyl-tRNA reductase activity; IEA.
GO; GO:00044; F:shikimate 5-dehydrogenase activity; IEA.
GO; GO:0006779; P:porphyrin biosynthesis; IEA.
InterPro; IPR001343; GlutR.
InterPro; IPR001343; GlutR.
Pfam; PF05201; GlutR. N; 1.
Pfam; PF05201; GlutR. N; 1.
Pfam; PF05201; GlutR. N; 1.
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R Pfam; PF00412; LIM; 2.

R PRINTS; PR00024; HOMEOBOX:

R PCDOOm; PD0000010; LIM; 2.

R SWART; SM00389; HOX; 1.

R SMART; SM00389; HOX; 1.

R SMART; SM00132; LIM; 2.

R PROSITE; PS00071; HOMEOBOX 1; 1.

R PROSITE; PS50071; HOMEOBOX 2; 1.

R PROSITE; PS50073; LIM DOMAIN 1; 2.

R PROSITE; PS01359; ZF FHD 1; UNKNOWN 1.

R PROSITE PS01359; ZF FHD 1; UNKNOWN 1.

R PROS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88.9%; Score 48; DB 2; Length 640; 92.3%; Pred. No. 1.4e+02; ive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67760 MW; A1A10F826018C98E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001, integrated into UniProtKB/TrEMBL.
01-MAR-2001, sequence version 1.
01-FEB-2006, entry version 17.
Glutamyl-tRNA reductase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     339 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9FYS1 HORVD PRELIMINARY;
Q9FYS1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  189 AAIAAAAAAAA 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      640 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; Q9UXR8; 1GPJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gramene; Q9FYS1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=112509;
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Query Match
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X MEDLINE-238825; PubMed-12477932; DOI=10.1073/pnas.242603899;

X Itausher R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Itausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A patchench L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A batchench M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

A stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

A Brownstein M.J., Usdin T.B., TOShiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

B Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

W Yillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K.,
Nakajima Y., Mizuno T., Morinaga M., Ota T., Suzuki Y., Obayashi M.,
Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            378 AA; 42533 MW; 1E7E5C741ACF6BA6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AK000315; BAA91078.1; -; mRNA.
Ensembl; ENSG0000091542; Homo sapiens.
GO; GO:005506; F:iron ion binding; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
InterPro; IPR005123; 20G-FeII_Oase.
Pfam; PF03171; 20G-FeII_Oxy; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2003, integrated into UniProtKB/TrEMBL. 01-JUN-2003, sequence version 1. 07-FBZ-2006, entry version 20. Hypothetical protein Ofoxd.
                                                                                                                                                  01-0CT-2000, integrated into UniProtKB/TrEMBL. 01-0CT-2000, sequence version 1. 07-FBB-2006, entry version 18. Hypothetical protein FLJ20308. Homo sapiens (Human).
                                                                                                          378 AA.
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                                                                                                                PRT;
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                                                                                                        Q9nxde_human preliminary;
Q9nxde;
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12; Conservative
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0800050 MOUSE

0800050

DT 01-JUN-20

DT 07-FEB-20

DF Hypotheri

DF Hypotheri

DF Manmelia-

OC Manmalia-

OC MANDIA

OC MANDIA

NUCLEOTII

RC STRAIN-CC

RX MEDLINE-2

RA Altschul

RA Altschul

RA Altschul

RA Bloaset

RA Altschul

RA Bloaset

RA Bloaset

RA Bloaset

RA Bloaset

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09NXD6 HUM
10 01-07
07 01-07
07 07-07
08 Hypo
08 Hypo
09 Hypo
09 Hypo
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Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield X.S.N., Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2003, integrated into UniProtKB/TrEMBL.
01-MAR-2003, sequence version 1.
07-FBB-2006, entry version 2.
0 day neonate eyeball cDNA, RIKEN full-length enriched library,
clone:E130207K11 product:hypothetical Alanine-rich region/Type 1
antifreeze protein/20G-Fe(II) oxygenase superfamily containing
protein, full insert sequence (2 cells egg cDNA, RIKEN full-length
enriched library, clone:B202011005 product:Hypothetical alanine-rich
region/type I antifreeze protein/20G-Fe, full insert sequence) (Novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=CS7BL/67; TISSUE-Egg, and Eyeball;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Davis M.J., Wilming L.G., Aidinis V., Allen J.E., Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L., Bansal M., Baxter L., Belsel K.W., Bersano T., Bono H., Chalk A.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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92.3%; Pred. No. 1.3e+02;
tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              NIH MGC Project;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0005566; Filton ion binding; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
InterPro; IPR005123; 20G-FeII Oase.
Ppfam; PF03171; 20G-FeII Oxy; I.
Hypothetical protein; Iron; Oxidoreductase.
SEQUENCE 395 AA; 44410 MW; 4CE25B4FB5B04DEB CRC64;
                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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PubMed=16141072; DOI=10.1126/science.1112014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carninci P., Hayaahizaki Y.;
"High-efficiency full-length cDNA cloning.";
Methods Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 395 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; BC052076; AAH52076.1; -; mRNA.
Ensembl; ENSMUSG00000042650; Mus musculus.
MGI; MGI:2144489; AW050020.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QBEKCI MOUSE PRELIMINARY; PRT; QBEKCI;
                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C57BL/6; TISSUE=Mouse;
                                                                                                                                                                                                                                               and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AAFAAAAAAAA 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12; Conservative
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NUCLEOTIDE SEQUENCE.
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Nature 420:563-573 (2002).

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RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,

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RA Mahlestedt C., Mattick B., Stumer A., Kand C., Sasaki D., Tomaru Y.,

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RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,

RA Tamaja M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki T., Saya STRAIN=CS7BL/6J; TISSUB=Egg, and Byeball;
PubMed=16141073; DOI=10.1126/science.1112009;
RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium;
"Antisense Transcription in the Mammalian Transcriptome."; "The transcriptional landscape of the mammalian genome."; Science 309:1559-1563(2005). Science 309:1564-1566(2005). NUCLEOTIDE SEQUENCE NUCLEOTIDE SEQUENCE Tagami M., Waki Hayashizaki Y.; 

60,770 full-length cDNAs.";

Carralledure Sergeam Second Se NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/G0; TISSUE=Egg, and Eyeball;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
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STRAIN=C57BL/6J; TISSUB=Egg;
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Hori F., Iida J., Imamura K., Imotani K., Itch M., Kanagawa S.,
Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
Muramatsu M., Hayashizaki Y.,
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases. STRAIN-C57BL/6J; TISSUB-Egg, and Byeball;
MEDLINE-20530913; PubMed-11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Yanamoco R., Matsumoro R., Hazama M., Nishine T., Harada A., Yanamoco R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa M., Ohara E., Watshiwagi K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., RKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequence:"; annotation of a full-length mouse cDNA collection."; NUCLEOTIDE SEQUENCE. STRAIN=C57BL/6J; TISSUE=Eyeball; Nature 409:685-690(2001). NUCLEOTIDE SEQUENCE NUCLEOTIDE SEQUENCE. Hayashizaki Y.; "Functional anno 

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                                                                                                                                   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninol P., Hayeshizaki Y.;
"High-efficiency Hayeshizaki Y.;
"High-efficiency Hayeshizaki Y.;
Methods Enzymol. 303:19-44(1999).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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On-MAR-2006, entry version 6.
On vitro fertilized eggs cDNA, RIKEN full-length enriched library, clone: 7420402B17 product: Hypothetical alanine-rich region/type I antifreeze protein/20G-Fe, full insert sequence.
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                                                             Tracey A.;
Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                GO; GO:0005566; F:iron ion binding; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
InterPro; IPROS123; 20G-FeII Oase.
Pfam; PF03171; 20G-FeII Oxy; I.
Hypotherical protein; Iron; Oxidoreductase.
SEQUENCE 395 AA; 44411 MW; 2822BF4BFFFEE7FF CRC64;
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                                                                                                                                                                                                                    EMBL; AK053695; BAC35478.1; -; mRNA.
EMBL; AK163294; BAE37281.1; -; mRNA.
EMBL; ALS96386; CA135332.1; -; Genomic_DNA.
Ensembl; ENSMUSG00000042650; Mus_musculus.
MGI; MGI:2144489; AM050020
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Matches 12; Conservative
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Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                      STRAIN=CS7BL/6J; TISSUE=Eyeball; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninoi P., Hayashizaki Y.; Hidah-efficiency Full-length cDMA cloning."; Methods Enzymol. 303:19-44(1999).
     01-MAR-2003, integrated into UniProtKB/TrEMBL.
01-MAR-2003, sequence version 1.
07-MAR-2006, entry version 24.
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                                                                                                                                 Name=AW050020;
       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bolunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Maalma N., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Suzuki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-Oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Manalla M., Rodriguez I., Sakamoto M., Wanghaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6J; TISSUE=In vitro fertilized eggs; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y., Inoh M., Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-CSTBL/65; TISSUE-In vitro fertilized eggs; MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibata K., Ttoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Sumi N., Ishi Y., Malshi K., Hazama M., Tashiro H., Itoh M., Yanamoto R., Matsumoto R., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiwagi K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., "RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
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Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
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Shibata K., Shizaki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
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                                                                                                                                                                                                                    "Functional annotation of a full-length mouse cDNA collection.";
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395 AA; 44494 MW; 1F3B93E0E71AF27D CRC64;
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GO; GO:0005506; F:iron ion binding; IEA.

GO; GO:0016491; F:oxidoreductase activity; IEA.

InterPro; IPR005123; 20G-FeII oase.

Pfam; PF03171; 20G-FeII oxy; I.

Hypotherical protein.

SEQUENCE 395 AA; 44494 MW; IF3B93E0E71AF27D
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les 12; Conserv
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NCLENTILE SEQUENCE:

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RY CARDINGS FBL/63; TISSUE-Expeball;

RY CARDINGS FBL/63; TISSUE-Expeball;

RY CARDINGS FBL/641072; DOI-10.1156/science.1112014;

RY CARDINGS FBL/641072;

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RY CHAINTING LG., Addinis V., Allen J.E.,

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Gaps

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395 AA.

PRT;

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RESULT 20 Q8BKB9 N ID Q8E AC Q8E

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RA Negati Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., RA Saitaido I., M., Kanapin A., Matsuda H., Schombach C., Gojobori T., RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schrini L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., RA Blake J.A., Bradt D., Brusic V., Chothin C., Corbani L.E., Cousins S., RA Blake J.A., Bradt D., Brusic V., Chothin C., Gough J., RA Gangh J., Rawaji H., Kawasawa Y., Kedzierski R.M., King B.L., RA Kanai A., Kawaji H., Kawasawa V., Kedzierski R.M., King B.L., RA Maglott D.K., Maltais L., Marchionni L., McKenzie L., Miki H., RA Magashima T., Nummata K., Okido T., Pavan W.J., Pertea G., Pesole G., Petrovsky N., Pillais L., Marchionni L., McKenzie L., Miki H., RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Nerardo R., Wagner L., Wahllestedd C., Wang Y., Watanabe K., Wagner L., Wahllestedd C., Wang Y., Watanabe K., Wagner L., Wahllestedd C., Wang Y., Wang I., Yang I., Waki K., Kawai J., Alzawa M., Sakazume N., Sakou M., Satok M., Hara A., Hashizume W., Imctani K., Ishii Y., Itoh M., Kagawa I., RA Hara A., Yashikawa T., Kawai J., Ahizawa K., Arakawa T., Rohino M., Waterston R., Shinagawa A., Yashaisaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yanalysis of the mouse transcriptome based on functional annotation of R., Nather M., Ph. Mather C., Nather M., Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Itoh M., Atakawa T., Hara A., Shibata K., Yoshino H., Itoh M., Itoh Saito T., Saito R., Saito T., Saito R., Saito T., Monthaw H., Hume D.A., Kamiya M., Lee N.H., Iyons P., Marchiomi L., Mashima J., Mazarelli J., Monthaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Wanghawa Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., STRAIN=C57BL/6J; TISSUE=Eyeball; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y., Nuramatsu M., Hayashizaki Y.; Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000). MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600; MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection."; STRAIN-C57BL/61; TISSUE-Byeball; MEDLINE=21085660; Pubmed=11217851; DOI=10.1038/35055500; STRAIN=C57BL/6J; TISSUE=Eyeball; 60,770 full-length cDNAs."; Nature 420:563-573(2002). Nature 409:685-690(2001). NUCLEOTIDE SEQUENCE NUCLEOTIDE SEQUENCE. NUCLEOTIDE SEQUENCE 

Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License NOULDENIE STANDARY IN STREE SYCHAIL;

Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Furuno M., Hanagaki T., Haracka T., Hirozane T., Hori K., Hayashida K., Hayatisu N., Hiramoto K., Hiracka T., Kinotani K., Hohimaya T., Kodo S., Konno H., Kaukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Rouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibatu K., Shinagawa A., Shiraki T., Soqabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. MEDLINE-9701-256; PubMed=8861101; DOI=10.1016/0925-4773(96)00507-2; Medline 20. Monaghan A.P.; Expression of the winged helix genes fkh-4 and fkh-5 defines domains in the central nervous system."; Mech. Dev. 55:221-230(1996). Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia, Eutheria, Euarchoncoglires, Glires, Rodentia, Sciurognathi; Muroidea, Muridae, Murinae, Mus. Gaps Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; Rira R., Hayashizaki Y.; Rira R., Hayashizaki Y.; sequencing pipeline with 34 multicapillary sequencer."; Genome Res. 10:1757-1771(2000). ö Length 395; 1; Indels Hypothetical protein. SEQUENCE 395 AA; 44415 MW; 6D22C26B1A99EDA8 CRC64; 01-NOV-1997, sequence version 1. 07-FEB-2006, entry version 31. Forkhead box protein B2 (Transcription factor FKH-4) 01-NOV-1997, integrated into UniProtKB/Swiss-Prot. 87.0%; Score 47; DB 2; I 92.3%; Pred. No. 1.3e+02; GO; GO:0005506; F:iron ion binding; IEA. GO; GO:0016491; F:oxidoreductase activity; IEA. 428 AA. 0; Mismatches Ensembl; ENSMUSG00000042650; Mus musculus. MGI; MGI:2144489; AW050020. EMBL; AK053700; BAC35481.1; -; mRNA. PRT; NUCLEOTIDE SEQUENCE OF 4-114. Forkhead box protein B2 (Tr Name=Foxb2; Synonyms=Fkh4; 1 AAFAAAAAAAA 13 36 AAVAAAAAAAA 48 12; Conservative STANDARD; Mus musculus (Mouse). NUCLEOTIDE SEQUENCE. NUCLEOTIDE SEQUENCE. Sest Local Similarity NCBI\_TaxID=10090; FOXB2 MOUSE Query Match FOXB2 MOUSE Q6473<u>3</u> Matches RESULT ð 셤

Kaestner K.H., Lee K.H., Schloendorff J., Hiemisch H., Monaghan A.P.,

MEDLINE=93361500; PubMed=7689224;

STRAIN=129

"Six members of the mouse forkhead gene family are developmentally regulated.";

Proc. Natl. Acad. Sci. U.S.A. 90:7628-7631(1993).
-!- SUBCELLULAR LOCATION: Nucleus.
-!- DEVELOPMENTAL STAGE: Expressed during embryogenesis.

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NCBI_TaxID=8364;
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Qeglgi;
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                                Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                            MGI: 1347468) FOXD2.
InterPro; IRR01766; TF Fork head.
InterPro; IRR011991, Wing llx DNA_bd.
Pfam; PF001250; Fork head; 1.
PRINTS; PR00053; FORKHEAD.
PRODOM; P0000425; TF Fork head; 1.
SMART; SM00339; FR; HEAD 1; 1.
PROSITE; PS00659; FORK HEAD 1; 1.
PROSITE; PS00659; FORK HEAD 2; 1.
PROSITE; PS00339; FORK HEAD 2; 1.
DRASITE; PS00339; FORK HEAD 2; 1.
CHAIN 1 428 FORKHEAD 3; Transcription regulation.
CHAIN 1
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
GO; GO:0006350; P:transcription; IEA.
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Pred. No. 1.4e+02;
0; Mismatches 1; Indels
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-!- SIMILARITY: Contains 1 fork-head DNA-binding domain.
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Fork-head.
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07-DEC-2004, sequence version 1.
07-FEB-2006, entry version 12.
OTTHOMRO00000021510.
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                                                                                                                                                                                 Ensembl; ENSMUSG0000056829; Mus musculus.
                                                                                      EMBL; X92591; CAA63335.1; -; mRNA.
EMBL; X71942; CAA50744.1; -; Genomic_DNA.
PIR; D47746; D47746.
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Poly-His.
Poly-Pro.
Poly-Ala.
Poly-Ala.
Poly-Ala.
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InterPro; IPR011991; Wing_hlx DNA bd.
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92.3%;
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QSVYVO;
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428 AA;
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MEDLINE-2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;

X trausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X trausher R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

X Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A tlschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

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Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robask S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

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Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Raha S.S., Loquellano N.A., Sodergren E.J., Lu X., Gibbs R.A.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rotterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Shuterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

But Generation and initial analysis of more than 15,000 full-length human
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Ensembl; ENSXETG00000021355; Xenopus tropicalis.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR009910; HMG 12 box.
Pfam; PF00505; HMG_box; I.
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07-FBB-2006, entry version 16.
874/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1.
Name=smarce1-prov;
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Pred. No. 1.4e+02;
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92.3%; Pred. No. 1...
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Pfam; PF00250; Fork head; 1.
PRINTS; PR00053; FORKHEAD.
ProDom; PD000425; TF_Fork_head; 1.
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NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
TISSUB=Brain;
PubMed=14702039; DOI=10.1038/ng1285;
                                                                                                                                                                                                                                       Acheta domesticus (House cricket).
                                                                                                                                                                                  11-OCT-2005, sequence version 1. 21-FEB-2006, entry version 7. BroadZ1 isoform.
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Pfam; PF00096; zf-C2H2; 2.
SMART; SM00225; BTB; 1.
SMART; SM00355; ZnF_C2H2; 2.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 47; DB 2; Length 458;
Pred. No. 1.5e+02;
0; Mismatches 1; Indels
                                                                          Length 435;
                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH MGC Project;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51409 MW; 88ACCDA9992B5AEB CRC64;
                   PROSITE; PS50118; HMG BOX 2; 1.
SEQUENCE 435 AA; 48441 MW; 6F227A5D387A9CA2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; BC062339; AAH62339.1; -; mRNA.
Ensembl; ENSG0000091542; Homo sapiens.
GO; GO:0005606; F::ron ion binding; IEA.
GO; GO:0016491; F::ronidoreductase activity; IEA.
InterPro; IPR065123; 2OG-FEII Oase.
Pfam; PP03171; 2OG-FEII Oxy; I.
Hypothetical protein; Iron; Oxidoreductase.
SEQUENCE 458 AA; 51409 MW; 88ACCDA9992B5AEB
                                                                        87.0%; Score 47; DB 2; I
92.3%; Pred. No. 1.4e+02;
tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                     Q6P6C2;
05-UUL-2004, integrated into UniProtKB/TrEMBL.
05-UUL-2004, sequence version 1.
05-FBB-2006, entry version 16.
Hypothetical protein OFOXD.
                                                                                                                                                                                                                                                                                   458 AA.
                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                   QEP6C2_HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 92.3%;
Matches 12; Conservative
                                                                                           Local Similarity 92.3%;
les 12; Conservative
                                                                                                                                                                          1 AAFAAAAAAAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences.
     SMART; SM00398; HMG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                 Name=OFOXD;
                                          SEQUENCE
                                                                              Query Match
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                                                                                                                  Matches
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Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                             Erezyilmaz D.F., Riddiford L.M., Truman J.W.; "An ancestral role for a metamorphosis-determining factor in a direct-
                                                                                                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    developing insect.";
Submitted (AUG-2005) to the EMBL/GenBank/DDBJ databases.
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PROSITE; PSO5097; BTB; 1.
PROSITE; PSO1028; ZINC FINGER C2H2 1; 2.
PROSITE; PSO50157; ZINC FINGER C2H2 2; 2.
Metal-binding; Nuclear protein; Zinc; Zinc-finger.
SEQUENCE 506 Aa; 54175 MW; F4FCCA9BE6415EC0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QBNAP8; Q5VXR5;
C4CAPR-2004, integrated into UniProtKB/Swiss-Prot. 01-0CT-2002, sequence version 1. 07-MAR-2006, entry version 25. 25. 21nc finger and BTB domain-containing protein 8. Name-2PTB8; Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87.0%; Score 47; DB 2; I
92.3%; Pred. No. 1.6e+02;
tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, DQ176003; ABA02190.1; -; mRNA.
GO, GO:0005634; C:nucleus; IEA.
GO, GO:0003676; F:nucleic acid binding; IEA.
GO, GO:0008270; F:proctein binding; IEA.
GO, GO:0008270; F:zinc ion binding; IEA.
InterPro; IPR001010; BTB.
InterPro; IPR001089; ZIE_C2H2.
                                                         11-OCT-2005, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            512 AA.
506 AA.
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   PRT;
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Page T., Seranki N., Wilhikhaso T., Otanki T., Sujayama T., Itie R., Andermer, M., Obayanki M., Wilhikhaso T., Chunki T., Sujayama T., Itie R., Andermer, D., Saito K., Kawai Y., Isano Y., Bakanura Y., Mirakami K., Yasada T., Kuwan Y., Mirakami K., Wasada T., Ivawangi T., Wagatama M., Shiracoti A., Saido M., Mananco C., Saito K., Kawai Y., Itakanura Y., Mirakami M., Sanda M., Kaku Y., Kaku Y., Kadura H., Kondo H., Sujawara M., Manancha M., Mana
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DB 1; Length 512;

Score 47;

87.08;

Query Match

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                    Gaps
                                                                                                                                                                                                                                                                    Anopheles gambiae str. PEST.
Eukaryota; Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
Anophelinae; Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Anopheles gambiae Sequence Committee;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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92.3%; Pred. No. 1.6e+02;
ive 0; Mismatches 1; Indels
                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                           The Anopheles gambiae Sequence Committee; "Anopheles gambiae re-annotation."; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55760 MW; 68A0C7DEA9FE24DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AAAB01008933; EAA09944.3; -; Genomic_DNA. GO; GO:0003676; F:nucleoide acid binding; IEA. GO; GO:0000166; F:nucleotide binding; IEA. InterPro; IPR012677; a b_plait_nuc_bd. InterPro; IPR00532; PolyU_bd. InterPro; IPR0050594; RNII_RNA_bd. InterPro; IPR0030594; RNM I. RNA_D: IPR007954; RNM I. POLYU_half_pint; 2.
   Pred. No. 1.6e+02; ); Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-JUL-2005, integrated into UniProtKB/TrEMBL.
19-JUL-2005, sequence version 1.
07-FBB-2006, entry version 4.
Hypothetical protein.
ORFNAmes=UM05773.1;
                                                                                                                                                                                     15-DEC-2003, integrated into UniProtKB/TrEMBL 07-DEC-2004, sequence version 2. 07-FEB-2006, entry version 16. ENSANGPO0000016225.
                                                                                                                                                          521 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00366; RRM; 3.
SMART; SM00361; RRM 1; 1.
TIGRFAMM; TIGRO1645; half-pint; 1.
PROSITE; PSG0102; RRM; 3.
SEQUENCE 521 AA; 55760 MW; 68A0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q4P290 USTMA PRELIMINARY; PRT;
Q4P290;
                                                                                                                                                          PRT;
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0
                                                                                                                                                                                                                                                  ORFNames=ENSANGG0000013746;
 92.3%;
                                                                                                                                                          Q7PPS0_ANOGA PRELIMINARY;
                                                                             136 AAVAAAAAAAA 148
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339 AAVAAAAAAAAA 351
                                                1 AAFAAAAAAAA 13
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Best Local Similarity 92.3
Matches 12; Conservative
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nes 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
STRAIN=PEST;
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                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                              STRAIN=PEST:
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Q7PPS0 ANO
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Q4P290 UST
ID Q4P29
AC Q4P29
DT 19-JU
DT 07-FE
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GN ORFNA
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Protein sister of
                                                                                                                                                                                                                                                      NCBI_TaxID=7227;
                                                        Q9VQS7; Q24571;
                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila.
                                          DROME
                SOB_DROME
                                          RESTRAIN-521;

RA AIT-Cabhra M., Allen N., Allen T., An P., Abouelleil A., Adekoya E.,

RA AIT-Cabhra M., Allen N., Allen T., An P., Anderson M., Anderson S.,

RA Arachchi H.M., Armbruster J., Bidnari D., Baldwin J., Barry A.,

RA Arachchi H.M., Armbruster J., Bidnar J., Boguelavskiy L.,

RA Arachchi H.M., Armbruster J., Bidnar J., Boguelavskiy L.,

RA Calvo S.E., Camarata J., Campo K., Chang J., Cheshatsang Y.,

RA Clowe C., David R., Dawer T., Degray S., Dodge S., Dooley K.,

RA Chomer C., David R., Dawer T., Degray S., Dodge S., Dooley K.,

RA Dorje P., Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T.,

RA Bngels R., Erickson J., Farlan J., Galagan J.E., Gearin G., Gnerre S.,

RA Anirke A., Goyette A., Graham J., Grandbois E., Heller A., Higgins H.,

RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,

RA Hand D., Landers T., Loger J., Levins D., Lewis E., Labutti K.,

RA Anirke D., Jones C., Kamal M., Kamata A., Kamysselis M., Karlson E.,

RA Manning J., Marbbit R., Machola S., Lewis D., Lewis T.,

RA Manning J., Marbbit R., Machola S., Lewis D., Lewis T.,

RA Manning J., Marbbit R., Machola S., Labutti K.,

RA Manning J., Marbbit R., Machola S., Lewis D., Lewis T.,

RA Manning J., Marbbit R., Machola S., Lawis D., Lewis T.,

RA Manning J., Marbbit R., Machola S., Lawis D., Lewis T.,

RA Manning J., Marbbit R., Machola S., Lawis D., Lewis T.,

RA Manning J., Marbbit R., Machola S., Ray V., Raymond C.,

RA Morsu N., O'Donnell P., O'Roawo O., O'Leary S., Omccebe B.,

RA Norbu N., O'Donnell P., O'Roawo O., O'Leary S., Marbo T.,

RA Norbu N., O'Bonnell P., News C., News C., Nguyen C.,

RA Norbu N., O'Bonnell P., Seamen C., Settipali S., Rachupbach R., Seamen C., Settipali S., Rachupbach R., Seamen C., Settipa M., Rameau R., Ray V., Raymond C.,

RA Retta R., Richardson S., Rise C., Rodiguez J., Rubban R.,

Rangels R., Mandil T., Willer E. S., Theodore J., Wullee D., Wassille H.,

RA Mandil T., Whittaker C., Wilkinson J., Wassille W.,

RA Mandil T., Whittaker C., Wilkinson J., Wassille W.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AACF01000212; EAK86012.1; -; Genomic_DNA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:000355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR000679; Znf_GATA.
Pfam; PF00120; GATA; 1.
SWART; SM00401; ZnF_GATA; 1.
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Eukaryoca, Fungi, Basidiomycota, Ustilaginomycetes,
Ustilaginomycetidae, Ustilaginales, Ustilaginaceae, Ustilago.
NCBI_TaxID=237631;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38cv ....,
87.0%; Score 47; DB 2; Length 22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l protein.
529 AA; 53820 MW; D5ABC2C8EA96B06D CRC64;
                                                                    [1]NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 92.3
nes 12; Conservative
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1 AAFAAAAAAAA 13 AAVAAAAAAAA 88

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MEDLINE=22426069; PubMed=12537572; Matthews B.B., Campbell K.S., Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whiffield E.J., Bayraktaroglu L., Berman B.P., Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
                                                                                                                                                                                                                                                         Hart M.C., Wang L., Coulter D.E.; "Comparison of odd-skipped and two "Comparison of the structure and expression of odd-skipped and two related genes that encode a new family of zinc finger proteins in
                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE [MRNA], AND TISSUE SPECIFICITY
                           16-AUG-2005, integrated into UniProtKB/Swiss-Prot. 01-MAY-2000, sequence version 1. 07-MAR-2006, entry version 30.
                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
578 AA.
PRT;
                                                                                                                                                                                                                              STRAIN=Canton-S; TISSUE=Embryo;
MEDLINE=97032935; PubMed=8878683;
                                                                               odd and bowel.
                                                                                                                                                                                                                                                                                                                           Genetics 144:171-182(1996)
                                                                                              Name=sob; ORFNames=CG3242
STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RI DIMENDAL-LAIL TELIBLE-1003).

RET Mech. Dev. 120:1139-1151(2003).

LIFE TOWCTION: Pair-rule protein that determines both the size and polarity of even-numbered as well as odd-numbered parasegments during embryogenesis. DNA-binding transcription factor that acts during embryogenesis. DNA-binding transcription factor that acts primarily as a transcriptional repressor but can also function as a transcriptional activator, depending on the stage of development and spatial restrictions (By similarity). May function redundantly with odd and drm in leg joint formation during the larval stages, acting downstream of Notch activation.

LISSUE SPECIFICITY: Has two temporally distinct modes of expression during early embryogenesis; expressed in seven stripes at the blastoderm stage. Also expressed in a non-periodic domain at the anterior of the embryo. During gastrulation, the seven primary stripes are supplemented by seven secondary stripes that appear in alternate segments. This results in the latensity at appear in alternate segments in the avenage, gaining in intensity at gastrulation. Expressed in the invaginating stomodeum and proctodeum of the embryonic gut. By stage 13, expressed in the region that will form the partogentic supplementally engage 13, expressed in the region that will form the pathyonic gut. By stage 13, expressed in the gut through the remainder of embryogenesis. Expressed has pattern in the leg disk at the distal edge of each presumptive leg segment in the lasts and pharmane and pattern in the leg disk at the distal edge of each presumptive leg segment and segment all edge of each presumptive leg segment and segment and pharmane event in target and segments and pharmane event in the areal segments.
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                                                                                                                                         STRAIN-Berkeley; TISSUE-Embryo; Stapleton M., Carlson J., Champer M., Champe M., Mundalez M., Guarin H., Kronmiller B., Li P.W., Liao G., Miranda A., Mungall C.J., Nunoo J., Pacleb J.M., Paragas V., Park S., Patel S., Phouanenavong S., Wan K.H., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                POSSIBLE FUNCTION, AND TISSUE SPECIFICITY.
PubMed=1459720; DOI=10.1016/j.ydbio.2003.07.011;
Hao I., Green R.B., Dunaevsky O., Lengyel J.A., Rauskolb C.;
"The odd-skipped family of zinc finger genes promotes Drosophila leg
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22930851; PubMed=14568103; DOI=10.1016/j.mod.2003.08.001; Johansen K.A., Green R.B., Iwaki D.D., Hernandez J.B., Lengyel J.A., "The Drm-Bowl-Lin relief-of-repression hierarchy controls fore- and
                                                       "Annotation of the Drosophila melanogaster euchromatic genome: a
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ensembl; CG3242; Drosophila melanogaster.
FlyBase; FBgn0004892; sob.
GO; GO:0003674; C:nucleus; ISS.
GO; GO:0003677; F:DNA binding; ISS.
GO; GO:0016563; F:transcriptional activator activity; ISS.
GO; GO:0016564; F:transcriptional repressor activity; ISS.
GO; GO:0007350; P:blastoderm segmentation; ISS.
                                                                                                                                                                                                                                          Patel S., Phouanenavong S., Wan K.H., Yu C., Lewis S.E., Celniker S.E.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                         Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Contains 5 C2H2-type zinc fingers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE003579; AAF510871; -; Genomic_DNA.
EMBL; BT003205; AA024960.1; -; mRNA.
PIR; S72227; S72227.
HSSP; P07248; 2ADR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               segments 1
                                                                                                                             NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U62004; AAC47282.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                        Biol. 263:282-295(2003).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE SPECIFICITY.
                                                                              systematic review
                                                                                                                                                                                                                                                                                                                                                                                            segmentation
                                         Lewis S
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GO; GO: 0016348; P:1eg joint morphogenesis (sensu Endopterygota); IMP.

GO; GO: 000122; P:negative regulation of transcription from R. .; ISS.

RO; GO: 0004594; P:periodic partitioning by pair rule gene; ISS.

RO; GO: 0004594; P:positive regulation of transcription from R. .; ISS.

RO; GO: 0004594; P:positive regulation of transcription from R. .; ISS.

RO; GO: 0004594; P:positive regulation of transcription from R. .; ISS.

RO; GO: 0004594; P:positive regulation of transcription from R. .; ISS.

RESURTS ROSON RESULTS RE
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                                                                                                                                                                             . .; ISS.
                                                                         . .; ISS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87.0%; Score 47; DB 1; Length 578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0F600954CFA7D8D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S -> P (in Ref. 1).
SS -> G (in Ref. 1).
P -> L (in Ref. 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-2000, sequence version 1.
07-MAR-2006, entry version 27.
Hypothetical protein FLJ10572 (Kelch-like 11)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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501
501
529
256
176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      578 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=KLHL11;
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entry version 21.

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Muridae; Mus.
                                          Adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone: B230201M16 product: Mi-2 autoantigen 240 kDa protein homolog (Fragment).
   01-MAR-2003, integrated into UniProtKB/TrEMBL.
                    01-MAR-2003, sequence version 1.
                                                                                                                                                                  NCBI_TaxID=10090;
   MEDLINE-2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;

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R. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K., Nakadima Y., Mizuno T., Morinaga M., Sasaki M., Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T., Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K., Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R., Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.; "Complete sequencing and characterization of 21,243 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 47; DB 2; Length 708;
Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH MGC Project; Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80148 MW; 38733CE875172E12 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO, GO:0005515; F:protein binding; IEA.
InterPro; IPR011705; BACK.
InterPro; IPR010210; BTB.
InterPro; IPR013069; BTB.
InterPro; IPR006552; Kelch_rep.
Pfam; PF07707; BACK; 1.
Pfam; PF00551; BTB; 1.
Pfam; PF00651; BTB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; BC034470; AAH34470.1; -; mRNA.
Ensembl; ENSG00000178502; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AK001434; BAA91689.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87.0%;
92.3%;
                                                                                                                                                         Nat. Genet. 36:40-45(2004).
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Best Local Similarity 92...
Best Local 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HGNC; HGNC:19008; KLHL11.
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PROSITE; PS50097; B1
                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                             CDNAS."
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RA Carminci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Davis M.J., Wilming L.G., Adidnis V., Allen J.E., Shimokawa K., Ra Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Davis M.J., Wilming L.G., Adidnis V., Allen J.E., Bailey T.L., Rabeai-Impionbato A., Apweiler R., Aturaliya R.N., Balley T.L., Ambeai-Impionbato A., Apweiler R., Aturaliya R.N., Balley T.E., Choudhary V., Christoffels A., Clutterbuck D.R., Barbers M., Engetrom P., Fagiolini M., Faulkner G., Glageras T.R., Golobort T., Green R.E., Golobort T.K., Hirokawa N., Libing D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T., Katoh M., Katoh M., Kawasawa Y., Kelso J., Kitamura H., Katoh M., Katoh M., Kawasawa Y., Kelso J., Kitamura H., Katoh M., Larearevic D., Lipovich L. Liu J., Liu J.,
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Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
Hayashizaki Y.;
NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6J, TISSUE-Corpora quadrigemina;
MEDLINE-99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=16141073; DOI=10.1126/science.1112009; RIKBN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium; "Antisense Transcription in the Mammalian Transcriptome."; Science 309:1564-1566(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The transcriptional landscape of the mammalian genome.";
                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-C57BL/6J; TISSUB-Corpora quadrigemina; PubMed=16141072; DOI=10.1126/science.1112014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6J; FISSUE=Corpora quadrigemina;
PubMed=16141073; DOI=10.1126/science.1112009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
                                                                                                                                           Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning."; Methods Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 309:1559-1563(2005).
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Gaps

ö

1; Indels

0; Mismatches

1 AAFAAAAAAAA 13

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4 AAVAAAAAAAA 16

708 AA.

PRT;

PRELIMINARY;

RESULT 31 QBBR71 MOUSE ID QBBR71 MOUSE AC QBBR71;

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MEDINE-Z.539483; Furnace_Listobell_JUD=10_LIDS/INGIRCHICLOLS

A MADINE-Z.539483; Furnace_Listobell_JUD=10_LIDS/INGIRCHICLOLS

A Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

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Balke J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

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MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60,770 full-length cDNAs.";
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Mus musculus (Mouse).
Bukaryota; Mctazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Muxinae; Mus.
NCBI_TaxID=10090;
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GO; GO:0016581; C:chromatin remodeling complex; IDA.
GO; GO:0016581; C:NuRD complex; IDA.
GO; GO:0006331; P:protein binding; IPI.
GO; GO:0006333; P:chromatin assembly or disassembly; IDA.
InterPro; IPR010598; CHD N.
InterPro; IPR010953; Chromo.
InterPro; IPR010965; Znf PHD.
Pfam; PF060385; Chromo; 1.
Pfam; PF00628; PHD; 2.
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                                                                                                                 STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMR; QBBR71; 464-519.
Ensembl; ENSMUSG0000018474; Mus musculus.
MGI; MGI:1344395; Chd3.
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PROSITE; PS50013; CHROMO 2; 2.
PROSITE; PS50016; ZF PHD 2; 2.
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07-FEB-2006, entry version 20.
                                                             Genome Res. 10:1757-1771 (2000)
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SMART; SM00249; PHD; 2.
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Matches 12; Conservative
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R BAJIC V.B. No. 1126/Geience.1112014;

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MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
Adama M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000, sequence version 1.
21-FEB-2006, entry version 39.
Protein pygopus (Gammy legs protein).
Name-pygo; Synonyma-gam; ORFNames-CG11518;
Drosophila melanogaster (Fruit fly).
Bukaryota; Merazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Erachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                     87.0%; Score 47; DB 2; Length 709; 92.3%; Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                              709 AA; 80429 MW; BA3DB8D4CA6FEB7A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-SEP-2002, integrated into UniProtKB/Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                               EMBL; AK029101; BAC26297.1; -; mRNA.
Ensembl; ENSMUSG0000048732; Mus musculus.
MGI; MGI:238648; KIbl11.
GO; GO:0005515; F:protein binding; IEA.
INTERPO; IPR011705; BACK.
INTERPO; IPR0103069; BTB.
INTERPO; IPR013069; BTB.
INTERPO; IPR013069; BTB.
Pfam; PF07707; BACK; 1.
Pfam; PF07707; BACK; 1.
Pfam; PF0144; Kalch_rep.
Pfam; PF0144; Kalch_rep.
FMART; SM00225; BTB; 1.
                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                               3 AAVAAAAAAAAA 15
                                                                                                                                                                                                                                                                                                                                                                                       1 AAFAAAAAAAA 13
                                                                                                                                                                                                                                                                                                                                                             12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                  Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DROME
                                                                                                                                                                                                                                                                                                             SEQUENCE
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Balton G.C. Westenn J.R. Vandell B.D. Zhang O. Chen L.R.
Balton G.C. Westenn J.R. Vandell B.D. Zhang O. M. Feliffer B.D.
Balton G.C. Abrill J. T. Adabyani A. An H.J. Andrews-Feanhoch C.R. Balddrin D. Abrill J. T. Adabyani A. An H.J. Andrews-Feanhoch C.R. Balddrin D. Abrill J. T. Adabyani A. An H.J. Andrews-Feanhoch C.R. Balddrin D. Abrill J. T. Adabyani A. An H.J. Andrews-Feanhoch C.R. Balddrin D. Baldbakov S. Balton K.Y. Benos P.V. Berma B.P. Bhundari D. Baldbakov S. Balton K.Y. Benos P.V. Berma B.P. Bhundari D. Baldbakov S. Balton B. Barton B. Balton B. B. Mannal B. Mannal B. B. Mannal B. M

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Ensembl; CGI1518; Drosophila melanogaster.

R Flybase; Regn0043900; pygo.

R BioCyc; DMEL-XXX-02:DMEL-XXX-02-014325-MONOMER; -.

R GO; GO:0005634; C:nucleus; NAS.

GO; GO:001528; F:transcription regulator activity; IPI.

GO; GO:003174; P:eye-antennal disc development; IMP.

R GO; GO:001717; P:positive regulation of Wnt receptor signali. ..; IPI.

GO; GO:001717; P:positive regulation of Wnt receptor signaling pathway; IMP.

R GO; GO:001017; P:positive regulation of Wnt receptor signaling pathway; IMP.

R GO; GO:0010155; Znf_PHD.

R PROSITE; PS013195; ZF_PHD.; 1.

R PROSITE; PS013159; ZF_PHD.; 1.

R ROSITE; PS013159; ZF_PHD.; 1.

R ROSITE; PS01016; ZF_PHD.; 1.

R Complete protecome; Developmental protein; Metal-binding;
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                                                                                                                                                                                                                                                                                                                                               Nuclear protein; Segmentation polarity protein; Wnt signaling pathway; Zinc; Zinc-finger.

CHAIN 1 815 Protein pygopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-0CT-2005, integrated into UniProtKB/TrEMBL.
11-0CT-2005, sequence version 1.
07-FBB-2006, entry version 5.
B16 F10Y cells cDNA, RIKEN full-length enriched library,
clone:6370031D15 product:SH3 multiple domains 2, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia; Butheria, Buarchontoglires; Glires; Rodentia, Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning."; Methods Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                         PHD-type.—
Nuclear localization signal (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87.0%; Score 47; DB 1; Length 815; 92.3%; Pred. No. 2.3e+02; tive 0; Mismatches 1; Indels
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S -> P (in Ref. 1).
369FD5A5D34BC136 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                 Protein pygopus.
/FTId=PRO_000097124.
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    EMBL; AY058500; AAL13729.1; -; mRNA.
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39 45 Nuu
48 65 All
123 749 Asi
393 393 S
815 AA; 80493 MW;
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Q3UG42;
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Les 12; Conservative
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MOTIF
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O30G42 MOU
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AC 030G44
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A Quetincich S., Harbers W., Hayashi Y., Hensch T.K., Hirokawa N., R. M. Hill D., Humbinschi L., Loseno N., Isbor Y., Kapan J., Kitamas H., Kitano H., Kanol H., Caplian C., Karishans S.P., Kruger. A., Edumarischi S.K., Kitano H., Lazisi K., Caprischi J., Lazisvo, D., Liporich L., Lill J., Karischkin I.V., Lazisvo, D., Liporich L., Lill J., Karischkin I.V., Lazisvo, D., Liporich L., Lill J., Marteuda H., Mateurasa S., While H., Makano N., Nakaduhi H., Naye S., Morris K., Marteuda H., Mateurasa S., While H., Makano N., Nakaduhi H., Naye S., Morris K., Mateudi H., Mateuda H., Mateurasa S., While H., Makano N., Nakaduhi H., Naye S., Morris K., Mateudi H., Mateudi H., Mateudi H., Mateudi H., Mateuda H., Mateudi H., Mateud
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Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Azakaa T., Haraa A., Pountishi Y., Konno H., Addedi J., Photuda S., Alzawa T., Lawa M., Mishi K., Kyosawa H., Kondo S., Vamanaka I., Rakawa T., Zakawa T., Zakip B., Zakawa T., Zakip T., Zakip B., Zakip B., Zakawa T., Zakip B., Zaki
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                                                                                                                                                                                                                                                                                                                                                              Name-shamd2, Synonyms-POSH;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98151363; PubMed=9482736; DOI=10.1093/emboj/17.5.1395; Tapon N., Nagata K., Lamarche N., Hall A.; Tapon N., Nagata K., Lamarche N., Hall A.; "A new rac target POSH is an SH3-containing scaffold protein involved in the JNK and NF-kappaB signalling pathways.";
                                                                                                                   Gaps
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                                                                                87.0%; Score 47; DB 2; Length 828;
92.3%; Pred. No. 2.3e+02;
ive 0; Mismatches 1; Indels
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HISP, 199071; T09071.

MISI, P19878; IK4U.

MGI; MGI:19313066; Sh3md2.

GO; GO:0030027; C:lamellipodium; IDA.

GO; GO:000578; F:MAP-Kinase scaffold activity; IDA.

GO; GO:0005518; F:MAP-Kinase scaffold activity; IDA.

GO; GO:0005218; F:Protein binding; IPI.

GO; GO:0005218; P:regulation of JNK cascade; IDA.

InterPro; IPR00108; Neu_Cyt_fact_2.

InterPro; IPR001841; Znf_RING.

Ffam; PF00018; SH3 1; 4.

PFam; PF00007; zf-G3HC4; 1.
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                                                   72FE525B907FE0FB CRC64;
                                                                                                                                                                                                                                                                                              01-AUG-1999, integrated into UniProtKB/TrEMBL. 01-AUG-1998, sequence version 1. 07-FEB-2006, entry version 26. Plenty of SH38.
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PRINTS; PRO0429; P67PHOX.
PRINTS; PRO0422; SH3DOMAIN.
PRODOM; PD0000066; SH3; 4.
SWART; SM00126; SH3; 4.
PROSITE; PS50002; SH3; 4.
PROSITE; PS500018; ZF RING 1; 1.
PROSITE; PS500089; ZF RING 1; 1.
PS50002; SH3; 3.
PS00518; ZF RING 1; 1.
PS50089; ZF RING 2; 1.
828 AA; 86192 MW; '
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NCBI_TaxID=10090;
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                                                                                                                                                                                 419 AAVAAAAAAAA 431
                                                                                                                                                1 AAFAAAAAAAAA 13
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                                                                                                                12; Conservative
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                                                                                                  Best Local Similarity
                                                                                   Query Match
                                  PROSITE;
                                                 SEQUENCE
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Q9VE88 DROME

RESULT 36

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RN MUCLEOTIDE SEQUENCE.

RA Adams M. D. (Celniker S.E. 1. Holt R.A. Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A. Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A. Evans C.A., Gocayne J.D.,

RA George R.A. Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Button G.G., Wortman J.E., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.H.C., Blazel R.G., Chang M., Feleifer B.D.,

RA Bandon R.C., Rogers Y.H.C., Blazel R.G., Chang M., Feleifer B.D.,

RA Ballew R.M., Bears B. E., Richards S. E., Rollomb C., Baldwin D.,

Ballew R.M., Baus A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Ballew R.M., Cawley S., Daller R., Cadieu B., Center A., Chindra I.,

RA Buttis K.C., Busam D.A., Butler H., Cadieu B., Center A., Chindra I.,

RA Buttis K.C., Busam D.A., Butler H., Cadieu B., Center A., Chindra I.,

Ra Dodgon K., Delcher A., Deng Z., Mays A.D., Dew II., Dietz S.M.,

RA Podeon K., Deng E., Downes M., Dugan-Rochs S., Dunkov B.C., Dunn P.,

RA Dodgon K., Delcher A., Heiman T.J., Hernandez J.R., Houck J.,

RA Dodgon K., Duy L.E., Downes M., Dugan-Rochs S., Pleischmann W.,

RA Dodgon K., Duy L.E., Deng Z., Mays A.D., Dew II., Dietz S.M.,

RA Dodgon K., Duy L.E., Melman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D.A., Heiman T.J., Weiner S., Fleischmann W.,

Rabkop P., Lei Y., Leviteky A.A., Li J.H., Li Z., Liang Y., Lin X.,

Liu X., Mattel B., Mollosh T.C., Mocled M.D., Morbry C.,

RA Hostin D. R., Mellina N.V., Mobarry C., Morris J., Mong G., M., Nelson D.L.,

RA Merkulow G., Milshina N.V., Mobarry C., Morris J., Morris C., Stenher H.,

RA Belazz K., Siden K.A., Wixon K., Nusskern D.R., Pacele D.J., Mang C.-Y., Wassarman D.A., Weinsteck G.M., Warny D.M., Narry D.M., Wang Z.-Y., Wassarman D.A., Weinster E., Spradling A.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.B., Rubin G.M., Ashburner M., Celniker S.B., "The transposable elements of the Drosophila melanogaster euchromatin: a genomics perspective.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=2246665; PubMed=12537568;

Celniker S. E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Sylrskas R., Tabor P.E., Wan K., Stapleron M., Sutron G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; Finishing a whole-genome shotgun: release 3 of the Drosophila
                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                       Q9VE88;
01-MAY-2000, integrated into UniProtKB/TrEMBL
01-OCT-2002, sequence version 2.
21-FEB-2006, entry version 28.
897 AA.
                                                                                                                                                                     Name=CG15803; ORFNames=Dmel CG15803;
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PRELIMINARY; PRT;
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     Q9VE88 DROME
  REPRESENTED TO THE PROPERTY OF THE PROPERTY OF
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Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                          MEDILNE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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TISSUB=smbryonic tail;
PubMed=15368895; DOI=10.1093/dnares/11.3.205;
Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                              Frise E., George R.
Svirskas R., Smith
                                                                                                                                                                                                                                                                Lewis S.E.;
"Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                 Berkeley Drosophila Genome Project,
Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E.,
Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R
Yu C., Rubin G.,
"Drosophila melanogaster release 4 sequence.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JAN-2006) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        897 AA; 94372 MW; 3A74789E08FD1A2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9VBP2:CG5053; NDExp=1; IntAct=EBI-172540, EBI-205
Q9VQW7:ed; NDExp=1; IntAct=EBI-172540, EBI-85823;
SIMILARITY: Contains 4 PDZ (DHR) domains.
                                                                                                                                                                                                                                                                                                                                         Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002)
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92.3%; Pred. No. 2.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FlyBase; FBgn0038606; CG15803.
GO; GO:0005515; F:protein binding; IPI.
InterPro; IPR001478; PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QE9Z11 MOUSE PRELIMINARY; PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEam, PF00595, PDZ; 4.
SWART; SM00228, PDZ; 4.
PROSITE; PS50106; PDZ; 4.
SEQUENCE 897 AA: 94777
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                                                                                                                                                                                                                                                                                                                   systematic review.";
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11-OCT-2005, sequence version 1.
07-FEB-2006, entry version 5.
Adult male medulla oblongata cDNA, RIKEN full-length enriched library, clone:6330596E03 product:hypothetical Transforming protein Ski/SAND-like/Putative DNA binding containing protein, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=CS7BL/6J; TISSUB=Medulla oblongata;
PubMed=16141072; DOI=10.1126/science.1112014;
Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
Saga Y., Seino S., Nishimura M., Kaisho T., Hoshino K., Kitamura H., Nagase T., Ohara O., Koga H.;
Nagase T., Ohara O., Koga H.;
Prediction of the coding sequences of mouse homologues of KIAA gene:
IV. The complete nucleotide sequences of 500 mouse KIAA-homologous cDNAs identified by screening of terminal sequences of cDNA clones randomly sampled from size-fractionated libraries.";
DNA Res. 11.205-218(2004).
-! SIMILARITY: Contains 1 KING-type zinc finger.
-! SIMILARITY: Contains 4 SH3 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
MEDLINE=99279553; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Methods Enzymol. 303:19-44(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                             EMBL; AK173185; BAD32463.1; -; mRNA.
MGI; MGI:1913066; Sh3md2.
GO; GO:0030027; C:lamellipodium; IDA.
GO; GO:0005078; F:MAP-kinase scaffold activity; IDA.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:004528; P:requilation of JNR cascade; IDA.
InterPro; IPR00108; Neu cyt_fact_2.
InterPro; IPR001452; SH3.
InterPro; IPR01841; Znf RING.
Pfam; PF00018; SH3.1; 4.
PF00097; zf-G3HC4; 1.
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PRINTS; PR00452; SH3DOMAIN.
Prodom; PD000066; SH3; 4.
SMART; SM00126; SH3; 4.
PROSITE; PS50002; SH3; 4.
PROSITE; PS50018; ZF RING 1; 1.
PROSITE; PS50089; ZF RING 2; 1.
Metal-binding; SH3 domain; Zinc-finger.
NON_TER
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QJUYA4;
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nes 12; Conservative
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SEQUENCE
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MOUSE
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KEATIMECIALL SEQUENCE.

KAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arawawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., A Arawawa T., Isawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Ashburner M., Batalov S., Casavant T., A Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Ruhl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., A Sakai K., Okido T., Furuno M., Aono H., Badarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Bronstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Buchinoich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N. H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez T., Sakamoco N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Whintawer C., Wilming L., Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.; Handar B.S., Rogers J., Hayashizaki Y.; Hanalysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=C192L/6J; TISSUE=Medulla oblongata; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Nomalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA lbraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Nagaoka S., Sasaki N., Carninci P., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoco R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rike integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
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GO:0005634; C:nucleus; RCA.
GO:0005634; C:nucleus; IDA.
GO:0005667; C:transcription factor complex; IDA.
GO:0005615; F:protein binding; IPI.
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                                                                                                                                     Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 409:685-690(2001).
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NUCLEOTIDES ESQUENCE.

REPAIRS AGONG: PubMed=10731132; DOI=10.1126/science.287.5461.2185; MCLEOTIDES ESQUENCE.

RA Adams N.D. Cellniker S.E., Holt R.A. Hoskins R.A., Galle R.F., Adams N.D., Cellniker S.E., Holt R.A., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Holt R.A., Andrews P.A., Galle R.F., Bandell M.D., Zhang Q., Chen L.X., Baction G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Barton G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Barton G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Barton G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Barton R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Bart K., Basu A., Baxendale J., Bandari D., Bolshakov S., Ballew R.M., Basu A., Baxendale J., Bandari D., Bolshakov S., Borkova D., Bockhan M.R., Buck J., Brokktein P., Broktein P., Borkova D., Bockhan M.A., Buller H., Cadleu E., Center A., Chandra I., Cawley S., Downes M., Buris K.C., Busam D.A., Buller H., Cadleu E., Center A., Chandra I., Cherry J.M., Cawley S., Downes M., Duran-Noche S., Burkov B.C., Dunn P., Borsler C., Gabriellan A.E., Garg N.S., Galbart W.M., Glasser K., Gong P., Gorrell J.H., Gu Z., Glann P., Harris M., Glasser K., Gong P., Gorrell J.H., Gu Z., Glann P., Harris M., Glasser K., Andrei B., Mollock A., Heilman T.J., Wei M.-H. Index D., Lai X., Mattel B., Mollock M., Weitel B., Mollock M., Wobbarty C., Morris J., Lin X., Lasko P., Lei Y., Levitzky A.A., Li J.H., Li Z., Liang Y., Lin X., Lasko P., Lei Y., Mollock M., Wobbarty C., Morris J., Wobsker D., M., Nattel B., Mollock M., Nukskern D.R., Mattel B., Mollock M., Nukskern D.R., Mohang C., Scheeler F., Shen H., Rainen B.C., Siden Klanes R., Moy M., Wurphy B., Murphy B., Mur
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Drosophila melanogaster (Fruit fly).
Bukaryote; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Nooptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
GO; GO:0003714; F:transcription corepressor activity; IDA. GO; GO:0050875; P:cellular physiological process; RCA. GO; GO:0016481; P:negative regulation of transcription; IDA. InterPro; IPR003180; Transform_Ski. Pfam; PR02437; Ski. Sno; 1.
                                                                                                                                                                       Length 935;
                                                                                                                                  935 AA; 96933 MW; A9C2953F4A77E367 CRC64;
                                                                                                                                                                              87.0%; Score 47; DB 2; I
92.3%; Pred. No. 2.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                              QOVIGO DROME PRELIMINARY; PRT;
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                                                                                                                                                                                                                                                                                                          484 AAVAAAAAAAA 496
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                                                                                                                                                                    MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R., Patel S., Fribe E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
NUCLECTIDE SEQUENCE.
MEDLINE=22456065; Pubmed=12537568;
Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstrock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M., "Finishing a whole-genome shoqun: release 3 of the Drosophila melanogaster euchromatic genome sequence."
                                                                                                                                                                                                                                                                                     MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochnik S.B.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Berkeley Drosophila Genome Project;
Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.
                                                                                                                                                                                                                                                                                                                                                                                           "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE003672; AAF54032.3; -; Genomic_DNA.
FlyBase; FBgn0003263; rn.
GO; GO:0007456; P:eye development (sensu Endopterygota); IMP.
GO; GO:0007480; P:leg morphogenesis (sensu Endopterygota); IMP.
InterPro; IRR07080; Znf C2H2.
ProDom; PD000003; Znf_C2H2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 47; DB 2; Length 946; Pred. No. 2.6e+02; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JAN-2006) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Drosophila melanogaster release 4 sequence.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PSSO15; ZINC_FINGER_C2H2_1; 6.
PROSITE; PSSO157; ZINC_FINGER_C2H2_2; 6.
Metal-binding; Nuclear_protein; Zinc; Zinc-finger.
SEQUENCE 946 AA; 100948 MW; 05EA01C8F64F61A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                     Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
                                                                                                                                                                                                                                    a genomics perspective.";
Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002)
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92.3%;
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nes 12; Conservative
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RC STRAIN-G57BL/6J; TISSUB-GECEPBELIUM, and Testis; R. PUGLECTIDE SEQUENCE ILARGE SCALE MRNA, and Testis; R. PARIN-G57BL/6J; TISSUB-GECEPBELIUM, and Testis; R. PARIN-G57BL/6J; TISSUB-GECEPBELIUM, and Testis; R. Parinci P., Kasukawa T., Kacayama S., Gough J., Frith M.C., Maeda N., Rajic V. B., Bernner S. E., Batalov S., Forrest A.R., Zavolan M., Bajic V. B., Bernner S. E., Batalov S., Forrest A.R., Bailey T.L., Ambesi-Impiombato A., Apweiler R., Atlan J.E., Bono H., Chalk A.M., Chistochabto A., Apweiler R., Atlan J.E., Bono H., Chalk A.M., Chistochabto D., Down T., Engetrom P., Fegiolini M., Faulkner G., Adishima T., Furuno M., Feed Bono B., Della Gatta G., R. Choughany V., Christoche B.P., Regiolini M., Faulkner G., R. Action D., Down T., Engetrom P., Fegiolini M., Faulkner G., R. Gingers T.R., Gojobori T., Green R.E., Adishima T., Furuno M., Feed J., Kilshod T.K., Hirokawa T., Alith D., Huminiacki L., Iacono M., Ikeo G., Libpovich L., Liu J., Aktion A., Aktion M., Kawasawa Y., Kelso J., Kitamura H., Kuronkin I., Lareau L.P., Lazarevec D., Lippovich L., Liu J., Aktion H., Kollias G., Kitishnan S.P., Kruger A., Kummerfeld S.K., Mortiskin S., Madan Babu M., Madera M., Marchionni L., Methaud H., Kollias G., Mishikawa S., Nori F., Ohara O., Avazaki Y., Otlando V., Pang K.C., Pavan W.J., Pavesi G., Pescole G., Rochbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y., Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y., Hammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Takmada K., Silva D., Sinclair B., Tammoja K., Tan S.L., Tang S., Rasa M., Waleston W., Wan S., Nori K., Van Waleston S., Kanamoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Takmada K., Shimada K., Sananishi H., Zabarovsky E., Zhu S., Kai C., Sasaki D., Tonmura K., Toh M., Kato T., Kawashima T., Kayanishi M., Plessof C., Shibata K., Shiraki Y., Rawashima T., Kayanima M., Koho S., Konno H., Nakano W., Nami J., Kawashima T., Kojama M., Rawashima T., Suzuki M., Nakanisaki Y., Shiraki Y., Shiraki Y., Shiraki Y., Shiraki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mizuhara E., Nakatani T., Minaki Y., Sakamoto Y., Ono Y., "Corll, a novel neuronal lineage-specific transcriptional corepressor for the homeodomain transcription factor Lbx1."; J. Biol. Chem. 280:3645-3655 (2005).
                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                          Ladybird homeobox corepressor 1 (Transcriptional corepressor Corll).
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-!- FUNCTION: Acts as a transcriptional corepressor of LBX1-!- SUBUNIT: Interacts with LBX1.
-!- INTERACTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 1 AND 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NGCLEOTIDE SEQUENCE [MRNA] (ISOFORM 2), FUNCTION, SUBCEL
LOCATION, TISSUE SPECIFICITY, AND INTERACTION WITH LBX1
                                QBBX45; QSW812; Q8C0T2; 21-JUN-2005, integrated into UniProtKB/Swiss-Prot. 01-MAR-2003, sequence version 1. 07-FEB-2006, entry version 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=15528197; DOI=10.1074/jbc.M411652200;
                                                                                                                                                                                                                                                                  Name=Lbxcorl; Synonyms=Corll;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Embryonic brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI TaxID=10090;
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Matches

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Gaps

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                                                                                                                                                                                                                                                                  IsoId=08BX46-3; Sequence=VSP_014178, VSP_014180, VSP_014181; Note=No experimental confirmation available; Note=No experimental confirmation available; TISSUE SPECIFICITY: Expressed in brain with higher levels in embryo than adult. Also expressed in adult testis. In embryonic brain, expressed in a subset of postmitotic neurons generated posterior to the midbrain-hindbrain border. In the developing spinal cord, selectively expressed in dorsal horn interneurons. SIMILARITY: Belongs to the SKI family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Missing (in isoform 3).
/FTId=VSP 014178.
Missing (in isoform 2).
/FTId=VSP 014179.
LQGGGCGGA -> PARGRRRRR (in isoform 3).
/FTId=VSP 014180.
Missing (in isoform 3).
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Alternative splicing; Coiled coil; Nuclear protein; Repressor; Transcription; Transcription regulation.
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/FTId=PRO_0000129391.
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                                                                                                                                                 Note=No experimental confirmation available;
-!- SUBCELLULAR LOCATION: Nucleus.
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /FTId=VSP 014181.
Q -> P (in Ref. 1)
                                                                                                                                                                                                                 IsoId=Q8BX46-2; Sequence=VSP_014179;
                                                                                                                          IsoId=08BX46-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AB185113; BAD69568.1; -; mRNA.
EMBL, AK029916; BAC26674.1; -; mRNA.
EMBL, AK049035; BAC33520.1; -; mRNA.
HSSP, P12755; 1MR1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                    September
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing:
                                                                                                            Title:
Perfect score:
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N

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Gaps

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98

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                      developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 39441; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 417;
85;
100.0%; Score 54; DB 8; Length 13; 100.0%; Pred. No. 0.024;
                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster polypeptide SEQ ID NO 39441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 42;
Pred. No. 8
                                                                                                                                                                                                                                                          ABB70883 standard; protein; 417 AA.
                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-2001; 2001WO-US009231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77.8%;
76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 225 ASTSAAAAAAAA 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid
genes from Drosophila and
interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 75..
Loca 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ASMSAASAASMAA 13
                                                                                                                                       ASMSAASAASMAA 13
                                                                                                                                                                                                                                                                                                                                                     26-MAR-2002 (first entry)
                                                                                               1 ASMSAASAASMAA 13
                                                  13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-656860/75.
N-PSDB; ABL14986.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PEKE ) PE CORP NY
                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 417 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila; de
pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Venter JC,
    Query Match
Best Local S
Matches 13
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ABP27418
                                                                                                                                                                                                             RESULT 2
                                                                                                                                                                                                                                       ABB70883
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comprising: (a) an MHC class II component comprising at least a portion

comprising: (a) an MHC class II component comprising at least a portion

of an MHC class II alpha chain and MHC class II beta

chain form a peptide binding groove; (b) a spaceholder molecule; and (c)

an effector component, where the effector component is linked to the MHC

class II component. Also described: (I) a pharmaceutical composition

comprising the MHC class II molecule and a carrier; (2) a method of

producing an MHC class II compound; (3) a method of directly identifying

an antigen-specific T cell; (4) a method of directly identifying

an autigen-specific T cell; (4) a method of tracting an immune response ex vivo in a subject;

(6) a method of regulating an immune response ex vivo in a subject; and

(7) a method of treating an immune disorder ex vivo in a subject; and

(7) a method of treating an immune disorder ex vivo in a subject;

(1) can be used for preparing a composition for treating immune

cativities, and can be used in gene therapy. The MHC class II compound

(I) can be used for preparing a composition for treating immune

cativities, neoplastic disease, autoimmunity or tractions, parasitic

infections, neoplastic disease, autoimmunity or tractions, parasitic

an MHC class II compound from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                               MHC class II compound; MHC class II component; MHC class II alpha chain; MHC class II beta chain; peptide binding groove; spaceholder molecule; effector component; immune response; immune disorder; virucide; antibacterial; antiparasitic; cytostatic; immunosuppressive; gene therapy; viral infections; bacterial infection; parasitic infection; neoplastic disease; autoimmunity; toxicity; human.
                       Aay37630 Chlamydia
Aef77642 Rat 3-hyd
Aef77640 Mouse 3-h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New MHC class II compound, useful for preparing a composition for treating immune disorders e.g. viral infections, bacterial infections, parasitic infections, neoplastic disease, autoimmunity or toxicity.
                                                                                                                                                                                                                                                                                                                                                                                                       Human MHC class II compound spaceholder molecule SEQ ID NO:5.
                                                                                                                                                 ALIGNMENTS
       ADO03023
AAY37630
AEF77642
AEF77640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 11; SEQ ID NO 5; 92pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (DAND ) DANA FARBER CANCER INST INC.
                                                                                                                                                                                                                                                                    ADI29009 standard; peptide; 13 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-JUL-2002; 2002US-0395494P.
22-JUL-2002; 2002US-0397893P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-JUL-2003; 2003WO-US021767
           1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seth N;
                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wucherpfenning KW,
           64.8
64.8
64.8
64.8
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Synthetic.

RESULT 1

AD129009

ID AD129009

XXX
AD129009

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AD129009

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AD129009

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AD129009

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AD129009

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AD129009

BE Huma
AD129009

XXX
AD129009

BE Huma
AD20009

Homo

ADI29009;

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Gaps

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Indels

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ABP27418 standard; protein; 970 AA.

ABP27418;

Sequence 13 AA;

13

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New nucleic acid molecule encoding a hyperimmune serum reactive antigen, useful for the manufacture of a vaccine against Streptococcus agalactiae
                                immune stimulation; antigen; bacterial surface display; hyperimmune serum reactive antigen; vaccine; bacterial infection; antibacterial; infection.
S agalactiae hyperimmune serum reactive antigen seqid 326.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 12; SEQ ID NO 326; 221pp; English.
                                                                                                                                                                                                                                                                                                                                                    Meinke A, Nagy E, Hanner M,
                                                                                                                                                                                                                    06-MAY-2004; 2004WO-EP004856.
                                                                                                                                                                                                                                                    07-MAY-2003; 2003EP-00450112.
28-NOV-2003; 2003EP-00450266.
                                                                                                         Streptococcus agalactiae
                                                                                                                                                                                                                                                                                                             (INTE-) INTERCELL AG
                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-821662/81.
                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ADU69414
                                                                                                                                             WO2004099242-A2.
                                                                                                                                                                                 18-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infection.
The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN6604-ABN71256 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used to recombinantly produce (I) and may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
                                                                                  Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Streptococcus protein for the treatment or prevention of infection disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Fraser C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 42; DB 5; Length 970; Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Masignani V, Margarit Y RosI, Grandi G,
                                                   Streptococcus polypeptide SEQ ID NO 4012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 3556; 4525pp; English
                                                                                                                                                                                                                                                                                                           2000GB-00026333.
2000GB-00028727.
                                                                                                                                                                                                                                                                       29-OCT-2001; 2001WO-GB004789
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             (first entry)
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Best Local Similarity 69.27
Best Local 9; Conservative
                                                                                                                                                            Streptococcus agalactiae.
                                                                                                                                                                                                                                                                                                                                                                                    (CHIR-) CHIRON SPA. (GENO-) INST GENOMIC RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-352536/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ABN68049.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 970 AA;
                                                                                                                                                                                                WO200234771-A2
             02-JUL-2002
                                                                                                                                                                                                                                                                                                           27-OCT-2000;
                                                                                                                                                                                                                                                                                                                               24-NOV-2000;
                                                                                                                                                                                                                                     02-MAY-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Telford J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tettelin H;
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Prustomersky S;

Kallenda S,

Horky M,

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The invention describes an isolated nucleic acid molecule encoding a hyperimmune serum reactive antigen or its fragment. Also described are: a vector comprising the nucleic acid molecule; a host cell comprising the vector comprising the nucleic acid molecule and comprising a sequence corocating the nucleic acid molecule and consisting of e.g., 85, 299, 467 consisting of peptides comprising e.g., 76, 134, 221 or 576 amino acids; consisting of peptides comprising e.g., 76, 134, 221 or 576 amino acids; a process for producing a Streptococcus agalactiae hyperimmune serum reactive antigen; a process for producing a cell that expresses a S. agalactiae hyperimmune serum reactive antigen; a pharmaceutical composition, especially a vaccine, comprising the hyperimmune serum composition, especially a vaccine, comprising the hyperimmune serum composition, especially a vaccine, comprising the hyperimmune serum control antibody; an antigonist that binds to the hyperimmune serum-reactive antigen; a method for identifying an antigonist capable of binding to the hyperimmune serum-reactive antigen; a method for identifying an antagonist capable of reducing or inhibiting the interaction activity of antagonist capable of reducing or inhibiting the interaction activity of a process for in vitro diagnosis and process for in vitro diagnosis of the hyperimmune serum-reactive antigen; and a process for in vitro diagnosis of the hyperimmune serum-reactive antigen; and a process for in vitro diagnosis of the hyperimmune serum-reactive antigen; and a process for in vitro diagnosis of the hyperimmune serum-reactive antigen; and a process for in vitro diagnosis of the hyperimmune serum-reactive antigen; and a process for in vitro diagnosis of the hyperimmune serum-reactive antigen; and a process for in vitro diagnosis of the hyperimmune serum-reactive antigen; and a process for in vitro diagnosis of the hyperimmune serum-reactive antigen; and a process for in vitro diagnosis of the hyperimmune serum-reactive antigen; and a process for in vi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hyperimmune serum reactive antigen is useful for isolating, purifying and/or identifying an interaction partner of the hyperimmune serum reactive antigen. The hyperimmune serum reactive antigen is useful for generating a peptide binding to the hyperimmune serum reactive antigen, where the peptide comprises anticalines, or for the manufacture of a functional nucleic acid comprising aptamers or spiegelmers. The nucleic acid molecule is useful for the manufacture of a functional ribonucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acid comprising ribozymes, antisense nucleic acids or siRNA. The nucleic acid molecule, hyperimmune serum-reactive antisen or antibody is useful for the manufacture of a vaccine against S. agalactiae infection. This ithe amino acid sequence of a Streptococcus agalactiae hyperimmune serum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Pred. No. 2.9e+02;
4; Mismatches 0; Indels
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69.2%;
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Best Local Similarity 69.2%,
Best Local Similarity 69.4%,
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Gaps

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1 ASMSAASAASMAA 13

ADU69631 standard; protein; 1310 AA.

RESULT 4 ADU69631 (first entry)

10-FEB-2005

ADU69631;

1 ASMSAASAASMAA 13

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ADV89548;

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The present invention relates to novel Streptococcus agalactiae

nucleotide sequences (1; ADV78860-ADV78998 and ADV83341-ADV85476) and

nucleotide sequences (1; ADV78899-ADV81203 and ADV812054ADV83340). The

convel polypeptides (11; ADV78899-ADV81203 and ADV81205-ADV83340). The

concleotide sequences encode polypeptides of S. agalactiae involved in the

concleotide metabolism, cell membranes, intermediate (central)

concleotide metabolism including purines, pyrimidines and/or nucleosides,

concleotide metabolism including purines, pyrimidines and/or nucleosides,

crequlatory functions, replication, transcribtion, translation, protein

transport, adaptation to atypical conditions, sensitivity to medicines

confactors, prosthetic groups and transporters, cell membrane proteins and

cofactors, prosthetic groups and transporters, cell membrane proteins and

cofactors, prosthetic groups and transporters, cell membrane proteins

cof nucleic acids. Pharmaceutical composition comprising (1) or (11) are

of nucleic acids. Pharmaceutical composition comprising (1) or (11) are

cof nucleic acids. Pharmaceutical composition comprising (1) or (11) are

cof nucleic acids. Pharmaceutical composition comprising (1) or (11) are

cof nucleic acids. Pharmaceutical composition of comprising (1) or (11) are

present patent is an equivalent for the basic patent FR2824074A1, which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomic nucleotide sequences encoding polypeptides of Streptococcus agalactiae for the development of vaccines, diagnostic tools, DNA chips and identification of therapeutic targets.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Frangeul L, Lalioui L;
Poyart C, Trieu-Cuot P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 42; DB 8; Length 1310;
Pred. No. 2.9e+02;
4; Mismatches 0; Indels
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                                                                Streptococcus agalactiae protein, SEQ ID 1942.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antibacterial; vaccine; bacterial infection.
                                                                                                             Antibacterial; vaccine; bacterial infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chevalier F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rusniok C, Chevalier F,
Couve E, Buchrieser C,
                                                                                                                                                                                                                                                                                                                                                                                                     (INSP ) INST PASTEUR.
(CNRS ) CNRS CENT NAT RECH SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contains only 2344 sequences.
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                                                                                                                                                                                                                                                                                                            26-APR-2002; 2002WO-IB003059.
                                                                                                                                                                                                                                                                                                                                                         26-APR-2001; 2001FR-00005642
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781 ASMSASTSASMSA 793
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                      24-FEB-2005 (first entry)
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Matches 9; Conservative
                                                                                                                                                                 Streptococcus agalactiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-101891/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1310 AA;
                                                                                                                                                                                                                WO200292818-A2
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                                                                                                                                                                                                                                                               21-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glaser P,
Zouine M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADV82959;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to novel Streptococcus agalactiae
nucleotide sequences (I; ADV87607-ADV87745) and novel polypeptides (II;
ADV87746-ADV8950). The nucleotide sequences encode polypeptides of S.
agalactiae involved in the synthesis of amino acids, cell membranes, intermediate (central) metabolism, energetic metabolism, fatty acid and phospholipid metabolism, nucleotide metabolism including putnines, comprising and/or nucleosides, regulatory functions, replication, transport, adaptation to atypical conditions, sensitivity to medicines and/or analogues, functions related conditions, sensitivity to medicines and/or analogues, functions related transpoorts, cell membrane proteins and cellular machinery. (I) are useful for the detection and/or amplification of nucleic acids.
Pharmaceutical composition comprising (I) or (II) are useful for the detectial S. agalactiae infection. Note: WO20029818A2 is equivalent for the present basic patent FR2824074A1. WO200292818A2 contains 6617 sequence whereas the present patent only contains 2344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genomic nucleotide sequences encoding polypeptides of Streptococcus agalactiae for the development of vaccines, diagnostic tools, DNA chips and identification of therapeutic targets.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Frangeul L, Lalioui L;
Poyart C, Trieu CP, Kunst F;
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Pred. No. 2.9e+02;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                               Streptococcus agalactiae protein sequence, SEQ ID 1942.
                                                                                                                                                                                                                                                                                                                   Antibacterial; Vaccine; bacterial infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 6; SEQ ID NO 1942; 2687pp; French.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chevalier F,
                                                                                                                            ADV89548 standard; protein; 1310 AA.
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(CNRS ) CNRS CENT NAT RECH SCI
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    781 ASMSASTSASMSA 793
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                                                                                                                                                                                                                                                                                                                                                                     Streptococcus agalactiae
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Best Local Similarity
9; Conserve
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Glaser Zouine

ADV89548

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XXX ADV8

BPN FR28

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sednences

Streptococcus agalactiae.

ADV80801;

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RESULT 6 ADV80801

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21-NOV-2002

Glaser P, Zouine M,

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded protesins (ABB37737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             osteopathic; vulnerary; cytostatic; gene therapy; diagnosis; forensics; gene mapping; mutation identification; biodiversity; chromosome marker; immune response; myeloid cell disorder; lymphoid cell disorder; bone cartilage; tendon; ligament; nerve tissue growth; wound healing; burns; incision; ulcer; cancer.
                                                                                                                                                                                                           New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 21255; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhang J, Zhao QA,
ou P, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 510;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74.1%; Score 40; DB 4; I 69.2%; Pred. No. 2.2e+02; ive 3; Mismatches 1;
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Xue AJ, Wehrman T, Weng G, Zhou P,
                                                                                                     Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADI60138 standard; protein; 276 AA.
                                                                                                     Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-SEP-2002; 2002WO-US029636.
23-MAR-2000; 2000US-0191637P
11-JUL-2000; 2000US-00614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-SEP-2001; 2001US-0323349P
16-SEP-2002; 2002US-00323349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 ASMSASMSASMSA 113
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                                                                                                     Adams M,
                                                                                                                                            WPI; 2001-656860/75.
N-PSDB; ABL08924.
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N-PSDB; ADI60483.
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                                                              (PEKE ) PE CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 510 AA;
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                                                                                                                                                                                                                               genes from Dr
interactions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-MAR-2003
                                                                                                     Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tang YT,
Ghosh M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADI60138;
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ADI60138
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nucleotide sequences (1, ADV78860-ADV78998 and ADV83341-ADV85476) and

nucleotide sequences (1; ADV78899-ADV81203 and ADV81205-ADV83340). The

nucleotide sequences encode polypeptides of S. agalactiae involved in the
synthesis of amino acids, cell membranes, intermediate (central)

mucleotide metabolism including purines, pyrimidines and/or nucleosides,
regulatory functions, replication, transcription, translation, protein

transport, adaptation to atypical conditions, sensitivity to medicines

and/or analogues, functions related to transposons, biosynthesis of
cofactors, prosthetic groups and transporters, cell membrane proteins and
cellular machinery. (1) are useful for the detection and/or amplification
of nucleic acids. Pharmaceutical composition comprising (1) or (11) are
useful for treatment of a bacterial S. agalactiae infection. The complete
genome of Streptococcus agalactiae is given in ADV81204. Note: The
present patent is an equivalent for the basic patent FR2824074Al, which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                    Genomic nucleotide sequences encoding polypeptides of Streptococcus agalactiae for the development of vaccines, diagnostic tools, DNA chips and identification of therapeutic targets.
                                                                                                                                                                                                                                                                          Kunst F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila; developmental biology; cell signalling; insecticide;
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Pred. No. 2.9e+02;
4; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                      Poyart C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 6; SEQ ID NO 4100; 439pp; French.
                                                                                                                                                                                                                                                Chevalier F,
                                                                                                                                                                                                                                                                      Buchrieser C,
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                                                                                                                                                                                 (INSP ) INST PASTEUR.
(CNRS ) CNRS CENT NAT RECH SCI
                                                                                                 26-APR-2002; 2002WO-IB003059.
                                                                                                                                          26-APR-2001; 2001FR-00005642.
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69.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         contains only 2344 sequences.
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781 ASMSASTSASMSA 793
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nes 9, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster
                                                                                                                                                                                                                                            Rusniok C,
                                                                                                                                                                                                                                                                    Couve E,
                                                                                                                                                                                                                                                                                                               WPI; 2004-101891/11
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                   WO200292818-A2
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Wang J;

26-MAR-2002

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ABB64821;

RESULT 8 ABB64821

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Query Match Best Loc Matches 27-SEP-2001

New polynucleotides and secreted proteins, useful for treating myeloid or lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve tissue growth or regeneration, in wound healing, and in tissue repair and replacement

Claim 20; SEQ ID NO 173; 243pp; English.

The invention relates to novel isolated polymucleotides or a sequence encoding a polypeptide with biological activity, where the polymucleotide corrections to the polymucleotide under stringent hybridization conditions or has greater than 99% sequence identity with the polymucleotide. The corresponding identification of mutations responsible for genetic gene mapping, identification of mutations responsible for genetic consources or supplements. The polymucleotides may also be used as molecular sources or supplements. The polymucleotides may also be used as molecular cources or supplements. The polymucleotides may also be used as molecular cources or supplements. The polymucleotides may also be used as molecular corresponding polypeptides or elicit immune response. The polympoptide is expressed, for re-engineering collophypeptide is expressed, for re-engineering collophypeptide is expressed, for re-engineering continguation, in wound healing myeloid or lymphoid cell corresponding polypeptide is proved and regeneration, in wound healing, in tissue repair and replacement, in the corresponds to a protein sequence of the invention.

Sequence 276 AA;

Gaps ; 72.2%; Score 39; DB 7; Length 276; 61.5%; Pred. No. 1.7e+02; ive 5; Mismatches 0; Indels 1 ASMSAASAASMAA 13 Best Local Similarity 61.5 Matches 8; Conservative Query Match 8

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ADW17198 standard; protein; 311 AA. ADW17198; RESULT 10 ADW17198 

24-MAR-2005 (first entry)

plant; transcription; gene regulation; gene expression; transgenic plant; drought resistance; disease resistance; salt tolerance; cold tolerance; freezing tolerance; flowering; flavor enhancer; flower color.

E\_grandis transcription factor protein C2C2 (co-like) family Seq 948.

Eucalyptus grandis

WO2005001050-A2.

06-JAN-2005.

07-JUN-2004; 2004WO-US017965.

06-JUN-2003; 2003US-0476189P.

(ARBO-) ARBORGEN LLC.

Magusin A; K, Wood M; Emerson SJ, kir. A, Lund ST, Mague. Gause K, Connett MB, Emerson SJ, Higgins C, Lasham A, Lund Veerakone S, Westwood C, N, Bryant C, Grigor M, F Puthigae S, 2005-075542/08. Bloksberg LN, Forster RLS, G Phillips J, Pu

N-PSDB; ADW16412

New polynucleotides isolated from plants encoding transcription factors, and polypeptides encoded by such polynucleotides, useful for regulating gene transcription and gene expression.

This invention relates to novel isolated plant nucleic acid molecules, or variants thereof, that encode transcription factors. Specifically, it refers to transcription factor proteins that are capable of binding to no refers to regulate gene transcription and gene expression in a plants, in particular Eucalyptus grandis and Pinus radiata. The present invention describes DNA constructs containing DNA encoding a present containing DNA encoding a ranscription factor that regulates the promoter, which is operably linked to the desired nucleic acid to be expressed. It further provides transgenic plants expressing a transcription factor that confers a trait to the plant such as increased drought, salt or disease tolerance, height changed; enhanced cold/ frost tolerance, enhanced color, health and characteristics, as well as improved taste, starch composition, flower longevity and germination, amongst others.

CC Accordingly, such plants that are successfully transfected with a DNA construct can be characterized by a difference in flower color, petal or transcription factor protein sequence of the invention. ö transgenic; plant; enhanced tolerance to abiotic stress; glyphosphate tolerance; hormone sensitivity; disease resistance; sugar sensing; flower structure; stem bifurcation; branching pattern; apical dominance; trichome; stem morphology; root growth; root hair; seed development; call proliferation; call differentiation; premature senescence; necrosis; plant size; leaf morphology; seed morphology; seed biochemistry; root anthocyanin; plant anthocyanin; lapht response; shade avoidance; bioinformatic; Gaps ö Score 39; DB 9; Length 311; Pred. No. 1.9e+02; Mismatches 2; Indels 1; Mismatches Claim 31; SEQ ID NO 948; 1265pp; English. ADI42807 standard; protein; 395 AA. Plant transcription factor #459. transcription factor; gene; ds 25-FEB-2003; 2003US-00374780. 72.2%; 76.9%; 18-APR-2001; 2001US-00837944 155 AAASAASAAA 167 22-APR-2004 (first entry) 1 ASMSAASAASMAA 13 Query Match Best Local Similarity 76.9 Matches 10; Conservative SHERMAN B K. RIECHMANN J L. HEARD J E. HAAKE V. CREELMAN R A. RATCLIFFE O. ADAM L J. REUBER T L. KEDDIE J. BROUN P E. Sequence 311 AA; US2004019927-A1 JIANG C Oryza sativa. 29-JAN-2004. ADI42807; (HAAK/) (CREE/) (RATC/) (ADAM/) (REUB/) (KEDD/) (BROU/) (PILG/) SHER/) (JIAN/) (HEAR/) RIEC/) RESULT 11 ADI42807 8 셤

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04-MAR-2004
    The invention describes a transgenic plant comprising a recombinant bolynucleotide of any one of more than 500 nucleotide sequences fully defined in the specification or its complement. The method of the invention can be used to produced a plant having altered traits such as: chhanced tolerance to abiotic stress; glyphosphate tolerance; hormone sensitivity; disease resistance; sugar sensing; early or late flowering; altered flower structure, change in steem bifurcations, altered branching pattern, reduced apical dominance, reduced trichome density; lack of trichomes; reduced trichome development; altered trichome trichome trichome number; altered stem morphology; increased root growth, increased root hairs; altered seed development; altered cell proliferation or cell differentiation; rapid development; premature senescence; increased necrosis; increase in seedling or plant or size; decreased plant size; leaf morphology; seed morphology; seed size; decreased plant size; leaf morphology; seed morphology; seed coloments, increase in remarkable transgenic plant, polynucleotides and polypeptides are useful in blonk bloinformatic search methods. This is the amino acid sequence of a plant transcription factor, and an orthologue of Arabiodopsis thaliana transcription of a transgenic plant with altered traits.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cold tolerance; heat tolerance; drought; osmotic strees; phosphate limitation; potassium limitation; nitrogen limitation; potassium limitation; nitrogen limitation; hormone sensitivity; disease resistance; sugar sensing; seed germination; flowering; inflorescence architectural change; meristem cell differentiation; phyllotaxy; apical dominance; trichome development; seed development; premature sensecence; delayed sensecence; lethality; necrosis; plant size; leaf morphology; secondary metabolism; light response; shade avoidance.
                                                                                                                               New transgenic plant comprising a recombinant polynucleotide of any one of more than 500 nucleotide sequences, useful in bioinformatic search
                                                    Haake V;
Keddie J, Broun PE;
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Pred. No. 2.5e+02;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thalecress transcription factor, Rice orthologue #82.
                                                    Riechmann JL, Jiang C, Heard JE, Ratcliffe O, Adam LJ, Reuber TL,
                                                                             Pineda O, Yu G;
                                                                                                                                                                                  Claim 1; SEQ ID NO 1270; 435pp; English.
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                                                                Creelman RA, Ratcliffe O,
Pilgrim ML, Dubell AN, P
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Best Local Similarity 69.2-
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DUBELL A N.
PINEDA O.
                                                                                                      WPI; 2004-132245/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 395 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US2004045049-A1.
                            (YUGG/) YU G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa.
                                                   Sherman BK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AD003010;
(DUBE/) [
                                                                                                                                                          methods.
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polynucleotide having a polynucleotide sequence or its complementary sequence comprising a sequence encoding a polypeptide, that initiates transcription (i.e. a transcription factor) from Arabidopsis, Soybean, Rice, Rape or Corn, comprising any of the sequences appearing as AD001588 -AD003527 or AD003530-AD003559. Also included are using a transgenic plant to grow a progeny plant, an expression cassette (comprising a constitutive, inducible or tissue-specific promoter and a recombinant polynucleotide described above), a host cell comprising the expression cassette, producing a modified plant having a modified trait, identifying a factor that is modulated by or interacts with a polypeptide encoded by the polynucleotide sequence and identifying at least one downstream polynucleotide sequence that is subject to a regulatory effect of any of the polypeptides encoded by the polynucleotide described above. The transgenic plant is useful for producing a plant that has an altered transgenic plant is useful for producing a plant that has an altered transgenic plant, enhanced tolerance to abiotic stress (increased tolerance to chilling, germination in cold conditions, freezing tolerance to theat, tolerance to semotic stress, tolerance to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New transgenic plant, useful in developing phenotypes with altered or improved characteristics or traits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a transgenic plant comprises a recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fromm ME, Heard JE, Riechmann JL, Adam LJ, Broun PE; Reuber TL, Keddie JS, Yu G, Jiang C, Samaha RS; L, Creelman RA, Dubell AN, Ratcliffe O, Kumimoto R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 1424; 213pp; English.
                                                                                                                                                                                        22-MAR-2000; 2000US-00533030.
22-MAR-2000; 2000US-00533030.
22-MAR-2000; 2000US-00533030.
6-APR-2000; 2000US-00533030.
16-NOV-2000; 2000US-00530948.
16-NOV-2000; 2000US-00713994.
17-APR-2001; 2001US-00819142.
17-APR-2002; 2002US-00958131.
14-JUN-2002; 2002US-00255066.
09-AUG-2002; 2002US-00255067.
                                                                                21-JAN-2000; 2000US-00489376.
17-FEB-2000; 2000US-00506720.
22-MAR-2000; 2000US-00532591.
22-MAR-2000; 2000US-00533029.
10-APR-2003; 2003US-00412699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-DEC-2002; 2002US-0434166P
25-FEB-2003; 2003US-00374780
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JIANG C.
SAMAHA R S.
PILGRIM M L.
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FROMM M E.
HEARD J E.
RIECHMANN J I
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BROUN P E.
PINEDA O.
REUBER T L.
KEDDIE J S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RATCLIFFE O. KUMIMOTO R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SHERMAN B K
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Pilgrim ML,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sherman BK;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BROU/)
(PINE/)
(REUB/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (JIAN/)
(SAMA/)
(PILG/)
(CREE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (FROM/)
(HEAR/)
(RIEC/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZHAN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (KEDD/)
(YUGG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (RATC/)
(KUMI/)
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calt, tolerance to phosphate limitation, tolerance to potassium

Imitation, decreased sensitivity to nitrogen limitation), altered

bormone sensitivity, reduced sensitivity to abscisic acid, an altered

cesponse to ethylene, disease resistance, altered susceptibility to

botrytis, altered susceptibility to Fusarium, altered susceptibility to

Erysiphe, altered susceptibility to Pseudomonas syringae, altered

susceptibility to Sclarctinia, altered sugar sensing, improved seed

cusceptibility to Sclarctinia, altered sugar sensing, improved seed

germination and seedling vigor, early flowering, late flowering, extended

germination and seedling vigor, early flowering, late flowering, a change in

stem bifurcations, altered phyllotaxy, altered branching pattern, reduced

apical dominance, reduced trichome density, ectopic trichome development,

altered trichome development, altered stem morphology, increased root

growth, increased root hairs, altered seed development, altered cell

proliferation/cell differentiation, premature sensescence, delayed

cyproliferation/cell differentiation, premature sensescence, delayed

growth, increased root hairs, altered seed development, altered cell

proliferation/cell differentiation, premature sensescence, delayed

growth, increased plant size, a change in leaf morphology, increased

cleaf cell expansion, change in seed morphology, altered seed coloration,

increased seed size, decreased leaf with a manufactation of leaf farty acid

content, increased leaf anthocyanins, an alteration of leaf fatty acid

content, increased leaf anthocyanins, an alteration of leaf fatty acid

content, increase in seed fatty acid content, decrease in seed coloration

content, alteration of genes involved in secondary metabolism, increase

content, alteration in seed prenyl lipid content, decrease in seed

content, alteration in seed prenyl lipid content, altered seed sold soldens and altered on in

content, alteration in seed prenyl acid content, altered sold soldens and altered soldens and alter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plant; transcription factor; transgenic plant; abiotic stress tolerance; osmotic stress tolerance; cold tolerance; heat tolerance; low nitrogen tolerance; low phosphate tolerance; fungal disease; glyphosate resistance; flowering; fertility; seed development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
to phosphate limitation, tolerance to potassium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72.2%; Score 39; DB 8; Length 395; 69.2%; Pred. No. 2.5e+02; ive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADO62431 standard; protein; 395 AA
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24-APR-2003; 2003US-0465809P.
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264 AAMSASSAAAAAA 276
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nes 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 395 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-SEP-2002;
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ADO62431
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The present invention relates to novel plant transcription factor proteins (I) and nucleotide sequences (II) (ADO61394-ADO6379). The equences can be used to produce transgenic plants, which overexpress (II), where the transgenic plant has an altered trait as compared to a not-transgenic plant or wild-type plant. The transgenic plant comprises an altered trait selected from increased tolerance to abiotic stress, increased tolerance to cold, increased tolerance to disease, increased tolerance to cold, increased tolerance to disease, including increased tolerance to disease, including town phosphate conditions, increased tolerance to disease, including town multiple fungal pathogens, increased tolerance to disease, including town multiple fungal pathogens, increased tolerance to glyphosate, increased sensitivity to ABC, altered sensitivity to ABA, reduced sensitivity to ABA, reduced sensitivity to ABC, altered sensitivity to ABC, altered sensitivity to ABC, altered sensitivity to ABA, reduced sensitivity to ABC, altered sensitivity to ABA, reduced sensitivity to ABC, altered sensitivity to ABA, reduced sensitivity to ABC, altered sensitivity to ABC, altered sensitivity to ABC, altered sensitivity to ABC, altered sensitivity altered flower structure, leared trichome structure, altered sensitivity, altered benefit, altered seed trichome structure, altered obsent, altered benefit, altered benefit, altered seed trichome structure, altered coll expension, altered benefit, altered call proliferation, altered coll expension, altered call proliferation, altered cell expension, altered cell proliferation, altered cell expension altered cell proliferation, altered seed latered sension or gray leaves, glossy leaves, altered abaxial/adaxial polarity, green leaves, glossy leaves, altered abaxial/adaxial polarity, and content, altered seed protein content, altered seed and mass, large 
                                                                                                       New recombinant polynucleotide encoding transcription factor polypeptides, useful for producing transgenic plants with advantageous properties compared to a reference plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
Reuber TL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
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                        Sherman BK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 39; DB 8; Length 395;
Pred. No. 2.5e+02;
3; Mismatches 1; Indels
  Adam LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster polypeptide SEQ ID NO 3390.
Jiang C, Heard JE, Ratcliffe O, Creelman RA, Riechmann JL, Haake V, Dubell AN, Keddie JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       format directly from WIPO at
                                                                                                                                                                                              claim 1; SEQ ID NO 898; 510pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB58866 standard; protein; 793 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72.2%;
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Best Local Similarity 69.4.
Best Local 9, Conservative
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                                                                   WPI; 2004-330163/30
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ABB58866
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The invention relates to novel abiotic stress responsive polynucleotides and polypeptides. Also disclosed are vectors, expression cassettes, host cells, and plants containing such polynucleotides. Also disclosed are methods for using the polynucleotides and polypeptides to alter the responsiveness of a plant to abiotic stress. The invention is useful in agriculture. The nucleic acid is useful for determining whether a test plant has been exposed to an abiotic stress condition. It is also useful for selecting an agent that alters abiotic stress regulated polynucleotide expression in a plant cell, and to identify a homolog or ortholog to an abiotic stress responsive polynucleotide. The nucleic acid molecule and the polypeptide encoded by it are useful in altering the responsiveness of a plant to an abiotic stress, such as cold stress, salt stress, osmocic stress cany of their combinations. The present sequence is used in the exemplification of the invention
                                                                                                                           responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold stress, salt stress or osmotic stress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MHC class II compound; MHC class II component; MHC class II alpha chain; MHC class II beta chain; peptide binding groove; spaceholder molecule; effector component; immune response; immune disorder; virucide; antibacterial; antiparasitic; cytostatic; immunosuppressive; gene therapy; viral infections; bacterial infection; parasitic infection; neoplastic disease; autoimmunity; toxicity; human.
  Katagiri F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New MHC class II compound, useful for preparing a composition for
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                                                                                                        New stress-responsive nucleic acid, useful for altering the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72.2%; Score 39; DB 7; Length 930; 76.9%; Pred. No. 6.1e+02; ive 1; Mismatches 2; Indels
  Goff SA,
Glazebrook J,
J, Zhu T;
                                                                                                                                                                                          Claim 1; SEQ ID NO 7444; 89pp; English.
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  Kreps J, Briggs SP, Cooper B, Gl
Moughamer T, Provart N, Ricke D,
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22-JUL-2002; 2002US-0397893P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 930 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
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ADI29006
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    셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABBS7737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          abiotic stress tolerance; transgenic plant; plant; cereal; agriculture.
                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 39; DB 4; Length 793;
Pred. No. 5.2e+02;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rice abiotic stress responsive polypeptide SEQ ID NO:7444
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 3390; 21pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                                                                                                                                                          Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABM89198 standard; protein; 930 AA.
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                                                                                                                                                                                                                                                                          PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-AUG-2001; 2001US-0314662P.
26-SEP-2001; 2001US-0325277P.
                                                                                                                       23-MAR-2001; 2001WO-US009231
                                                                                                                                                                23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
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Drosophila melanogaster
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Best Local Similarity
                                                                                                                                                                                                                                                                        Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                               WPI; 2001-656860/75
                                                                                                                                                                                                                               (PEKE ) PE CORP NY
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                                       WO200171042-A2
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                                                                                  27-SEP-2001
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The present invention describes an isolated MHC class II compound (I) comprising: (a) an MHC class II component comprising at least a portion of an MHC class II alpha chain and at least a portion of an MHC class II alpha chain and mHC class II beta of action form a peptide binding groove; (b) a spaceholder molecule; and (c) an effector component, where the effector component is linked to the MHC class II molecule and a carrier; (2) a method of producing an MHC class II molecule and a carrier; (2) a method of producing an MHC class II compound; (3) a method of directly identifying an antigen-specific T cell; (4) a method of regulating an immune response ex vivo in a subject; (5) a method of treating an immune disorder in a subject; and (7) a method of treating an immune response ex vivo in a subject; and (7) a method of treating an immune disorder and immunosuppressive activities, and can be used in gene therapy. The MHC class II compound (1) can be used for preparing a composition for treating immune catcions, parasitic disorders, e.g., viral infections, bacterial infections, parasitic infections, parasitic infections, parasitic infections, parasitic and infections, parasitic and infections, parasitic and memore represent sequence represents a spaceholder molecule peptide, which can be used in an MHC class II compound from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P; Dussurget O, Chetouani P, Nedjari H, Glaser P, Kunst F, Cossart P; Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA; Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A; Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L; Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N; Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J; Rose M, Voss H;
treating immune disorders e.g. viral infections, bacterial infections, parasitic infections, neoplastic disease, autoimmunity or toxicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin B12; bacterial infection; disease.
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Pred. No. 8.5;
1; Mismatches 0; Indels
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                                                            Claim 11; SEQ ID NO 2; 92pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB49912 standard; protein; 328 AA
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1 AAMAAAAAAAAA 12
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Best Local Similarity
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WPI; 2002-010914/01

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The present invention relates to the genome sequence of Listeria

monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of
it are useful for selecting probes and primers for detecting genes in L.

monocytogenes and related organisms, and for studying genetic
comportogenes and related organisms, and for studying genetic
comportogenes and related organisms.

CC expressed from the genome sequence are useful for raising specific
cantibodies, identification of L. monocytogenes and related organisms, and
cfor biosynthesis and biodegradation, especially biosynthesis of Vitamin
CC for biosynthesis and biodegradation, especially biosynthesis of Vitamin
CC selecting compounds that regulate gene expression and cell replication
CC selecting compounds that regulate dene expression and cell replication
CC and modulate L. monocytogenes-related diseases. In addition, the genome
CC vaccines compositions for the treatment or prevention of infections by L.
CC monocytogenes and related organisms. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from NIPO at
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Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and related polypeptides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 38; DB 5; Length 328
Pred. No. 2.9e+02;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster polypeptide SEQ ID NO 40827.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Myers EW
                                                                                        SEQ ID NO 2617; 192pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB71345 standard; protein; 508 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sest Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 328 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200171042-A2.
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                                                                                        Claim 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel nucleotide fragment encoding polypeptides having receptor-like protein kinase activity, caleosin-like activity, useful for altering oil phenotypes in plants such as sunflower, coconut, soybean, wheat and rice.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B;
The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Li C, Oliveira IC, Sakai H, Shen B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plant; oil trait; oil phenotype; altered lipid profile; MAP kinase; receptor-like protein kinase; mitogen activated protein kinase; oil; LIP15-like transcription factor caleosin; ATP citrate lyase; SNF1; CKC-like transcription factor; antisense inhibition; co-suppression;
                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oil trait related protein sequence SEQ ID NO:216.
                                                                                                                                                                                                                                                          Length 508;
                                                                                                                                                                                                                                                        70.4%; Score 38; DB 4; Length 508
69.2%; Pred. No. 4.7e+02;
ive 3; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABR40698 standard; protein; 589 AA.
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Klein TM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                          449 ASVAAASAAAAA 461
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                                                                                                                                                                                                                                                                        Local Similarity 69.2
nes 9; Conservative
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MC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Allen SM, Allen WB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-201509/
N-PSDB; ACC00733.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transgenic plant
                                                                                                                                                                                                                      Sequence 508 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycine
                                                                                                                                                                                                                                                                                              Matches
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ABR40698
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oil obtained from (V). (I) or its part can be used in antisense inhibition or co-suppression in a transformed plant. (III) is useful for altering the oil phenotype in a plant such as corn, soybean, wheat, rice, canola, Brassica, sorghum, sunflower or coconut. (III) is also useful for creating transgenic plants having altered lipid profiles. (I) can also be used as a hybridisation probe. ACCOOGS to ACCOOGS and ABR40591 to ABR40879 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cold
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 stress tolerance; transgenic plant; plant; cereal; agriculture.
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                                                                                                                                                                                                                                     Gaps
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an abiotic stress such as
                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rice abiotic stress responsive polypeptide SEQ ID NO:6244.
                                                                                                                                                                                                   Length 589
                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                Score 38; DB 6; I
Pred. No. 5.5e+02;
2; Mismatches 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glazebrook J,
J, Zhu T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New stress-responsive nucleic acid, useful responsiveness of a plant, e.g. cereal, to stress, salt stress or osmotic stress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; SEQ ID NO 6244; 89pp; English:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SYGN ) SYNGENTA PARTICIPATIONS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ricke D,
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                                                                                                                                                                                                                                                                                                                                                                                                     ABM87998 standard; protein; 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-JUN-2001; 2001US-0300112P.
24-AUG-2001; 2001US-0314662P.
26-SEP-2001; 2001US-0325277P.
21-NOV-2001; 2001US-0332132P.
                                                                                                                                                                                                  70.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                          67 ASFRSASASSMAA 79
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Moughamer T, Provart N,
                                                                                                                                                                                                                                   9; Conservative
                                                                                                                                                                                                                                                                        1 ASMSAASAASMAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-248011/24.
                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                Sequence 589 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2003008540-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-JUN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JAN-2003
                                                                                                                             invention
                                                                                                                                                                                                                                                                                                                                                                                                                                       ABM87998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 abiotic
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
                                                                                     developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 22404; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 37; DB 4; Length 285; Pred. No. 3.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein encoded by Prokaryotic essential gene #35899.
                                                   Drosophila melanogaster polypeptide SEQ ID NO 22404.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                  Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABU50372 standard; protein; 375 AA.
                                                                                                                                                                                                                                                                                                                                                                                  Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-MAR-2002; 2002WO-US009107.
                                                                                                                                                                                                                                                       23-MAR-2001; 2001WO-US009231.
                                                                                                                                                                                                                                                                                       23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
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61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       158 AAVAASAAAVAA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-JUN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid
genes from Drosophila and
               26-MAR-2002 (first entry)
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                                                                                                                                           Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                    Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-656860/75.
N-PSDB; ABL09307.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 285 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yersinia pestis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200277183-A2
                                                                                                                                                                               WO200171042-A2
                                                                                                       pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-OCT-2002
                                                                                      Drosophila;
                                                                                                                                                                                                                   27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                  Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABU50372;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a substantially purified nucleic acid molecule encoding a nitrite reductase of SEQ ID NO. 11926. Further disclosed is a recombinant DNA construct for expression of a nitrite reductase gene in a plant cell, and a plant cell comprising the recombinant DNA construct. The nucleic acid is useful for determining gene expression, identifying mutations in a gene of interest, and for constructing mutations in a gene of interest and for sEQ IDS 9692-16825 represent a group of 7134 Mxyococcus xanthus proteins and peptides. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encoding a nitrite reductase, useful for determining gene expression, identifying mutations in a gene of interest, and for constructing mutations in a gene of interest.
                                                                                                                                                                                                                                                                                                                                                                                        Transgenic plant; DNA replication; gene regulation; gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   substantially purified Myxococcus xanthus nucleic acid molecule
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                                     Length 45;
                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wiegand RC;
                                   Score 37; DB 7;
Pred. No. 51;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; SEQ ID NO 11882; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                    M. xanthus protein sequence, seq id 11882.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Slater SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB65204 standard; protein; 285 AA.
                                                                                                                                                                                                                                          ABM92683 standard; protein; 170 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MONS ) MONSANTO TECHNOLOGY LLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-JUL-2001; 2001US-00902540.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-JUL-2000; 2000US-0217883P.
                                   68.5%;
61.5%;
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Best Local Similarity 75...
For a 9, Conservative
                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                           1 ASMSAASAASMAA 13
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| ASLTAASASAMIA 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hinkle GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2005-028716/03.
                                                                                                                                                                                                                                                                                                                                                                                                                             Myxococcus xanthus.
                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 170 AA;
   Sequence 45 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               US6833447-B1
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                                                                                                                                                                                                                                                                                                                02-JUN-2005
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ABM92683

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ABM8

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                                                                                                                                                                                                                                                                                                                                                                                  the inventory issues of an interest acts to where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense another acid; (2) a host cell containing the vector; (3) an isolated concleic acid; (2) a host cell containing the vector; (3) an isolated containing the polypeptide of its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide (5) producing the polypeptide; (6) inhibiting cellular containing the polypeptide; (6) inhibiting cellular containing the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway contained for proliferation, or that inhibits cellular proliferation; (8) centured for cellular proliferation of an compound that inhibits proliferation of an compound that compound that inhibits proliferation of an compound; a activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent compound; a ctivity; (11) a culture comprising strains in which the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the compound contains; or (13) identifying the target of a compound that inhibits the contained contains or screening for homologous nucleic acids required contains and activity; (13) activity of compound that inhibits cellular proliferation of an organism. The antisense nucleic acids are useful for cellular proliferation of an organism. The activity of acids are useful for cellular proliferation of an organism contains and acids are useful for cellular proliferation of an organism contains and acids are useful for cellular proliferation of an organism contai
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                                                                                                                                                                                                                                                                      screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Breast and ovarian cancer associated antigen protein sequence SEQ ID 506.
                                                                                                                                                                                                                                                                                                                                                                         invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                           Zyskind JW;
Xu HH;
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t
                                                                                                                                                                                                                                                             New antisense nucleic acids, useful for identifying proteins or so for homologous nucleic acids required for cellular proliferation isolate candidate molecules for rational drug discovery programs.
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                                                                                                                                                           Ohlsen KL,
Forsyth RA,
                                                                                                                                                            Haselbeck R,
                                                                                                                                                                             Yamamoto R,
                                                                                                                                                                                                                                                                                                                                  Claim 25; SEQ ID NO 78296; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB58798 standard; protein; 434 AA.
                                                                                                                                                         Malone C,
Carr GJ,
                21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
                                                                     2002US-00072851.
                                                                                     06-MAR-2002; 2002US-0362699P
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                                                                                                                      (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 SAASVASMAA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 SAASAASMAA 13
                                                                                                                                                         Zamudio C,
Trawick JD,
                                                                                                                                                                                                              2003-029926/02
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Best Local Similarity
                                                                                                                                                                                                                              N-PSDB; ACA54242
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                                                                   08-FEB-2002;
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BXZXXXB
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or antagonist sequences exhibit cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiucher; vulnerary; anticonvulsant; antidacterial; antifugal; antiparasitic and cardiant activity. The polymucleotide and protein sequences are used in the diagnosis of cancer, particularly breast and ovarian cancer. The nucleic acid sequences, proteins, agonists and agonists may also be used in the diagnosis, prevention and treatment of immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                isolation and characterisation of the DNA and protein sequences of the invention. The breast and ovarian cancer associated DNA, protein, agonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disease, multiple scleroais, rheumatoid arthritis and ulcerative colitis; cardiovascular disorders such as myocardial ischaemias; wound healing; neurological diseases such as cerebral anoxia and epilepsy; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequences AAF21614 - AAF22031 represent DNA sequences encoding human proteins ABES9711 - AAB59128. The DNA and protein sequences are associated with breast and ovarian cancer. Included in the invention are sequences AAF22032 - AAF22040 and AAB59129 which are used in the
nootropic; neurpprotective; antiviral; antiallergic; hepatotropic;
antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant;
                                                                     antibacterial; antifungal; antiparasitic; cardiant; immune disorder; Addison's disease; allergy; autoimmune haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; Crohn's disease; amultiple sclerosis; rheumatoid arthritis; ulcerative colltis; cardiovascular disorder; wound healing; neurological disease.
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Pred. No. 5.7e+02;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11; Page 940-942; 1299pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0124270P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-MAR-2000; 2000WO-US005881.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-NOV-2004 (first entry)
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Matches 8; Conservative
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8 ASVSTAAAAALAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neurological diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-611515/58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           infectious diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAF21701.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 434 AA;
                                                                                                                                                                                                                                                                                                                                                                            WO200055173-A1
                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-SEP-2000.
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ADR43053
ID ADR43
XX
AC ADR43
XX
DT 18-NO
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The present invention relates to a novel recombinant DNA polynucleotide comprising a cell cycle regulated promoter, such as a cyclin promoter, that functions in plants operably linked to a DNA polynucleotide encoding an isopentenyl transferase. The present sequence is one such isopentenyl transferase. The present sequence is one such isopentenyl transferase. Also claimed are transgenic plants comprising the recombinant polynucleotide is useful for producing transgenic plants expressing cytckinin biosynthetic genes, and also provides an improved method of producing transgenic plants with increased yield and vigor. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to Pseudomonas aeruginosa polypeptides and the polymucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics,
                                                                                             New recombinant DNA polynucleotide comprising a cell cycle regulated promoter and encoding an isopentenyl transferase, useful for producing transgenic plants expressing cytokinin biosynthetic genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacterial infection; Pseudomonas aeruginosa infection; antibacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 37; DB 10; Length 455; Pred. No. 6e+02; t; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bush
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 20621; 455pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ú
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas aeruginosa polypeptide #4050
                                                                                                                                                                                        Disclosure; SEQ ID NO 128; 21pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Deloughery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABO71875 standard; protein; 493 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68.5%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-00252991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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110 SLAAATAASIAA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 SMSAASAASMAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-615309/58.
                                                            WPI; 2006-088763/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ABD05446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 455 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rubenfield MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-JUL-2004
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                    He SS;
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Matches
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ABO71875
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to an isolated polynucleotide comprising a plant promoter directing transcription of an operably linked polynucleotide in at least one of the tissues selected from abscission zone, root, pod, wall, apical meristem, and flower of plants. The polynucleotides and methods are useful for producing a plant having increased yield or a trait of agronomic interest when compared to a nontransformed plant of the same genotype. The present sequence represents a IPP-like structural protein. The sequence data for this patent is not represented in the printed specification but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transgenic plant; plant breeding; isopentenyl transferase; enzyme; plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotides comprising a plant promoter that directs its transcription into abscission zone(s), root, pod, wall, apical meristem, or flower of plants, useful for producing a plant having increased yield
                                   abscission zone; apical meristem; Plant Growth Regulant; Gene Therapy; A6; abscission zone promoter; IPT; isopentyl transfease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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66.7%; Pred. No. 6e+02;
ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                        Tennessen DJ;
                                                                                                                                                                                                                                                                                                                                                                     Nelson DE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 21; SEQ ID NO 135; 63pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isopentenyl transferase, SEQ ID 128.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AEF15580 standard; protein; 455 AA.
  IPT-like structural protein #112
                                                                                                                                                                                                                                                                                                                             (MONS ) MONSANTO TECHNOLOGY LLC
                                                                                                                                                                                                                                                                                                                                                                        Eilers RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-JUN-2005; 2005US-00156084.
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                                                                                                                                                                                                                                         13-FEB-2004; 2004WO-US004499.
                                                                                                                                                                                                                                                                                 14-FEB-2003; 2003US-0447833P.
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Query Match
Best Local Similarity 66./v,
Best Local 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-635562/61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          agronomic trait.
                                                                                                                                                                                                                                                                                                                                                                     Deng M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 455 AA;
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                                                                                                                                                    WO2004074442-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa
                                                                                                            Unidentified
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                                                                                                                                                                                                                                                                                                                                                                        Bhat DG,
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prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology, Sequences ABO67826-ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at
                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid comprising any one of
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Xu HH;
                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                            Score 37; DB 7; Length 493;
Pred. No. 6.5e+02;
0; Mismatches 3; Indels
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein encoded by Prokaryotic essential gene #7794.
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 25; SEQ ID NO 50191; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABU22267 standard; protein; 533 AA.
                                                                                                                                                                                                                     seqdata.uspto.gov/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-SEP-2001; 2001US-00948993.
25-0CT-2001; 2001US-0342923P
08-FEB-2002; 2002US-0372851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                            68.5%;
76.9%;
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Best Local Similarity 76.9
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Burkholderia mallei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-029926/02.
N-PSDB; ACA26137.
                                                                                                                                                                                                                                                          Sequence 493 AA;
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06-SEP-2001;
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Wall
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the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway can equired for the gene required for cellular proliferation; (8) inchipits against a proliferation, or that inhibits cellular proliferation; (8) at gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound; sactivity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent or which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids required for proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MHC class II compound; MHC class II component; MHC class II alpha chain; MHC class II beta chain; peptide binding groove; spaceholder molecule; effector component; immune response; immune disorder; virucide; antibacterial; antiparastic; cytostatic; immunosuppressive; gene therapy; viral infections; bacterial infection; parastic infection, neoplastic disease; autoimmunity; toxicity; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New MHC class II compound, useful for preparing a composition for treating immune disorders e.g. viral infections, bacterial infections, parasitic infections, neoplastic disease, autoimmunity or toxicity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 37; DB 6; Length 533
Pred. No. 7.1e+02;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (DAND ) DANA FARBER CANCER INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADI29007 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-JUL-2003; 2003WO-US021767.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68.5%;
61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-JUL-2002; 2002US-0395494P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seth N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 AGMNAATAAAVAA 138
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Best Local Similarity 61.5
Fra 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 533 AA;
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The present invention describes an isolated MHC class II compound (I) comprising: (a) an MHC class II component comprising at least a portion of an MHC class II alpha chain and at least a portion of an MHC class II alpha chain and mHC class II beta cof an MHC class II alpha chain and MHC class II beta chain form a peptide binding groove; (b) a spaceholder molecule; and (c) an effector component, where the effector component is linked to the MHC class II component. Also described: (1) a pharmaceutical composition comprising the MHC class II molecule and a carrier; (2) a method of producing an MHC class II compound; (3) a method of directly identifying an antigen-specific T cell; (4) a method of treating an immune response ex vivo in a subject; (5) a method of treating an immune disorder in a subject; and (7) a method of treating an immune disorder and immunosuppressive corruction, and can be used in gene therapy. The MHC class II compound (I) can be used for preparing a composition for treating immune corructions, neoplastic disease, autoimmunity or toxicity. The present infections, neoplastic disease, autoimmunity or toxicity. The present confider and incompound from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer; tumour; cytostatic; immunostimulant; vaccine; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fanger GR, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sleath PR;
                                                                                                                                                                                                                                                                                                                                                                                                                        66.7%; Score 36; DB 8; Length 13; 61.5%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human lung tumour clone peptide, SEQ ID No 2064.
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Carter D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Mismatches
             Claim 11; SEQ ID NO 3; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Watanabe Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Henderson RA, Wang T, Watanabe Y,
Johnson JC, Retter MW, Durham M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADH47583 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-OCT-2002; 2002WO-US034777.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-OCT-2001; 2001US-00017754
28-MAR-2002; 2002US-00113872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 61...
Best Conservative
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ASMSAASAASMAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AAMAAAAAAAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Johnson JC, Retter M
Bangur CS, Mcnabb A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2003037267-A2.
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human; clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAR-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADH47583;
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The invention relates to novel compositions and methods for the therapy

Example 38; SEQ ID NO 2064; 258pp; English.

New polypeptides and encoding polynucleotides, useful for diagnosing, preventing and/or treating lung cancer.

WPI; 2003-468346/44.

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Gaps

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The invention relates to novel compositions and methods for the therapy and diagnosis of cancer, particularly lung cancer. The compositions comprise one or more lung tumour polypeptides, immunogenic portions therof, polynucleotides that encode such polypeptides, antigen presenting cells that express such polypeptides, and T cells that are specific for cells expressing such polypeptides. The novel compositions have oytostatic and immunostimulant activity. The lung tumour antigens can be used in the creation of a vaccine. The polynucleotides that encode the lung tumour polypeptides can be used in gene therapy to help in the reatment of lung tumours. This sequence represents a human lung tumour clone polypeptide of the invention. This sequence was not shown in the specification. It has been taken from a World Intellectual Property
and diagnosis of cancer, particularly lung cancer. The compositions comprise one or more lung tumour polypeptides, immunogenic portions therof, polynucleotides that encode such polypeptides, antigen presenting cells that expressing such polypeptides, and T cells that are specific for cells expressing such polypeptides. The novel compositions have expostatic and immunostimulant activity. The lung tumour antigens can be used in the creation of a vaccine. The polynucleotides that encode the lung tumour polypeptides can be used in gene therapy to help in the treatment of lung tumours. This sequence represents a human lung tumour clone polypeptide of the invention. This sequence was not shown in the specification. It has been taken from a World Intellectual Property Organization CD ROM supplied with the specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lung cancer; tumour; cytostatic; immunostimulant; vaccine; gene therapy;
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Fanger GR, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encoding polynucleotides, useful for diagnosing,
                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                        7; Length 20;
                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human lung tumour clone peptide, SEQ ID No 2065.
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Durham M, Carter D,
                                                                                                                                                                                                                                                                                          Score 36; DB 7
Pred. No. 31;
2; Mismatches
                                                                                                                                                                                                                                                                                        DB 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 38; SEQ ID NO 2065; 258pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       preventing and/or treating lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADH47584 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-OCT-2002; 2002WO-US034777.
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28-MAR-2002; 2002US-00113872.
                                                                                                                                                                                                                                                                                          66.78;
69.28;
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                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 6>...
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       7 ASASSASSASA 19
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Johnson JC, Retter MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Johnson JC, Retter M
Bangur CS, Mcnabb A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptides and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-468346/44.
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                                                                                                                                                                                                                                                         Sequence 20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human; clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-MAY-2003.
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03-MAY-2001; 2
10-JUL-2001; 2
29-OCT-2001; 2
                                                                                                                                                                                                                                                                                                                                   28-OCT-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-MAR-2002;
                                                                                                                                                                                                                           04-NOV-2004
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                                                                                                                                                                                                                                                                                                                                                                      17-DEC-1999
                                                                                                                                                                                                                                                                                                                  13-NOV-2003
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                                                                                                                                                                                                                                                                                                                                                               15-OCT-1999
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                                                                                                                                           7
                                                                                                                                                                                                         ADJ21503;
                                                                                        Query Match
Best Local S
                                                                                                          Matches
                                                                                                                                                                       RESULT 33
                                                                                                                                                                             ADJ21503
ID ADJ
888888888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence chosen from any one of 40 lung tumour polypeptides or its complements, fragments or degenerate variants. The method of the invention has cytostatic applications and may be useful for detecting and treating lung cancer in a patient, as well as for inhibiting the development of lung cancer in a patient via incubating CD4+ and/or CD8+ T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a novel isolated polynucleotide comprising a
                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vedvick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for
                                                     ö
                                                                                                                                                                                       Human lung cancer-related L978P peptide fragment - SEQ ID 2064.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel polynucleotide encoding lung tumor polypeptides, useful diagnosing, preventing and treating cancer e.g. lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fanger GR,
                                    Length 20
                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sleath
supplied with the specification,
                                                                                                                                                                                                        lung tumour; cytostatic; lung cancer; human; L978P.
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Carter D,
                                    7;
                                   DB
31;
                                                    Mismatches
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                                    36;
No.
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                                    Score Pred. 1
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                                                                                                                                   ADJ21502 standard; peptide; 20 AA.
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06-OCT-2000; 2000US-00677419.
30-OCT-2000; 2000US-00702705.
13-DEC-2000; 2000US-007136457.
03-MAY-2001; 2001US-00846626.
10-JUL-2001; 2001US-00909941.
                                                                                                                                                                                                                                                                                              99US-00346492.
99US-00419356.
99US-00466867.
99US-00476300.
2000US-00533077.
2000US-00546259.
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2000US-00589184.
2000US-00614124.
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2000US-00671325.
2000US-00677419.
                                                                                                                                                                                                                                                                                                                                                                                        2000US-00651563
                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-OCT-2001; 2001US-00017754
28-MAR-2002; 2002US-00113872
                                  66.7%;
69.2%;
                                                                                                                                                                                                                                                                               2002US-00283017
                                                                                                                                                                      (first entry)
                                                                     1 ASMSAASAASMAA 13
                                                                                       ASASSASSASA 14
                                 Query Match
Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Henderson RA, Wang T,
Johnson JC, Retter MW,
Bangur CS, Mcnabb A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CORI-) CORIXA CORP.
Organization CD ROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-167010/16
                                                                                                                                                                                                                                           US2003211510-A1
                 Sequence 20 AA;
                                                                                                                                                                                                                                                                                                                                                              27-APR-2000;
05-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                11-JUL-2000;
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22-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                     10-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                        29-AUG-2000;
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                                                                                                                                                                                                                           Homo sapiens
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17-DEC-1999;
                                                                                                                                                                      04-NOV-2004
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                                                                                                                                                    ADJ21502;
                                                                                                                   RESULT 32
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SXS
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cells isolated from a patient with at least one component chosen from a polypeptide, polynuclectide or antigen presenting cell (APC) of the invention and administering an effective amount of the proliferated T cells to the patient. The current sequence is that of the human lung cancer-related peptide of the invention. The current sequence is not shown in the specification per se but is available on the USPTO web-site http:seqdata.uspto.gov/sequence.html?DocID=20030211510.
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                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human lung cancer-related L978P peptide fragment - SEQ ID 2065.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sleath PR;
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                                                                                                                                                                                                                                        Length 20;
                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lung tumour; cytostatic; lung cancer; human; L978P.
                                                                                                                                                                                                                                                                                      2,
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Carter D,
                                                                                                                                                                                                                                      Score 36; DB 8;
Pred. No. 31;
2; Mismatches
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Durham M, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADJ21503 standard; peptide; 20 AA.
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22-MAR-2000; 2000US-00519642.
27-APR-2000; 2000US-00546259.
27-APR-2000; 2000US-00546259.
11-JUN-2000; 2000US-00560184.
11-JUL-2000; 2000US-00561124.
29-AUG-2000; 2000US-00651124.
26-SEP-2000; 2000US-006511355.
66-CCT-2000; 2000US-006771355.
30-CCT-2000; 2000US-006771355.
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2001US-00849626.
2001US-00902941.
2001US-00017754.
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99US-00466867.
99US-00476300.
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69.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                  1 ASMSAASAASMAA 13
                                                                                                                                                                                                                                                                                                                                                                              19
                                                                                                                                                                                                                                                                                    9; Conservative
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Johnson JC, Retter MW,
                                                                                                                                                                                                                                                                                                                                                               ASASSASSASASA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-167010/16.
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                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US2003211510-A1.
                                                                                                                                                                                             Sequence 20 AA;
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Sequence 148 AA;

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The invention relates to a novel isolated polynucleotide comprising a sequence chosen from any one of 40 lung tumour polypeptides or its complements, fragments or degenerate variants. The method of the invention has cytostatic applications and may be useful for detecting and treating lung cancer in a patient, as well as for inhibiting the development of lung cancer in a patient via incubating CD4+ and/or CD8+ T cells isolated from a patient with at least one component chosen from a polypeptide, polynucleotide or antigen presenting cell (APC) of the invention and administering an effective amount of the proliferated T cells to the patient. The current sequence is that of the human lung cancer-related peptide of the invention. The current sequence is not cancer-related peptide of the invention. The current sequence is not the useful cancer is not the useful that it is available on the USPTO web-site http:seqdata.uspto.gov/sequence.html?DocID=20030211510.
              $$$$$$$$$$$$$$$$$$$
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Sequence 20 AA;

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Score 36; DB 8; Length 20;
Pred. No. 31;
                  2; Indels
                   Mismatches
                  2;
       66.78;
            69.28;
1 ASMSAASAASMAA 13
                                            ASASSAASASA 14
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Gaps

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ABB70649 standard; protein; 148 AA. (first entry) 26-MAR-2002 ABB70649; RESULT 34 

Drosophila; developmental biology; cell signalling; insecticide; Drosophila melanogaster polypeptide SEQ ID NO 38739. pharmaceutical

Drosophila melanogaster.

WO200171042-A2

23-MAR-2001; 2001WO-US009231 27-SEP-2001

23-MAR-2000; 2000US-0191637P. 11-JUL-2000; 2000US-00614150.

Claim 2; SEQ ID NO 9672; 14pp; English.

(PEKE ) PE CORP NY

Venter JC, Adams M,

Myers EW;

Li PWD,

WPI; 2001-656860/75. N-PSDB; ABL14752.

New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.

Disclosure; SEQ ID NO 38739; 21pp + Sequence Listing; English

The invention relates a recombinant DNA construct comprising a CC polymucleotide having any of 5544 mucleotide sequences (CDNAs SEQ ID NO: 1-5544) and encoding a polypeptide with any of 5544 amino acid sequences (SEQ ID NO: 5545-11089). The CDNAs and proteins are from corn, soybean, capabidopsis, wheat and rape but the specification does not indicate which sequences is derived from which organism. Also included is a method of producting a plant having an improved property, comprising transforming a plant with a recombinant DNA construct comprising a promoter region construct in a plant cell operably joined to a polynucleotide encoding a plant with a resombinant DNA construct comprising the transformed collypeptide associated with the property, and growing the transformed plant. The property is selected from improving plant cold tolerance, for plant. The property is selected from improving plant cold tolerance, for pathway, for improving plant drought tolerance, for providing increasing resistance to plant disease, for adactomannan production, for production of plant tolerance to herbicides, for increasing the rate of improving plant tolerance to extreme osmotic conditions, for improving plant tolerance to pathogens or pests, for yield improvement by modification of carbohydrate, nitrogen or phosphorus use and/or uptake and for yield improvement by read improvement by and for uptake and for yield improvement by read improvement by modification of carbohydrate, nitrogen or phosphorus use and/or uptake

18 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16177) and the encoded proteins (ABBS7737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

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                                                                                                                                                                                                                                                                                                                                                                                              new recombinant DNA constructs useful in the field of biochemistry and genetics, and in particular for producing transgenic plants with improved biological characteristics.
                                                                                                                                                                              plant; transgenic; cold tolerance; growth rate; drought tolerance; disease resistance; galactomannan production; plant growth regulator; heat tolerance; herbicide tolerance; lignin production; extreme osmotic condition tolerance; pathogens resistance; pest resistance; yield improvement; seed oil yield; seed protein yield.
                  Gaps
                  ö
Length 148;
                 3; Indels
Score 36; DB 4; I
Pred. No. 2.6e+02;
                  Mismatches
                                                                                                        ADT59595 standard; protein; 250 AA.
                   .
0
                                                                                                                                                               Plant polypeptide, SEQ ID 9672.
                                                                                                                                                                                                                                                                                                18-DEC-2003; 2003US-00739930.
                                                                                                                                                                                                                                                                                                                   28-APR-2003; 2003US-00424599.
28-APR-2003; 2003US-00425115.
66.78;
                                                                                                                                            13-JAN-2005 (first entry)
                                     1 ASMSAASAASMAA 13
                                                        50 ASASAAVAASAAA 62
                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-757369/74.
                                                                                                                                                                                                                                                                                                                                                (KOVA/) KOVALIC D K.
       Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                            US2004216190-A1.
                                                                                                                                                                                                                                          Viridiplantae.
                                                                                                                                                                                                                                                                               28-OCT-2004.
                                                                                                                                                                                                                                                                                                                                                                   Kovalic DK;
                                                                                                                          ADT59595;
 Query Match
                                                                                      RESULT 35
                                                                                               ADT59595
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development under at least one stress condition. The polynucleotide may also encode a plant transcription factor. The methods and compositions of the present invention are useful in the field of biochemistry and genetics, in particular for producing transgenic plants with improved biological characteristics such as increased yield, improved nitrogen flow, increasing plant tolerance to cold or heat, improving plant tolerance to extreme osmotic and drought conditions, and improving plant tolerance to plant pests or pathogens. They can also be used in physical arrays of molecules, plant breeding markers, computer-based storage and analysis systems. The present sequence is one of the 5344 plant protein sequences of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in collectual format directly from USFTO at sequence content of the sequence of the s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 36; DB 8; Length 250;
Pred. No. 4.6e+02;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nolling J, Deloughery C, Bush D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 31998; 455pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas aeruginosa polypeptide #15427.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABO83252 standard; protein; 268 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-00252991.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66.7%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 MSAASAASMA 12
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N-PSDB; ABD16823.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 250 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rubenfield MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US6551795-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-FEB-1998;
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The invention relates to a new isolated lung specific nucleic acid

molecule (I) comprising any of 113 fully defined nucleotide sequences

given in the specification, their encoded protein sequences, sequences

given in the specification, their encoded protein sequences, sequences

compositions of the nucleotide sequences. The methods and

compositions of the present invention are useful for identifying,

compositions of the present invention are useful for identifying,

compositions of the present invention are useful for identifying,

conditions of the lung. They are also used for identifying lung

concerous diseases of the lung. They are also used for identifying lung

concerous diseases of the lung. They are also used for identifying lung

concerous diseases of the lung. They are also used for identifying lung

concerous diseases of the lung. They are also used for identifying lung

concerous diseases of the lung. They are also used for identifying lung

confined and invention, gene therapy, production of transgenic

animals and production of engineered lung tissue for treatment and

cresearch. Lung specific genes (LSGS) were identified by a systematic

conalysis of gene expression data in the LIFESEQ Gold database using the

construction of confider and the second promatic search program

(CLASP). Genes were grouped into gene bins where each bin is a cluster of

sequences grouped together where they share a common contig.

Differentially expressed tissue-specific genes were selected based on the
                                                                                                                                                                                                                      ö
of Pseudomonas species using biochip technology. Sequences ABO67826-
BAD64396 represent P. aeruginosa polypeptides of the invention. Note: The
Sequence data for this patent did not form part of the printed
specification but was obtained in electronic format from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         identifying, diagnosing, monitoring, staging, imaging and treating lung cancer and non-cancerous diseases of the lung.
                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytostatic; gene therapy; vaccine; lung; diagnosis; cancer; non-cancerous lung disease; lung tissue; antagonist; gene therapy; transgenic animal; splice variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated human lung specific nucleic acid molecule, useful for
                                                                                                                                                                                                                      ö
                                                                                                                                                                         66.7%; Score 36; DB 7; Length 268; 81.8%; Pred. No. 4.9e+02;
                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lung specific gene splice variant encoded protein #89.
                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liu
                                                                                                                                                                                                                                                                                                                                                                                                                    ADR98917 standard; protein; 278 AA.
                                                                                          seqdata.uspto.gov/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sun Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-DEC-2002; 2002US-0431307P.
06-DEC-2002; 2002US-0431510P.
06-DEC-2002; 2002US-0431516P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-DEC-2003; 2003WO-US038896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                      9; Conservative
                                                                                                                                                                                                                                                                                                          152 MSPARAASMAA 162
                                                                                                                                                                                                                                                               3 MSAASAASMAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Turner LR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (DIAD-) DIADEXUS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-635553/61.
                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                  Sequence 268 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADR98917;
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Human; primer; detection; diagnosis; antisense therapy; gene therapy

Homo sapiens. EP1074617-A2. 27-AUG-1999; 99JP-00300253. 11-JAN-2000; 2000JP-00118776. 02-MAY-2000; 2000JP-00183767.

2000JP-00241899

09-JUN-2000;

(HELI-) HELIX RES INST.

28-JUL-2000; 2000EP-00116126

07-FEB-2001

29-JUL-1999;

Human protein sequence SEQ ID NO:14226.

26-JUN-2001 (first entry)

AAB94055;

AAB94055 standard; protein; 327 AA

**AAB94055** 

214 ASTSAAAAAAAA 226

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
percentage level in the targeted tissue versus all the other tissues. The expression levels for each gene in libraries of normal tissues or non-tumour tissues from cancer patients were compared with the expression levels in tissue libraries associated with tumour or disease. This sequence represents a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid detection reagent for detecting 1000 or more
genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                insecticides, therepoutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 27588; 21pp + Sequence Listing; English.
                                                                                                                                Length 278
                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster polypeptide SEQ ID NO 27588
                                                                                                                              Score 36; DB 8; I
Pred. No. 5.1e+02;
4; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                ABB66932 standard; protein; 327 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-2001; 2001WO-US009231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                                                  61.5%;
                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                 1 ASMSAASAASMAA 13
                                                                                                                                                                                                                     ij
                                                                                                                                                                   8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PEKE ) PE CORP NY
                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ABL11035.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 327 AA;
                                                                                                   Sequence 278 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          interactions
                                                                                                                                                                                                                                                                                                                                                                               26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Venter JC,
                                                                                                                                                                                                                                                                                                                                                ABB66932;
                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                 RESULT 38
ABB66932
                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                  888888
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Primer sets for synthesizing polynucleotides, particularly the 5602 full length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
                                                                                                                                        Yamamoto J;
                                                                                                                                                                                               Claim 8; SEQ ID NO 14226; 2537pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                    Length 327;
                                                                                                                                                                                                                                                                                                                                                    66.7%; Score 36; DB 4; Length 327
69.2%; Pred. No. 6.18+02;
ive 2; Mismatches 2; Indels
                                                                                                                                        Saito K, Ya
, Otsuki T;
                                                                                                                                        nikawa T, Hayashi K, S
Wakamatsu A, Nagai K,
                                                                                                                                        Ota T, Isogai T, Nishikawa
Ishii S, Sugiyama T, Wakama
                                                                                                                                                         WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                           Sequence 327 AA;
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Gaps

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1 ASMSAASAASMAA 13

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9; Conservative

Matches

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Gaps

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Score 36; DB 4; Length 327; Pred. No. 6.1e+02; 2; Mismatches 2; Indels

66.7%;

Query Match Best Local Similarity

2; Mismatches

1 ASMSAASAASMAA 13

<u>:</u>

9; Conservative

Matches

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New Stomach cancer-associated genes, useful as markers in blood tests for screening for the early stages of the disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to stomach cancer-expressed genes (AAI93842-AAI93917) and the encoded proteins (AAM93967-AAM94039). The genes can be used as markers in blood tests for screening for the early stages of the disease. The proteins and peptides can be used as targets for screening for compounds to treat the disease. They can also be used for predicting micro-metastases. The gene can predict peritoneal dissemination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Aburatani H;
Kodama T, Midorikawa Y;
                                                                                                                                            Human; stomach cancer, marker; screening; micro-metastasis; peritoneal dissemination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 66.7%; Score 36; DB 4; Length 327; Best Local Similarity 69.2%; Pred. No. 6.1e+02; Matches 9; Conservative 2; Mismatches 2; Indels
                                                                                                               Human stomach cancer expressed polypeptide SEQ ID NO 49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 119-120; 242pp; Japanese.
             AAM93990 standard; protein; 327 AA.
                                                                                                                                                                                                                                                                                                                               29-JUL-1999; 99JP-00248036.
27-AUG-1999; 99JP-00300253.
18-OCT-1999; 99US-0159590P.
11-JAN-2000; 2000JP-00118776.
17-FEB-2000; 2000JP-0018372P.
02-MAY-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-00183767.
                                                                                                                                                                                                                                                                                                 28-JUL-2000; 2000WO-JP005063
                                                                             13-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-570287/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAI93866.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 327 AA;
                                                                                                                                                                                                                                WO200109317-A1
                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                 08-FEB-2001
                                                AAM93990;
AAM93990
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Gaps ..

Search completed: September 9, 2006, 22:48:03 Job time : 103.418 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                     OM protein - protein search, using sw model
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September Run on:

9, 2006, 22:48:41; Search time 14.8101 Seconds (without alignments) 84.457 Million cell updates/sec

homectic protein e probable WRE1 ATP-transcription fact Clyorf4 protein -hypothetical prote hypothetical prote protein HGSC65.1 [ ecdysone-induced p ecdysone-induced p puff 74E protein -DNA-binding protei

myc-associated zin polyomavirus enhan zinc finger protei homeotic protein e

transcription fact

1 AAMAAAAAAAA 13 US-10-617-568-3 53 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

283416

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 100 summaries

1: pir1: \* 2: pir2: \* 3: pir3: \* 4: pir4: \* \*:08 PIR Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		di			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
	49	92.5	377	2	T04213	heat shock transcr
8	4		530	~	138558	
Э	4	92.5	577	7	\$72227	
4	49	92.5	892	~	T09071	SH3 domains-contai
2	49	92.5	1533	~	A46221	abdominal segment
9	49	92.5	2038	7	A43742	female sterile hom
7	48	90.6	451	~	D88395	protein F53A3.6 [i
æ	47	88.7	150	7	T12547	hypothetical prote
σ	47	88.7	220	7	JC5954	ribosomal protein
10	47	88.7	233	~	S11563	probable MASH-2 pr
11	47	88.7	238	7	A48279	
12	47	88.7	289	~	A43562	homeotic protein H
13	47	88.7	305	N	157039	genomic screen hom
14	47	88.7	314	N	JC5273	paired type homeob
15	47	88.7	323	N	S16318	homeotic protein H
16	47	88.7	328	N	AB1781	hypothetical prote
17	47	88.7	331	~	B47236	zinc-finger protei
18	47	88.7	333	N	A39065	homeotic protein E
19	47	88.7	334	~	G02409	protein kinase C-b
20	47	88.7	364	N	I48188	gene NKx6.1 protei
21	47	88.7		~	T03875	probable homeobox
22	47	88.7		N	T03874	probable homeobox
23	47	88.7		7	A44443	basic helix-loop-h
24	47	88.7	401	~	A48423	engrailed homeodom
25	47	88.7	403	~	A53662	homeotic protein H
26	47	88.7	420	~	T14911	bZIP DNA-binding p
27	47	88.7	443	-1	138239	
28	47	88.7	475	~	A43915	homeotic protein e
29	47	88.7	477	~	A47236	zinc-finger protei

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hypothetical prote finger protein esc homeotic protein c polyA binding prot segmentation prote homeotic protein e glucan 1, 4 alpha-g serine-rich protein parallel sister ch tegument protein -tegument protein -tegument protein -to fill protein -homeotic protein B homeotic protein B

castor protein - f neurogenic protein gene Delta protein neurogenic repetit hypothetical prote neurogenic locus m gene mastermind pr notch protein - fr

ovo protein - frui spalt protein - fr related to PAN2 pr sex comb protein -

bumetanide-sensit

dachshund protein dachshund protein dachshund protein stripe a/b protein bumetanide-sensiti

Gaps

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abdominal segment formation protein pumilio - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 21-Sep-1993 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: A46221; S22026
R;Barker, D.D.; Wang, C.; Moore, J.; Dickinson, L.K.; Lehmann, R.
A;Title: Pumilio is essential for function but not for distribution of the Drosophila at A;Reference number: A46221; MUID:93093466; PMID:1459455
A;Contents: embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:P25822; UNIPARC:UP1000016BD14; GB:L07943; NID:g158190; PID:g
A;Note: sequence extracted from NCBI backbone (NCBIN:120203, NCBIP:120204)
R;Macdonald, P.M.
B:Macdonald, P.M.
B:Macdonald, P.M.
A;Reference number: $22026
A;Accession: $22026
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A;Cross-references: UNIPARC:UF100001329FD; EMBL:X62589; NID:g8393; PID:g8394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:070254; UNIPARC:UP10000027BF6; EMBL:AF030131; NID:g3002587; A;Experimental source: cell line Ras-transformed NIH 3T3 cells
A;Note: activates JNK/SAPK cascade; Rac-binding protein
                                                                                                                                                                                                                                                                                                                                                                                           SH3 domains-containing protein POSH - mouse
C;Species: Mus musculus (house mouse)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 49; DB 2; Length 892;
Pred. No. 22;
1; Mismatches 0; Indels
                                                                                                  Length 577;
                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: T09071
K;Tapon, N; Nagata, K; Lamarche, N; Hall, A.
EMBO J. 17, 1395-1404, 1998
A;Reference number: Z16552; MUID:98151363; PMID:9482736
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                  5;
                                                                                            Score 49; DB 2
Pred. No. 16;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Keywords: signal transduction
F;8-58/Domain: RING finger homology <RRN>
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A,Cross-references: FlyBase:FBgn0003165
              A;Cross-references: FlyBase:FBgn0004892
C;Keywords: zinc finger
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                                                                                                  92.5%;
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12; Conserve
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A; Residues: 1-1533 <BAR>
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Best Local Similarity
Matches 12; Conserv
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A;Molecule type: mRNA
A;Residues: 1-361,'A',
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A;Gene: sob
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C;Species: Drosophila melanogaster
C;Date: 04-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C;Accession: S72227
Mang, L.; Coulter, D.E.
Genetics 144, 171-182, 1996
A;Fitle: Comparison of the structure and expression of odd-skipped and two related genes
A;Reference number: S7227; MUID:97032935; PMID:8878683
A;Status: preliminary
A;Status: preliminary
A;Residues: 1-577 < HAR.
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Mi-2 autoantigen 240 kDa protein - human (fragment)

Mi-2 autoantigen 240 kDa protein - human (fragment)

C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 05-Nov-1999

C;Accession: 138558

R;Ge, Q: Nilasena, D.S.; O'Brien, C.A.; Frank, M.B.; Targoff, I.N.

J. Clin. Invest. 96, 1730-1737, 1995

A;Title: Molecular analysis of a major antigenic region of the 240-kD protein of Mi-2 autoantic mumber: 138558; MUID:9601363; PMID:560064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPARC:UPI000016A09A; EMBL:U08379; NID:g761717; PIDN:AAC50228.1; PI
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                                                                                                                           heat shock transcription factor homolog T5C23.90 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C;Accession: T04213
R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft, submitted to the Protein Sequence Database, March 1999
A;Reference number: Z15261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cross-references: UNIPROT:024571; UNIPARC:UPI000007A28D; EMBL:U62004; NID:91480193;
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F;60-155/Domain: HSF DNA-binding domain homology <HSF>
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A;Molecule type: mRNA
A;Residues: 1-530 <RES>
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  ALIGNMENTS
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87 AAVAAAAAAAA 99
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Matches 12, Conservative
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A; Residues: 1-377 <BEV>
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A;Introns: 118/3
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Gaps

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C;Accession: JC5954
R;Tanaka, M; Tanaka, T.; Harata, M.; Suzuki, T.; Mitsui, Y.
Biochem. Biophys. Res. Commun. 243, 531-537, 1998
A;Title: Triplet repeat-containing ribosomal protein L14 gene in immortalized human end A;Reference number: JC5954; MUID:98153799; PMID:9480843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 specifically expressed in neuro
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A;Residues: 1-233 <JOH>
A;Cross-references: UNIPROT:P19359; UNIPARC:UPI0000047567; EMBL:X53725; NID:G56630; PID
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A;Residues: 1-220 <TAN>
A;Cross-references: UNIPARC:UPI000004E622; DDBJ:D87735; NID:g1620021; PIDN:BAA13443.1;
C;Superfamily: rat ribosomal protein L14
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C.Species: Rattus norvegicus (Norway rat)
C.Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C.Accession: 51158.
Nature 346, 958-861, 1990
A.Title: Two rat homologues of Drosophila achaete-scute specifically express A.Reference number: S11562; MUID: 90363294; PMID: 2392153
A.Reference number: S11563
A.Status: preliminary; nucleic acid sequence not shown
                                                                                                                                                                              hypothetical protein DKFZp586E1621.1 - human (fragment)
C,Species: Homo sapiens (man)
C,Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 02-Sep-2000
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                                                                                                                                                                                                                                                                                   Gassenhuber, J.; Wiemann,
                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-150 <OTT>
A;Residues: 1-150 <OTT>
A;Cross-references: UNIPROT:Q9Y4M1; UNIPARC:UP10000071DDD; EMBL:AL080235
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                                                                                                                                                                                                                                                      C,Accession: T12547
R;Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gasser submitted to the Protein Sequence Database, June 1999
A;Reference number: Z17528
A;Accession: T12547
A;Status: preliminary
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Pred. No. 10;
0; Mismatches
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Pred. No. 14;
0; Mismatches
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92.3%;
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Best Local Similarity 92.3
Matches 12, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ribosomal protein L14 - human
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein F53A3.6 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: D88395
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Title: sublished errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Status; preliminary
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                                                                                                                                                                                                                                                   female sterile homeotic protein, 205K - fruit fly (Drosophila melanogaster)
NyAlternate names: membrane protein fsh, 205K
NyChternate names: membrane protein fsh, 205K
NyContains: female sterile homeotic protein, 110K
C;Species: Drosophila melanogaster
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 31-Dec-2004
C;Accession: A43742; B43742
By Mare, S.R.; Mozer, B.A.; Bhatia-Dey, N.; Dawid, I.B.
Dev. Biol. 134, 246-257, 1989
A;Title: The Drosophila fsh locus, a maternal effect homeotic gene, encodes apparent A;Reference number: A43742; MUID:89276730; PMID:2267251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Keywords: alternative splicing; transmembrane protein
F;1-2038/Product: female sterile homeotic protein, 205K #status predicted <MA2>
F;1-1106/Product: female sterile homeotic protein, 110K #status predicted <MAT>
F;59-116/Domain: bromodomain homology <BRO1>
F;503-560/Domain: bromodomain homology <BRO2>
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A,Cross-references: UNIPARC:UPI000017A10F; EMBL:M23222
C,Genetics:
A,Gene: fsh
A,Cross-references: FlyBase:FBgn0004656
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Pred. No. 18;
0; Mismatches
  Pred. No. 33;
1; Mismatches
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1; Mismatches
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92.38;
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                                                                                                                            1050 AAVAAAAAAAA 1062
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                                                                               1 AAMAAAAAAAAA 13
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                             Conservative
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A;Molecule type: mRNA
A;Residues: 1-2038 <HAY>
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Matches 12; Conserv
Best Local Similarity
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A, Cross-references: UNIPARC: UP10000024E69; GB:S79041; NID:g1042008; PIDN:AAB34947.1; PID
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 16-Apr-1997 #sequence_revision 09-May-1997 #text_change 05-Oct-2004
C;Accession: JC5273
R;Yokoyama, M:; Nishi, Y.; Yoshii, J.; Okubo, K.; Matsubara, K.
B)NA Res. 3, 311-320, 1996
A;Title: Identification and cloning of neuroblastoma-specific and nerve tissue-specific
A;Reference number: JC5272; MuID:97191543; PMID:9039501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-314 < YOK>
A;Residues: 1-314 < YOK>
A;Residues: 1-314 < YOK>
A;Cross-references: UNIPROT:Q99453; UNIPARC:UPI0000131D16; DDBJ:D82344; NID:g1841337; PI
C;Comment: This protein is a transcriptional repressor involved in regulating gene expre C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;99-155/Domain: homeobox homology < HOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NyAlternate names: homeotic protein Hoxd-11
(),Species: Mus musculus (house mouse)
(),Species: Mus musculus (house mouse)
(),Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 05-Oct-2004
(),Accession: 816318; 846403; $557443
(),Rizpisua-Belmonte, J.C.; Falkenstein, H.; Dolle, P.; Renucci, A.; Duboule, D. R,Izpisua-Belmonte, J.C.; Falkenstein, H.; Dolle, P.; Renucci, A.; Duboule, A.; Title: Murine genes related to the Drosophila AbdB homeotic gene are sequentially expra A;Reference number: $16318.
A;Accession: $16318.
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A,Residues: 1-323 <1ZED-
A,FCROSACES: 1-323 <1ZED-
A,CTOSS-references: UNIPROT: P23813; UNIPARC: UPI0000029F10; EMBL: X60761; NID: 951420; PIDN
R,Gerard, M.; Duboule, D.; Zakany, J.
R,Gerard, M.; Duboule, D.; Zakany, J.
BMBO J. 12, 3539-3550, 1993
A,Title: Structure and activity of regulatory elements involved in the activation of the
A,Reference number: S40403; MUID: 94074553; PMID: 7902810
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A;Title: Gsh-2, a murine homeobox gene expressed in the developing brain. A;Reference number: 157039; MUID:95344993; PMID:7619729 A;Accession: 157039 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-305 <RES>
                                                                                                                                                                                                                                                                                                               C;Keywords: DNA binding; homeobox; nucleus; transcription regulation F;204-260/Domain: homeobox homology <HOX>
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Pred. No. 18;
0; Mismatches
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Pred. No. 18;
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92.3%;
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Best Local Similarity
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homeotic protein Hox D8 - mouse
homeotic protein Hox 4.3

N/Alternate names: homeotic protein Hox 4.3

C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: A4356
A;Title: Primary structure and embryonic expression pattern of the mouse Hox-4.3 homeobod A;Title: Primary structure and embryonic expression pattern of the mouse Hox-4.3 homeobod A;Reference number: A43562; MuID:91209232; PMID:1982431
A;Residues: 1-289 <1ZP>
A;Cross-references: UNIPROT:P23463; UNIPARC:UPI0000177DA6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: A48279
K;Ball, D.W.; Azzoli, C.G.; Baylin, S.B.; Chi, D.; Dou, S.; Donis-Keller, H.; Cumaraswam Proc. Natl. Acad. Sci. U.S.A. 90, 5648-5652, 1993
A;Title: Identification of a human achaete-scute homolog highly expressed in neuroendocr A;Reference number: A48279; MUID:93296195; PMID:8390674
A;Accession: A48279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Cross-references: UNIPROT:P50553; UNIPARC:UP10000047566; GB:L08424; NID:g306459; PID:q
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C;Species: Mus sp. (mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Oct-2004
C;Accession: IS7039
R;Hsieh-Li, H.M.; Witte, D.P.; Szucsik, J.C.; Weinstein, M.; Li, H.; Potter, S.S.
Mech. Dev. 50, 177-186, 1995
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C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 09-Jul-2004
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C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;196-252/Domain: homeobox homology <HOX>
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                                                                               88.7%; Score 47; DB 2; Length 233; 92.3%; Pred. No. 14; ive 0; Mismatches 1; Indels
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A;Molecule type: mRNA
A;Residues: 1-238 <RES>
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Matches 12; Conservative
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                                                                                                                                                                                                                                                                                       AAAAAAAAAAA 44
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Matches 12; Conservative
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les 12; Conserv
             C; Keywords: DNA binding
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Gaps

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Indels

Length 331;

5

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R.D'Esposito, M.; Morelli, F.; Acampora, D.; Migliaccio, E.; Simeone, A.; Boncinelli, E Genomics 10, 43-50, 1991
Genomics 10, 43-50, 1991
A;Title: EVXZ, a human homeobox gene homologous to the even-skipped segmentation gene, 3,8Reference number: A39065; MUID:91257849; PMID:1675198
A;Accession: A39065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: UNIPARC: UP1000016A2D0; EMBL: U48250; NID: 91199656; PIDN: AAC72247.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein kinase C-binding protein RACK17 - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Bacession: G02409
R;Kuroda, S.; Tokunaga, C.; Kiyohara, Y.; Konishi, H.; Kikkawa, U.
submitted to the EMBL Data Library, February 1996
                                                                                                                                                                                                                                                                                                                          homeotic protein EVX2 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 31-Dec-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Mesocricetus auratus (golden hamster)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Oct-2004
C;Accession: 148188
R;Rudnick, A.; Ling, T.Y.; Odaqiri, H.; Rutter, W.J.; German, M.S.
Proc. Natl. Acad. Sci. U.S.A. 91, 12203-12207, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GDB:127528; OMIM:142991
A;Map position: 242-4.3-2431
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;46-102/Domain: homeobox homology <HOX>
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Pred. No. 19;
0; Mismatches 1; Indels
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Pred. No. 19;
0; Mismatches
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                                                                                       0; Mismatches
                                   Score 47;
Pred. No.
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A, Cross-references: UNIPARC:UP1000017A29D
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92.3%;
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                                                                                       12; Conservative
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A;Accession: G02409
                                   Query Match
Best Local Similarity
Matches 12; Conserv
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Best Local Similarity
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hypotherical protein lin2792 [imported] - Listeria innocua (strain Clip11262)

C;Species: Listeria innocua
C;Species: Listeria innocua
C;Species: Listeria innocua
C;Species: Listeria innocua
C;Accession: AB1781

R;Glaser, D: Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
D; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001

A;Authors: Kreft, J.; Kunh, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mah, A.; Mathors: Kreft, J.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.;Reference number: AB1077; MUID:21537279; PMID:11679669

A;Scatus; preliminary
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C;Species: Mesocricetus auratus (golden hamster)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 05-Apr-1995
C;Accession: B47236
R;Kennedy, G.C.; Rutter, W.J.
Proc. Natl. Acad. Sci. U.S.A. 89, 11498-11502, 1992
A;Title: Pur-1, a zinc-finger protein that binds to purine-rich sequences, transactivate
A;Reference number: A47236; MUID:93087555; PMID:1454839
        PI
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C;Genetics:
A;Cross-references: UNIPARC:UP10000029F10; EMBL:X71422; NID:g397508; PIDN:CAA50553.1; IR;Takada, S.; Cook, M.; Kramlauf, R.; McMahon, A.P.
submitted to the EMBL Data Library, May 1991
A;Description: Genomic sequence of mouse Hox-4.6.
A;Reference number: S57443
A;Accession: S57443
A;Accession: S57443
A;Residues: 'MNDFDECGPSAAS', 1-323 <TAK>
A;Residues: 'MNDFDECGPSAAS', 1-323 <TAK>
A;Cross-references: UNIPARC:UP10000026A38; EMBL:X60395; NID:g871427; PIDN:CAA42943.1; IS
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C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;252-308/Domain: homeobox homology <HOX>
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                                                                                                                                                                                                                                                                                                                                                                                                             2; Length 323;
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Pred. No. 19;
2; Mismatches
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Pred. No.
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92.3%;
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Best Local Similarity
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                                                                                                                                                                                                                                                                            A, Gene: Hoxd-11
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Best Local S:
Matches 12
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Gaps

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Length 333;

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A;Cross-references: UNIPARC:UP100016DEBB; EMBL:D49704; NID:g1805615; PIDN:BAA08554.1; P A;Experimental source: cv. Nipponbare; splice form OSH42
C;Comment: For an alternative splice form, see PIR:T03875.
C;Genetics:
                                                                                                                                                           A;Introns: 174/3; 215/1; 277/3; 321/3; 367/2
C;Keywords: alternative initiators; alternative splicing; DNA binding; homeobox; nucleus
C;T-375/Product: probable homeobox protein OSH45, splice form OSH44 #status predicted <M
F;197-367/Product: probable homeobox protein OSH45, splice form OSH42 #status predicted
F;291-357/Product: probable homeobox protein OSH45, splice form OSH42 #status predicted
F;291-352/Domain: homeobox homology <HOX>
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C;Date: 01-Dec-1993 #sequence revision 18-Nov-1994 #text_change 31-Dec-2004
C;Date: 01-Dec-1993 #sequence revision 18-Nov-1994 #text_change 31-Dec-2004
C;Accession: A48423; S13009; A26629; A24778
R;Logan, C.; Hanks, M.C.; Noble-Topham, S.; Nallainathan, D.; Provart, N.J.; Joyner, A.I. Dev. Genet. 13, 345-358, 1992
A;Title: Cloning and sequence comparison of the mouse, human, and chicken engrailed gent A;Reference number: A48423; MUID:93185339; PMID:1363401
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PERS Lett. 277, 250-252, 1990
A,Title: Conservation of engralled-like homeobox sequences during vertebrate evolution.
A,Reference number: 813009; MUID:91099509; PMID:1980115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    basic helix-loop-helix transcription repressor H - fruit fly (Drosophila virilis)
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C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 02-Jul-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:102964, NCBIP:102966)
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A;Residues: 1-401 <LOG>
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A;Experimental source: CD-1, embryo
A;Note: sequence extracted from NCBI backbone (NCBIP:126620)
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Pred. No. 21;
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Pred. No. 21;
0; Mismatches
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0; Mismatches
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A;Molecule type: mRNA
A;Residues: 1-378 <WAI>
A;Cross-references: UNIPARC:UPI000017BEF1
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                 A;Gene: H45
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probable homeobox protein OSH45, splice form OSH42
C;Species: Oryza sativa (rice)
C;Species: Oryza sativa (rice)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-Oct-2004
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-Oct-2004
C;Accesion: T03874; T03876
R;Tamaoki, M.; Tsugawa, H.; Minami, E.; Kayano, T.; Yamamoto, N.; Kano-Murakami, Y.; Mathant J. 7, 927-938, 1995
A;Atle: Alternative RNA products from a rice homeobox gene.
A;Reference number: 215126; MUID:95322999; PMID:7599652
A;Accession: T03874
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: T03874
A;Accession: T03874
A;Accession: T03876
A;Accession: T03876
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A;Accession: T03876
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C;Keywords: alternative initiators; alternative splicing; DNA binding; homeobox; nucleus
F;291-352/Domain: homeobox homology <HOX>
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A;Molecule type: DAY
A;Rosidues: 1-374 <TAM>
A;Cossidues: 1-374 <TAM>
A;Cross-references: UNIPROT:P93423; UNIPARC:UP100000AB610; EMBL:D49704; NID:g1805615;
A;Experimental source: cv. Nipponbare
C;Comment: For alternative splice forms, see PIR:T03874.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable homeobox protein OSH45, splice form OSH45 [similarity] - rice C; Species: Oryza sativa (rice) C; Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change O5-Oct-2004 C; Accession: T03875 R; Tamaoki, M.; Tsuqawa, H.; Minami, E.; Kayano, T.; Yamamoto, N.; Kano-Murakami, Y.; Plant, J.; 7, 927-938, 1995 A; Title: Alternative RNA products from a rice homeobox gene. A; Reference number: Z15126; MUID:95322999; PMID:7599652 A; Reference number: Z15126; MUID:95322999; PMID:7599652
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A;Title: Pancreatic beta cells express a diverse set of homeobox genes.
A;Reference number: 148185; MUID:95083670; PMID:7991607
                                                                                                                                                                                                                                       A;Gene: Nix6.1
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;237-293/Domain: homeobox homology <HOX>
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A;Molecule type: DNA
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Pred. No. 20;
0; Mismatches
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Pred. No. 2
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92.3%;
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Local Similarity 92.3%;
hes 12; Conservative
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C;Accession: T14911
R;Kircher, S.; Ledger, S.; Hayashi, H.; Weisshaar, B.; Schafer, E.; Frohnmeyer, H.
Mol. Gen. Genet. 257, 595-605, 1998
A;Title: CPRF4a, a novel plant bZIP protein of the CPRF family: comparative analysis of
A;Reference number: Z18261; MUID:98265918; PMID:9604882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-443 <STE1>
A;Cross-references: UNIPROT:P41225; UNIPARC:UPI000003F546; EMBL:X71135; NID:g468790; PII
A;Accession: I38242
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A,Residues: 143-158,'P',160-218 <STE2>
A,Cross-references: UNIPARC:UPI0000071C8C; EMBL:X71137; NID:9468793; PIDN:CAA50467.1; P
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R;Dush, M.K.; Martin, G.R.
Bev. Biol. 151, 273-287, 1992
A;Title: Analysis of mouse Evx genes: Evx-1 displays graded expression in the primitive
A;Reference number: A43915; MUID:92249649; PMID:1349539
                                                                                                                                                                                                                                                A; Cross-references: UNIPROT: 082037; UNIPARC: UP100000A12C8; EMBL: Y10810; NID: 93336904;
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C;Superfamily: BZIP G-box-binding protein; fos/jun DNA-binding domain homology
C;Reywords: DNA binding; leucine zipper
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               homeoric protein even-skipped homolog Evx-2 - mouse
N;Alternate names: mesodermal cell dorsoventral fates determinator Evx-2
C;Species: Mus musculus (house mouse)
C;Date: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 31-Dec-2004
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                                                                                                                                       A,Accession: T14911
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1-420 <KIR>
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A,Gene: GDB:SOX3; SOX-3; SOXB
A,Crose-references: GDB:250376; OMIM:313430
A,Map position: Xq26-Xq27
C,Superfamily: human SOX3 protein; HMG box homology
P;136-211/Domain: HMG box homology <HMG>
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Pred. No. 23;
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22;
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Pred. No.
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Best Local Similarity 92.5
Loca 12; Conservative
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                                          A; Molecule type: nucleic acid
A; Residues: 321-380 -4NL>
A; Residues: 321-380 -4NL>
A; Residues: 321-380 -4NL>
A; Corner, A.L.; Martin, G.R.
R; Joyner, A.L.; Martin, G.R.
Genes Dev. 1, 29-38, 1987.
A; Title: En-1 and En-2, two mouse genes with sequence homology to the Drosophila engrail
A; Reference number: A91620; MUID:88112776; PMID:2892757
A; Molecule type: DNA; mRNA
A; Residues: 278-401 -4JOY>
A; Cross-references: UNIPARC:UP1000016CA7C; GB:Y00201; GB:M11987; NID:949587; PIDN:CAA683
A; Title: Expression during embryogenesis of a mouse gene with sequence homology to the D
A; Recerence number: A24778; MUID:86079501; PMID:2416459
A; Molecule type: DNA
A; Recerences: UNIPARC:UP1000017A2B0
C; Genetics:
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C;Species: Homo sapiens (man)
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 31-Dec-2004
C;Accession: A53662
R;Harrison, K.A.; Druey, K.M.; Deguchi, Y.; Tuscano, J.M.; Kehrl, J.H.
A;Harrison, R.A.; Druey, K.M.; Deguchi, Y.; Tuscano, J.M.; Kehrl, J.H.
A;Hitle: A novel human homeobox gene distantly related to proboscipedia is expressed in
A;Reference number: A53662; MUID:94327547; PMID:7914194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-403 <HAR>
A;Cross-references: UNIPARC:UPI000017A29E; GB:U07663
A;Note: the nucleotide sequence and conceptual translation as given are self-consistent
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bZIPD DNA-binding protein - parsley
C;Species: Petroselinum crispum (parsley)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 31-Dec-2004
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C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;313-369/Domain: homeobox homology <HOX>
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C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;244-300/Domain: homeobox homology <HOX>
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A, Status: preliminary; not compared with conceptual translation
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Pred. No. 22;
0; Mismatches
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A;Gene: GDB:HLXB9
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Score 47; DB 2; Length 494; Pred. No. 25;
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92.3%;
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F,174-183/Region: alanine-rich
F,207-230/Region: zinc finger
F,296-318/Region: zinc finger
F,324-346/Region: zinc finger
F,354-368/Region: zinc finger
F,373-405/Region: zinc finger
F,409-430/Region: zinc finger
F,452-468/Region: alanine-rich
                                                                                              396 AAAAAAAAAAAA 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AAMAAAAAAAA 13
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Matches 12; Conservative
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CiSpecies: Mus musculus (house mouse)
CiSpecies: Mus musculus (house mouse)
CiSpecies: Mus musculus (house mouse)
CiSpecies: Musculus (house mouse)
CiSpecies: Musculus (house mouse)
CiSpecies: A7236
R; Kennedy, G.C.; Rutter, W.J.
Proc. Natl. Acad. Sci. U.S.A. 89, 11498-11502, 1992
A; Reference number: A47236, MUID:93087555; PMID:1454839
A; Reference number: A47236
A; Status: preliminary: not compared with conceptual translation
A; Status: preliminary: not compared with conceptual translation
A; Residues: 1-477 < KEN>
A; Resi
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C;Species: Homo sapiens [man]
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C;Accession. JG7583
R;Fujimoto, K.; Shen, M.; Noshiro, M.; Matsubara, K.; Shingu, S.; Honda, K.; Yoshida, E. Biochem. Biophys. Res. Commun. 280, 164-171, 2001
A;Title: Molecular cloning and characterization of DEC2, a new member of basic helix-loc A;Accession: JG7583; MUID:21092582; PMID:11162494
A;Status: preliminary
A;Molecule type: DNA; mRNA
A;Residues: 1-475 <DUS>
A;Cross-references: UNIPROT:P49749; UNIPARC:UPI0000020BC6; GB:S34322; NID:g249137; PIDN:A;Note: sequence extracted from NCBI backbone (NCBIN:100478, NCBIN:100480, NCBIN:100482, C;Genetics:
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A;Cross-references: UNIPROT:Q9C0J9; UNIPARC:UPI0000052B52; DDBJ:AB044088
C;Comment: This protein, a novel member of the DEC subfamily of basic helix-loop-helix
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C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;192-248/Domain: homeobox homology <HOX>
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88.7%; Score 47; DB 2; Length 482;
Best Local Similarity 92.3%; Pred. No. 25;
Matches 12; Conservative 0; Mismatches 1; Indels
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C; Keywords: transcription factor
F;1-173/Region: highly conserved #status predicted
F;130-173/Domain: Orange #status predicted cORA>
                                                                                                                                                                                                                                                                                                                                                                                                           Score 47; DB 2
Pred. No. 24;
0; Mismatches
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basic helix-loop-helix protein, DEC2 - human
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Best Local Similarity 92.3%;
Matches 12; Conservative
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A; Residues: 1-482 <FU
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C;Species: Chlamydomonas reinhardtii
C;Species: Chlamydomonas reinhardtii
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T09084
R;Molendijk, A.J.; Irvine, R.F.
Plant Mol. Biol. 37, 53-66, 1998
A;Title: Inositide signalling in Chlamydomonas: Characterization of a phosphatidylinosit
A;Accession: T09084
A;Sctutus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-490 <MOL>
A;Cross-references: UNIPROT:004270; UNIPARC:UPI00009C6FA; EMBL:U97663; NID:g2109290; PI
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Biochemistry 31, 4102-4110, 1992
A,Title: Isolation of a novel cDNA encoding a zinc-finger protein that binds to two site A,Reference number: A42170; MUID:92232709; PMID:1567856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.Cross-references: UNIPROT: P56270; UNIPARC:UPI000017C427; GB:J05371
A;Notes: it is uncertain whether Met-18 is the initiator or whether translation is initial R;Bossone, S.A.; Asselin, C.; Patel, A.J.; Marcu, K.B.
Proc. Natl. Acad. Sci. U.S.A. 89, 7452-7456, 1992
A;Title: MAZ, a zinc finger protein, binds to c-MYC and C2 gene sequences regulating tra A;Reference number: A46153; MUID:92366479; PMID:1502157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N, Alternate names: MYC-associated zinc finger protein MAZ; zinc finger protein ZF87
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C;Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 09-Jul-2004
C;Accession: A42170; A46153
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A;Note: sequence extracted from NCBI backbone (NCBIN:110666, NCBIP:110667)
C; Keywords: DNA binding; zinc finger
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A;Residues: 18-417,'L',419-494 <BOS>
A;Cross-references: UNIPARC:UPI000012ECF8; GB:M94046
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Pred. No. 25;
0; Mismatches
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N.Alternate names: PEAZ alpha chain type 1; PEAZ alpha chain type 2; PEBP2 alpha chain type 2; PEBP2 alpha chain type 1; Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Jul-2004
C;Accession: A48233 B48233
R;Ogawa, E.; Maruyama, M.; Kagoshima, H.; Inuzuka, M.; Lu, J.; Satake, M.; Shigesada, K Proc. Natl. Acad. Sci. US.A. 90, 6859-6863, 1993
A;Title: PEBP2/PEAZ represents a family of transcription factors homologous to the prodict A;Reference number: A48233; MUID:93342088; PMID:8341710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-513 <OGA>
A, Cross-references: UNIPROF: Q08775; UNIPARC: UPI000002B2F8; GB: D14636; NID: g391766; PIDN
A, Accession: B48233
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A;Cross-references: UNIPARC:UPI000002B2F9; GB:D14637; NID:g391768; PIDN:BAA03486.1; PID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Gene: PEBP2alphaA
C,Superfamily: transcription factor CBF alpha 2
C,Keywords: alternative splicing; DNA binding; T-cell; transcription factor; transcript:
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C;Species: Drosophila melanogaster
C;Species: Os-Sep-1995 #sequence_revision 08-Sep-1995 #text_change 09-Jul-2004
C;Accession: A55529
R;Cheah, P.Y.; Meng, Y.B.; Yang, X.; Kimbrell, D.; Ashburner, M.; Chia, W.
Mol. Cell. Biol. 14, 1487-1499, 1994
A;Title: The Drosophila 1(2)35Ba/nocA gene encodes a putative Zn finger protein involved A;Reference number: A55929; MUID:94119100; PMID:8289824
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A,Molecule type: mRNA
A,Residues: 1-537 <CHE>
A,Cross-references: UNIPROT:Q24423; UNIPARC:UPI000007B356; GB:L14009; NID:g431289; PID:
                                                                                                                polyomavirus enhancer-binding protein 2 alpha chain type 1 - mouse
N/Alternate names: PEA2 alpha chain type 1; PEA2 alpha chain type 2; PEBP2 alpha chain
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C;Species: Drosophila melanogaster
C;Date: 27-Nov-1985 #sequence revision 27-Nov-1985 #text change 09-Jul-2004
C;Accession: A90862; A93354; Ā03321; A03322; A25682; S03667
C;Accession: A90862; A25682; B.; Kornberg, T. Cell 40, 37-43, 1985
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Pred. No. 27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 47; DB 2
Pred. No. 26;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
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A,Cross-references: FlyBase:FBgn0005771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88.7%;
84.6%;
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92.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AAMAAAAAAAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AAMAAAAAAAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 AAAAAAAAAAA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 92.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: A48233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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NyAlternate names: MAZ protein
NyAlternate names: MAZ protein
Cipacies: Homo sapiens (man)
Cibate: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 05-Nov-1999
Cibate: 31-Jan-1997 #sex Commun. 226, 801-809, 1996
Biochem: Biophys. Res. Commun. 226, 801-809, 1996
Biochem: Biophys. Res. Commun. 226, 801-809, 1996
A;Reference number: JC5076, MUID:96428591; PMID:8831693
A;Recession: JC5076
A;Reference number: JC5076
A;Rocession: J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Molecule type: DNA
A;Residues: 1-495 <HAR>
A;Residues: 1-495 <HAR>
A;Residues: 1-495 <HAR>
A;Cross-references: UNIPROT: P31361; UNIPARC: UPI0000029AAF; EMBL: M88299; NID: g200444; PIC
C;Superfamily: transcription factor Brn-1; homeobox homology; POU domain homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;27-49/Region: glycine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Keywords: phosphoprotein; zinc finger
1:146,204,480/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status pre
F:349/Binding site: phosphate (Tyr) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Hara, Y.; Rovescalli, A.C.; Kim, Y.; Nirenberg, M.
Proc. Natl. Acad. Sci. U.S.A. 89, 3280-3284, 1992
A;Title: Structure and evolution of four POU domain genes expressed in mouse brain.
A;Reference number: S31223; MUID:92228768; PMID:1565620
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                                                                                                                                                                                                                                                                                                                   transcription factor Brn-1 - mouse
N;Alternate names: class III POU domain protein brain-1
C;Species: Wus musculus (house mouse)
C;Date: 02-Dec-1993 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S31223
       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Pred. No. 25;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 47; DB 1; Length 495;
Pred. No. 25;
0; Mismatches 1; Indels
       Indels
       1,
   Mismatches
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F;316-383/Domain: POU domain homology <POU>F;402-458/Domain: homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F:101-112/Region: alanine-rich
F:162-180/Region: histidine/proline-rich
F:186-201/Region: alanine-rich
F:236-247/Region: glycine-rich
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92.3%;
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92.3%;
                                                                                                                                              113 AAAAAAAAAA 125
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                                                                       1 AAMAAAAAAAA 13
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12; Conservative
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A; Status: preliminary
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Best Local
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Gaps

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Length 627;

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C;Accession: $40382
R;Abel, T.; Michelson, A.M.; Maniatis, T.
Bevelopment 119, 623-633, 1993, 1993
A;Title: A Drosophila GATA family member that binds to Adh regulatory sequences is expre
A;Reference number: $40382; MUID:94244465; PMID:8187633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Molecule type: mRNA
A,Residues: 1-779 cABE.
A,Crons-references: UNIPROT:P52172; UNIPARC:UPI0000135F5F; EMBL:X76217; NID:9441491; PII
C,Coment: This transcriptional activator is the earliest known marker of the developing
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A,Cross-references: FlyBase:FBgn0003507
C,Superfamily: box A-binding factor; GATA-type zinc finger homology
C,Keywords: DNA binding; nucleus; transcription factor; transcription regulation; zinc
F;316-369/Domain: GATA-type zinc finger homology <GZF>
                  A,Molecule type: DNA
A,Residues: 1-627 <STO>
A,Cross-references: UNIPARC:UPI000017885F; GB:AE002093; NID:93413700; PIDN:AAC31223.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Drosophila sp. C;Species: Drosophila sp.)
C;Species: Drosophila sp.
C;Species: 18-Feb-1994 #sequence_revision 01-Dec-1995 #text_change 07-May-1999
C;Accession: S39356
R;Wimmer, B.A.; Jaeckle, H.; Pfeifle, C.; Cohen, S.M.
Nature 366, 690-694, 1993
A;Title: A Drosophila homologue of human Spl is a head-specific segmentation gene.
A;Reference number: S39356; MUID:94081952; PMID:8259212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Molecule 1.644 cWIM>
A;Cross-references: UNIPARC:UPI0000124C17; EMBL:Z29361; NID:g441283; PID:g441284
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N;Alternate names: ABF; transcription factor dGATAb
C;Species: Drosophila melanogaster
C;Date: 11-Jan-1995 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C;Accession: S40382
                                                                                                                                                                                                             A;Map position: 2
A;Introns: 40/1; 119/1; 160/3; 319/3
C;Superfamily: FtsH/SEC18/CDC48-type ATP-binding domain homology
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Best Local Similarity 92.3%; Pred. No.
Matches 12; Conservative 0; Mismatc
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                                                                                                                                               C;Genetics:
A;Gene: T19L18.5; At2g26140
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N;Alternate names: YTA11 protein homolog T19118.5
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 24.Mar-1999 #sequence_revision 24-Mar-1999 #text_change 31-Dec-2004
C;Accession: T02610; H84656
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, August 1998
A;Description: Arabidopsis thaliana chromosome II BAC T19118 genomic sequence.
A;Reference number: Z14681
A;Reference number: Z14681
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A;Reference number: Z14681
A;Reference number: C02610
A;Status: translated from GB/EMBL/DDBJ
A;Redidues: 1-672 <ROUN
A;Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
K;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
R;Lin, X.; Kaul, S.; Cronin, L.A.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
N;Thle: Sequence and analysis of Chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                         A, Accession: A93354
A, Molecule type: DNA
A, Residues: 447-485, E7, 487-518, VWH, <FUO>
A, Cross-references: UNIPARC:UPI00001745BF; GB:X01765; GB:X03059; NID:g8084; PIDN:CAA259G
A, Cross-references: UNIPARC:UPI00001745BF; GB:X01765; GB:X03059; NID:g8084; PIDN:CAA259G
A,Note: the translation of the nucleotide sequence from Fig. 5 is shown, not the transla
n in Fig. 6
R, Kassis, J.A.; Poole, S.J.; Wright, D.K.; O'Farrell, P.H.
EMBO J. 5, 3583-3589, 1986
A,Title: Sequence conservation in the protein coding and intron regions of the engrailed
A, Reference number: A91059; MNID:87161768; PMID:2881781
A, Contents: annotation; intron locations and sequences
R, Gay, N.J.; Poole, S.J.; Kornberg, T.B.
Nucleic Acids Res. 16, 6637-6647, 1988
A,Title: The Drosophila engrailed protein is phosphorylated by a serine-specific protein
A, Reference number: S03667; MUID:88289425; PMID:2899884
A, Contents: annotation; potential phosphorylation sites; homeobox domain
C, Comment: This protein specifies the body segmentation pattern.
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A,Cross-references: FlyBase:FBgn0000577
A;Aross-references: 78,62.0 (48A1-4)
A;Introns: 438/1; 470/3
C;Superfamily: engrailed homeotic protein; homeobox homology
C;Superfamily: engrailed homeotic protein; nucleus; segmentation; transcription regulati
F;26-35/Region: glutamine-rich
F;68-87/Region: alanine-rich
A;Title: The engrailed locus of Drosophila: structural analysis of an embryonic transcri
A;Reference number: A90862; MUID:85099327; PMID:3917855
                                                                                                                 A,Molecule type: mRNA
A;Residues: 1-552 <POO>
A;Cross-references: UNIPROT:P02836; UNIPARC:UP1000012CA13; GB:M10017; NID:g157363; PIDN:
R;Fjose, A.; McGinnis, W.J.; Gehring, W.J.
Nature 313, 284-289, 1985
                                                                                                                                                                                                                                                                                       A,Title: Isolation of a homoeo box-containing gene from the engrailed region of Drosophi
A,Reference number: A93354; MUID:90114393; PMID:2481829
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Pred. No. 27;
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F,320-368/Region: serine-rich
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Search completed: September 9, 2006, 23:01:49 Job time : 16.8101 secs

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GenCore version 5.1.9
(c) 1993 - 2006 Biocceleration Ltd
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                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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SMART; SMOO355; BTB; 1.
SMART; SMOO355; ZAF C2H2; 2.
PROSITE; PS50097; BTB; 1.
PROSITE; PS500189; ZINC_FINGER_C2H2_1; 1.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 2.
DNA-binding; Metal-binding; Nuclear protein; Repeat; Transcription; DNA-binding; Metal-binding; Nuclear protein; Repeat; Transcription; Zinc, Zinc-finger.
Zinc finger and BTB domain-containing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: May be involved in transcriptional regulation.
-!- SUBCELIULAR LOCATION: Nucleus (Potential).
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382 C2H2-type 2.
4149 Ala-rich.
53387 MW, B4FF082555B0CAIA CRC64;
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                                                                                                                         26-APR-2004, integrated into UniProtKB/Swiss-Prot. 01-MAR-2003, sequence version 1. 07-MAR-2006, entry version 22.
                                                                                                                                                                                  07-MAR-2006, entry version 22.
Zinc finger and BTB domain-containing protein 8.
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InterPro; IPR000210; BTB.
InterPro; IPR013069; BTB POZ.
InterPro; IPR007087; Znf_C2H2.
Pfam; PF00651; BTB; 1.
Pfam; PF00661; Zf-C2H2; 2.
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SMART; SM00225; BTB; 1.
SMART; SM00355; ZnF C2H2; 2.
                                                                                STANDARD;
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QBCII0;
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Length 484;

DB 1;

Score 53;

100.0%;

Query Match

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RA CATRING-07-10.1126/science.112014;

RA CATRING-07-10.1126/science.112014;

RA CATRING-07-10.1126/science.1122014;

RA CATRING-07-10.11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-OCT-2005, integrated into UniProtKB/TrEMBL.
11-OCT-2005, sequence version 1.
21-FEB-2006, entry version 7.
21-FEB-2006, entry version 7.
11 days embryo head cDNA, RIKEN full-length enriched library, clone:C130068L16 product:Linc finger and BTB domain containing 8, full insert sequence (0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:C230068H07 product:zinc finger and BTB domain containing 8, full insert sequence) (14, 17 days embryo head cDNA, RIKEN full-length enriched library, clone:3222401B20 product:zinc finger and BTB domain containing 8, full insert sequence).
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
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MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
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"High-efficiency full-length cDNA cloning.";
Methods Enzymol. 303:19-44(1999).
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                           Pred. No. 42; Mismatches
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100.08;
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-CSTBL/65. TISSUB=Cerebellum, and Head;
MEDLINE=21085660; PubMed=11217851; DOT=10.1038/3505500;
A Rawai J., Shinagawa A., Shibata K., Yoshino M., Itch M., Ishii Y.,
A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Abhburner M., Batalov S., Casavant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bareh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Rronstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Wunnibaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Winnibay-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               birney E., Hayashizaki Y., "Analysis of the mouse transcriptome based on functional annotation of
., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
                                                                                                                                                   STRAIN=C57BL/63; TISSUB=Cerebellum, and Head;
PubMed=16141073; DOI=10.1126/science.1112009;
RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium;
"Antisense Transcription in the Mammalian Transcriptome.";
Science 309:1564-1566 (2005).
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                                        "The transcriptional landscape of the mammalian genome."; Science 309:1559-1563(2005).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 420:563-573 (2002).
                                                                                                                              NUCLEOTIDE SEQUENCE
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  Tagami M.
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STRAIN=CS7BL/6J; TISSUB=Cerebellum, and Head; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;

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Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Wormalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630 (2000).
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Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.
Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibate K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Carninci P., Samamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Chazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AK140914; BAE24519.1; -; mRNA.
EMBL; AK163930; BAE37541.1; -; mRNA.
EMBL; AK13152; BAE20999.1; -; mRNA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0046872; F:metal ion binding; IEA.
GO; GO:003515; F:metal ion binding; IEA.
GO; GO:005515; F:protein binding; IEA.
GO; GO:000515; F:protein binding; IEA.
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PROSITE; PS00028; ZINC FINGER C2H2 1; 1.
PROSITE; PS50157; ZINC FINGER C2H2 2; 2.
Metal-binding; Nuclear protein; Repeat;
                                                                                                                                                                                                                                                                                                                                                                         Genome Res. 10:1757-1771(2000).
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InterPro; IPR013069; BTB POZ.
InterPro; IPR007087; Znf_C2H2.
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SMART; SM00355; ZnF_C2H2; 2.
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ProDom; PD000003; Znf_C2H2
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                                                                                                                             NUCLEOTIDE SEQUENCE
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NUCLEOTIDE SEQUENCE
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RESULT 3 Q6Z8T9 OR

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RA Borowsky M., Boukhgalter B., Brunache A., Butler J., Calixte N., RA Calvo S.E., Camarata J., Campo K., Chang J., Cheshatsang Y., Calroen M., Collymore A., Conadidne T., Cook A., Cooke F., Corum B., Cuomo C., David R., Dawore T., Degray S., Dodge S., Dooley K., RA Dorrie R., David R., David R., David R., Dorries L., Duffey N., Duges A., Elkins T., Bragels R., Erickson J., Farina A., Faro S., Ferreira P., Fischer H., Ragels R., Erickson J., Farina A., Galagan J.E., Gearin G., Gnerre S., Ragels M., Foloy K., Gage D., Galagan J.E., Gearin G., Gnerre S., Handre A., Graham J., Handbois E., Heller A., Higgins H., RA Handra T., Hond N., Hughes L., Hulme W., Husby E., Iliev I., RA Landers T., Leger J., Levine S., Lewis D., Lewis T., Lindblad-Toh K., Liu X., Leger J., Levine S., Lewis D., Lewis T., Landers T., Mander D., Mabbitt R., Machen C., Major J., Maclardy W., McDonough S., McGhee T., Meldrim J., Manceli E., McGarthy W., McDonough S., McGhee T., Meldrim J., Mencel E., Mallrain L., Munson G., Maylor J., Mencel J., Milalev A., Milalev A., Milalev A., Milalev A., Milalev R., Machen C., Newes C., Maylor J., Malalev A., Milalev R., Mallrain S., Perrin D., Phunkhang P., Piqani B., Norbu N., Obonnell P., Okoawo O., O'Leary S., Omotosho B., Norbu N., Obonnell P., Okoawo O., O'Leary S., Omotosho B., Norbu N., Obonnell P., Ghome C., Settipali S., Sharpe T., Senera R., Stone S., Stubbs M., Talamas J., Tchining P., Testage S., Teange -Thoman N., Satvopoulos S., Rageron K., Stone C., Stube S., Subbs M., Talamas J., Tochham R., Towey S., Tsamla T., Tsone Thomas J., Wu Y., Wang S., Wangchu K., Towey S., Tsamla T., Shenger E., Young G., Wang S., Wang S., Yang X., Veager S., Young G., Wang S., Wang S., Yang X., Yang S., Yang X., Yang S., Yang X., Yang X., Yang S., Yang X., Yang X., Yang S., Yang X., Yang X., Yang S., Yang X., Yang X., Yang X., Yang X., Yang X., Yang X.,
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92.3%;
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ORFNames=NCU08548.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sasaki T., Matsumoto T., Yamamoto K.,
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
-!- DOMAIN: The RING-type zinc finger domain is essential for ubiquitin ligase activity. It coordinates an additional third zinc
                                                                                                                                                                                                                               Zinc finger protein family-like.
Name=P0686H11.17;
Oryza sativa (japonica cultivar-group).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Ustilaginomycetidae, Ustilaginales, Ustilaginaceae, Ustilago.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gramene, QG2899, ...

GG GO:0005634; C:nucleus; IEA.

GO; GO:0005634; C:nucleus; IEA.

GO; GO:00046872; F:ubiquitin ligase complex; IEA.

R GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.

R GO; GO:0008270; F:sinc ion binding; IEA.

R GO; GO:0016570; F:protein ubiquitination; IEA.

R InterPro; IPR011841; Znf RING.

R InterPro; IPR010841; Znf RING.

R SWART; SW00184; RING; 1.

R SWART; SW00744; RING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 49; DB 2; Length 167;
Pred. No. 57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSTITE: PESSONS, TERMS 2; 1.
Metal-binding; Nuclear protein; Zinc; Zinc-finger.
SEQUENCE 167 AA; 17664 MW; 4729ACE00A901AE9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ion (By similarity).
SIMILARITY: Contains 1 RING-type zinc finger.
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1D Q4PEIS USTWA

AC Q4PEIS USTWA

TO 19-JUL-2005, integrated into UniProtKB/TrEMBL.

DT 19-JUL-2005, sequence version 1.

DT 19-JUL-2006, entry version 3.

DT 07-FEB-2006, entry version 3.

DT 07-FEB-2006, entry version 3.

DT 07-FEB-2006, entry version 3.

DE Wpotherical protein.

GN ORPHARMS=UM01475.1;

OC Bukaryota; Bungi, Basidiomycota; Ustilaginomyce C Ustilaginomyceridae; Ustilaginomyce OC Ustilaginomyceridae; Ustilaginales; Ustilaginomyce OC Ustilaginomyceridae; Ustilaginales; Ustilaginac OX NCBL TaxID=237631;

RN (1)

RP NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=521;

RA Ait-Zahra M., Allen N., Allen T., An P., Anders RA Atachchi H.M., Armbruster J., Bachantsang P., B A B Arachchi H.M., Armbruster J., Bachantsang P., B B B Bayul T., Blitshsteyn B., Bloom T., Blye J., Bo
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19-JUL-2005, sequence version 1.
07-FEB-2006, entry version 3.
Hypothetical protein.
                                                                                                                                                               Uni Prot KB/TrEMBL.
                                                                                                         167 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AP004762; BAD10011.1; -; Genomic_DNA.
                                                                                                              PRT;
                                                                                                                                                            05-JUL-2004, integrated into UniF
05-JUL-2004, sequence version 1.
07-FEB-2006, entry version 14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92.5%;
                                                                                                         QEZBT9 ORYSA PRELIMINARY;
Q6Z8T9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 92.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56 AAIAAAAAAAA 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                 Ehrhartoideae;
                                                                                      ORYSA
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neurospora crassa.
Bukaryota; Fungl; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordarlaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=74-0R23-1A / FGSC 987;
MEDLINE=22598136; PubMed=12712197; DOI=10.1038/nature01554;
                                                                  Length 361;
                                                                                                                      0; Indels
Hypothetical protein.
SEGUENCE 361 AA; 39615 MW; 038F774408202041 CRC64;
                                                                     Score 49; DB 2;
Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                              15-DEC-2003, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
                                                                                                                                                                                                                                                                                                                                                  368 AA
                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                             Q7SBK2_NEUCR PRELIMINARY; PRT;
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Mayer K.F.X., Schueller C., Wanbutt R., Murphy G., Volckaert G., Poll T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N., Haris B., Ansorge W., Brandt P., Grivell L.A., Rieger M., Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M., Meicheslgattner M., de Simone V., Obermaier B., Mache R., Mueller M., Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T., Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I., A. Os P., Hoheisel J., Zimmermann W., Wedler H., Ridley P., Langham S.-A., McCullagh B., Bilham L., Robben J., Vandenbussche F., Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F., A. Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E., Meitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M., Heitzenegger T., Bothe G., Ramsperger U., Hauf J., Koetter P., Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P., Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H., De Reyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R., Van Montagu M., Rogers J., Cronin A., Quail M.A., Bray-Allen S., A., Nettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S., Mayes R.,
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Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         097003; 098CW3;
01-DEC-2000, integrated into UniProtKB/Swiss-Prot.
01-MAY-2000, sequence version 1.
07-MAR-2006, entry version 37.
Heat shock factor protein 7 (HSF 7) (Heat shock transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear Cress).
Makaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; eudicotyledons; core eudicotyledons; cosids; eurosids II; Brassicales; Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                 Nature 422:859-868(2003).
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBU whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92.5%; Score 49; DB 2; Length 368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=HSF7; OrderedLocusNames=At4g11660; ORFNames=T5C23.90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AABX01000166; EAA33794.1; -; Genomic DNA.
SEQUENCE 368 AA; 35691 MW; 7AB0P69255969DD2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=cv. Columbia;
MEDLINE=20083488; PubMed=10617198; DOI=10.1038/47134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Pred. No. 1.1e+02; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            377 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         255 AMAAAAAAAAA 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 AMAAAAAAAA 13
                                                                                                                                                                                                                                                                                                                                         preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HSTF 7).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Bookeve D., Blocches H., Stanses A.C. Scinsfer M., Wallier-Auer S., R. Dones S. de Haan W., Mantres A.C. Scinsfer M., Wallier-Auer S., R. Massense O. Ouişley F., Clabaid G., Wendlein A., Febber R., A. Gabel G., Fronton S., Asylriou A., Vitale D., Lidgoorj R., Pitrandi B. B. Added S. M. Mantres S., Asylriou A., Vitale D., Lidgoorj R., Pitrandi B. B. Miller R., Schmidt W., Lecharity A., Aubourg S., Achief F., Schmidt W., Lecharity A., Aubourg S., Achief F., Schmidt W., Lecharity A., Aubourg S., Miller R., Schmidt W., Lecharity A., Aubourg S., Miller R., Schmidt W., Lecharity A., Aubourg S., Frishen D., Schwidt W., Lecharity A., Aubourg S., Miller R., Schmidt W., Lecharity A., Aubourg S., Miller R., Schmidt W., Mees H., Stocker S., Scholer P., Scholer P., Miller R., Scholer P., Miller R., Good D., Schulz S., Scholer P., Miller R., Good D., Schulz S., Miller R., M., Scholer P., Miller R., M., Scholer P., Scholer P., Miller R., M., Scholer P., Scholer P., Miller R., M., Scholer P., Scholer P., Scholer P., Scholer P., Miller R., M., Scholer P., Scholer
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395 AA

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RECOURTED STATEMENT OF THE STATE OF THE STATEMENT OF THE 
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                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92.5%; Score 49; DB 2; Length 395
92.3%; Pred. No. 1.1e+02;
tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF03171; 2GG-FeII Oxy; I.
Hypothetical protein; Iron; Oxidoreductase.
SEQUENCE 395 AA; 44410 MW; 4CE25B4FB5B04DEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; BC052076; AAH52076.1; -; mRNA.
Ensembl; BNSWUSG0000042656; Mus musculus.
MGI: MGI:2144489; AW050020.
GO; GO:0005506; F:irron ion binding; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
InterPro; IPR06513; 20G-FeII_Oase.
Pf-an. PF03171; 20G-FeII Oxy: 1.
                                                                               01-JUN-2003, integrated into UniProtKB/TrEMBL
                 PRT;
                                                                                                                 sequence version 1. entry version 20.
                                                                                                                                                                                                                                                                                                                                                  Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6; TISSUE=Mouse;
                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                 01-JUN-2003, sequence versi
07-FEB-2006, entry version
Hypothetical protein Ofoxd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AAMAAAAAAAA 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 92.3
Matches 12, Conservative
                                                                                                                                                                                                                                                        Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QBBKC1_MOUSE
QBBKC1;
                 Q80US0 MOUSE
Q80US0;
                                                                                                                                                                                                                             Name=Ofoxd;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
QBBKC1_MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BHHHAD
                        DDT THE BOOK SOCIOUS SEED THE 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                           PROSITE; PS00434; HSF_DOMAIN; 1.
Activator; DNA-binding; Heat shock; Nuclear protein; Phosphorylation; Transcription; Transcription regulation.
Transcription; Transcription regulation.
1 377 Heat shock factor protein 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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0
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0
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Pred. No. 1.1e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 49; DB 1; Length 377;
Pred. No. 1.1e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                            regulation.
Heat shock factor protein 7.
/FIIG=PRO 0000124588.
By similarity.
Poly-Gly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Poly-Gly.
Poly-Ala.
Poly-Ala.
G -> K in Ref. 3).
W, FDID5E595B7FC584 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  378 AA; 42533 MW; 1E7E5C741ACF6BA6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ensembl; ENSG0000091542; Homo sapiens.
GO; GO:0005506; F:iron ion binding; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
InterPro; IRF005123; 20G-FeII Oase.
Ffam; PF03171; 20G-FeII Oxy; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000, integrated into UniProtKB/TrEMBL. 01-OCT-2000, sequence version 1. 07-FBB-2006, entry version 18. Hypothetical protein FLJ20308. Home sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 378 AA
                        TAIR; At4g11660; ...
InterPro; IPR002341; HSF_BNA_bd.
InterPro; IPR002341; HSF_ETS_BNA_bd.
InterPro; IPR011991; Wing_hlx_Bn.
Pfam; PF00447; HSF_DNA-bind; I.
PRINTS; PR00056; HSFDOMAIN.
ProDom; PD001788; HSF_BNA_bind; I.
SWART; SM00415; HSF_INA_bind; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AK000315; BAA91078.1; -; mRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 151 BY
14 21 PO
32 50 PO
155 171 PO
202 207 PO
50 50 G
377 AA; 39705 MV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92.5%; S
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9NXD6_HUMAN PRELIMINARY;
Q9NXD6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 92.5
Best Local Similarity 92.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               155 AMAAAAAAAAA 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 AMAAAAAAAA 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   al Similarity
12; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
GeneFarm; 4072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA BIND
COMPBIAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEOUENCE
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Best Local
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Matches

RESULT 7

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8

01-MAR-2003, integrated into UniProtKB/TrEMBL. 01-MAR-2003, sequence version 1. 07-FEB-2006, entry version 22. 0 day neonate eyeball cDNA, RIKEN full-length enriched library, 395 AA.

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Gaps

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Length 395;

ω RESULT

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RC STRAIN-657BL/60; TISSUE-Egg, and Eyeball;
RUBDEGG=1614072; DOI-10.126/Geience.1112014;
RA STRAIN-657BL/60; TISSUE-Egg, and Eyeball;
RA Bajic V. B., Ravasal T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V. B., Brenner S. B., Batalov S., Forrest A. R., Zavolan M.,
RA Bajic V. B., Brenner S. B., Addinis V., Allen J. E.,
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Nortagui-Tabar S., Mishikawa S., Nori F., Ohara O.,
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Namanishi H., van Niwegen E., Werardo R., Wei C.L., Yagi K.,
Wannishestedt C., Mattick J.S., Hume D.A., Kai C.L., Yagi K.,
Mathestedt C., Mattick J.S., Hume D.A., Kai C., Saski D., Tonkan J.,
Havshieredt C., Sekiguchi K., Suzuki H., Nakaniaki Y.,
Ramaniaki H., Waki K.,
clone:E130207K11 product:hypothetical Alanine-rich region/Type I antifreeze protein/20G-Fe(II) oxygenase superfamily containing protein, full insert sequence (2 cells egg cDNA, RIKEN full-length enriched library, clone:B020011005 product:Hypothetical alanine-rich region/type I antifreeze protein/20G-Fe, full insert sequence) (Novel
                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6J; TISSUE=Egg, and Eyeball;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
High-efficiency full-length cDNA cloning.";
Methods Enzymol. 303:19-44(1999).
                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
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PubMed=16141073; DOI=10.1126/science.1112009;
                                                                                                                                            Name=AW050020; ORFNames=RP23-331121.1-001;
                                                                                                                                                                                                                                           Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                       musculus (Mouse).
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STRAIN=C57BL/6J; TISSUE=Egg, and Eyeball;

NUCLEOTIDE SEQUENCE.

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RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

RA Nikaido II., Osato N., Saitor R., Suzuki H., Yamanaka I., Kiyosawa H.,

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Rayasaki A., Hashizume W., Imotani W., Shibata R., Shibata R.,

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Saniraki R., Sakai K., Sakai W., Shibata R., Shibata R.,

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Saniraki R., Shibata R., Shibata R.,

Saniraki R., Shibata R.,

Saniraki R., Shibata R., Shibata R.,

Saniraki R., Shibata R.,

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"Analysis of the mouse transcriptome based on functional annotation of
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MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
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MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
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MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           full-length cDNAB.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 420:563-573(2002).
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NCBI_TaxID=10090;
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                                                                                             Adachi J., Alzawa K., Akinura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayastu N., Hiranoto K., Hiraoka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murala M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saitoh H., Sakai K., Sakai K., Sakazume N., Sano H., Sakai C., Sakai K., Sakazume N., Sano H., Tagawa A., Takahashi F., Takawu A., Shiraki T., Sogabe Y., Tagami M., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y., Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6J; TISSUE=Egg;
Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
Hori F., Iida J., Immunta K., Imotani K., Icoh M., Kanagawa S.,
Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
Muramatsu M., Hayashizaki Y.;
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11-0CT-2005, sequence version 1.
11-0CT-2006, entry version 6.
In vitro fertilized eggs CDNA, RIKEN full-length enriched library, clone:7420402E17, product:Hypothetical alanine-rich region/type I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
 Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer."; Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
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Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0015506; F:1ron ion binding; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
InterPro; IPR005123; 20G-FeII Oase.
Pfam; PF03171; 20G-FeII Oxy; I.
Hypochetical protein; Iron; Oxidoreductase.
SEQUENCE 395 AA; 44411 MW; 2822BF4BFFFEETFF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antifreeze protein/20G-Fe, full insert sequence.
Name=AW050020;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92.5%; Score 49; DB 2; I 92.3%; Pred. No. 1.1e+02;
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Q3TSG4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AKO53695; BAC35478.1; -; mRNA.
EMBL; AK163294; BAE37281.1; -; mRNA.
EMBL; AL566386; CA135332.1; -; Genomic DNA.
ENSEMbl; RNSWUSGO000042650; Mus musculus.
MGI; MGI:2144489; AW050020
GO; GO:0005506; F:iron ion binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                     STRAIN=C57BL/6J; TISSUE=Eyeball;
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hes 12; Conserv
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REAL STATEMENTS. TESTINGENER, WITTON CENTILIZED 6999; MUCLEOTIDE SEQUENCE.

REAL STATEMENTS. TESTINGENER, TO SEGUENCE 110016/80076-6879(99)00004-9; REALINGES. PRICE OF THE SEGUENCE.

REALINGES. PRICE TESTINGENER, THE SEGUENCE 1110014; PRICE MACKEDING 9990.

REALINGES. PRICE TESTINGENER, THE SEGUENCE 1110014; PRICE MACKEDING 9990.

REALINGES. PRICE THE SEGUENCE.

REALINGES. PRICE
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Maglott D. R. Waltels L. Marchinni L. Wergaris L. Will H. Wasabhian T. Numata A. Kucchinni L. Wergaris L. Will H. Wasabhian T. Numata A. Wordthorn L. Wergaris L. Will H. Wasabhian T. Numata K. Oldo T. Reid J. Na Rang B. J. Rangabla M., Rasabhian T. Numata K. Waltels J. Pontius J.U. Qi D. Rangchandran S. Ba Recrowley W. Pillas II. S. Pontius J.U. Qi D. Rangchandran S. Bandbain K. J. Rangabla R. J. Pallas R. Sandbain R. J. Pallas R. J. Marchinni R. J. Rangabla R. J. Rangabla R. J. Pallas R. J. Marchina R. J. Marchina R. J. Rangabla R. J. Rangabla R. J. Magan I. J. Rangabla R. J. Rangabla R. J. Rangabla R. J. Haydah R. J. Rangabla R. J. Rangabla R. J. Haydah R. J. Rangabla R. J. Rangabla R. J. Haydah R. J. Rangabla R. J. Rangabla R. J. Haydah R. J. Rangabla R. J. Rangabla R. J. Haydah R. J. Rangabla R. J. Rangabla R. J. Haydah R. J. Rangabla R. J. Rangabla R. J. Haydah R. J. Rangabla R. J. Rangabla R. J. Haydah R. J. Rangabla R. J. Rangabla R. J. Haydah R. J. Rangabla R. J. Rangabla R. J. Haydah R. J. Rangabla R. J. Rangabla R. J. Haydah R. J. Rangabla R. J.
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RESTANDENTIAL SEQUENCE.

RESTAIN-CSTBL/67; TISSUBE-Eyeball;

RA Carninci P., Kasukwa T., Katayama S., Gough J., Frith M.C., Maeda N., Ravasi T., Katayama S., Gough J., Frith M.C., Maeda N., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Rayasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Rabajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Ra Manbesi-Impiombato A., Apweiler R., Alten J.E., Baisel K.W., Bersano T., Bono H., Chalk A.M., RA Bansal M., Baxter L., Baisel K.W., Bersano T., Bono H., Chalk A.M., Crowe M.L., Dalla E., Dallar E., Dalla Gatta G., Adinis V., Christoffels A., Clutterbuck D.R., A., Crowe M.L., Dalla E., Dallar Cowe M.L., Dalla B., Churopels B.P., de Bono B., Della Gatta G., RA Growe M.L., Dallar B., Dallarymple B.P., Gobori T., Green R.E., Repetcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M., Ranapin A., Katoon M., Ikeo K., Iwama A., Ishikawa T., Rutano H., Kollias G., Krishnan S.P., Lipovich L., Liu J., A., Katoon M., Kanapin A., Katoon M., Rawaswa Y., Kelso J., Kitamura H., Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J., R., Kurochkin I.V., Lareau Babu M., Madera M., Marchian L., Matsuzawa S., Madan Babu M., Madera M., Marchian L., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.A. Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
                                                                               Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C57BL/6J; TISSUB=Eyeball; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninol P., Hayashlaski Y.; Hayashlaski Y.; Hidd-efficiency Full-length cDNA cloning."; Methods Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                              Gaps
Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
Muramatsu M., Hayashizaki Y.;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2003, sequence version 1.
07-MAR-2006, entry version 24.
0 day neonate eyeball cDNA, RIKEN full-length enriched library, clone:E130210021 product:hypothetical Alanine-rich region/Type antifreeze protein/20G-Fe(II) oxygenase superfamily containing protein, full insert sequence.
Name=AW050020;
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                                                                                                                                                                                                                                                                                                                                92.5%; Score 49; DB 2; Length 395; 92.3%; Pred. No. 1.1e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                      EMBL; AK162072; BAE36711.1; -; mRNA.
MGI; MGI:2144489; AW050020.
GO; GO:0005506; F:iron ion binding; IEA.
GO; GO:0016491; F:oxidoreductage activity; IEA.
InterPro; IPR05123; 20G-FeII Qase.
Pfam; PF03171; 20G-FeII_Oxy; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2003, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     395 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                      1 AAMAAAAAAAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                             36 AAVAAAAAAAA 48
                                                                                                                                                                                                                                                                                                                                                                              12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE
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NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qebkb9 Mouse
Qebkb9;
                                                                                                                                                                                                                                                                    Hypothetical
SEQUENCE 39
                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOUSE
                                                                                                                                                                                                                                                                                                                                                                              Matches
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Distributed under the Creative Commons Attribution-NoDerivs License
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STRAIN=C57BL/6J; TISSUE=Eyeball;

MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

A Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Asumino T., Intoh M., Nishine T., Harda A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikagami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watchiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Aokazaki Y., Miramatsu M., Inoue Y., Kitra A., Hayashizaki Y.;

RIKEN integrated sequence analysis (RISA) system.384-format

Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu N., Sugahara Y., Shibata K., Itoh M., Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Pukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hirancoto K., Hiraoka T., Hirozane T., Hayis K., Ishii Y., Itoh M., Kagawa I., Kaukawa T., Katoh H., Kawai J., Kojima Y., Itoh M., Kagawa I., Koda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Murata M., Nakamura M., Satoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases:
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Winshim Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                   Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
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Pred. No. 1.1e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C578L/6J; TISSUE=Eyeball;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
SEQUENCE 395 AA; 44415 MW; 6D22C26B1A99EDA8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AK053700; BAC35481.1; -; mRNA.
Ensembl; ENSMUSG0000042650; Mus musculus.
MGI; MGI:2144489; AW050020.
GO; GO:0005606; Firon ion binding; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
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STRAIN=C57BL/6J; TISSUE=Eyeball;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                               Nature 409:685-690(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00657; FORK HEAD 1; 1.
PROSITE; PS00657; FORK HEAD 2; 1.
PROSITE; PS00658; FORK HEAD 2; 1.
PROSITE; PS50039; FORK HEAD 3; 1.
DNA-binding; Nuclear protein; Transcription regulation.
CHAIN 1 428 Forkhead box protein B2.
                                                                                                                                                 MEDLINE=97014266; Pubmed=8861101; DOI=10.1016/0925-4773(96)00507-2; Kaestner K.H., Schuetz G., Monaghan A.P.; "Expression of the winged helix genes fkh-4 and fkh-5 defines domains
                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                         Kaestner K.H., Lee K.H., Schloendorff J., Hiemisch H., Monaghan A.P.,
                                                                                                                                                                                                                                                                                'Six members of the mouse forkhead gene family are developmentally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 49; DB 1; Length 428;
Pred. No. 1.2e+02;
.; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                           regulated.",
Proc. Natl. Acad. Sci. U.S.A. 90:7628-7631(1993).
-- SUBCELLULAR LOCATION: Nucleus.
-- DEVELODMENTAL STAGE: Expressed during embryogenesis.
-- SIMILARITY: Contains 1 fork-head DNA-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DESASEFDIE94AB10 CRC64;
          01-NOV-1997, integrated into UniProtKB/Swiss-Prot. 01-NOV-1997, sequence version 1. 07-FEB-2006, entry version 31. Forkhead box protein B2 (Transcription factor FKH-4). Name-Foxb2; Synonyms=FkH4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Forkhead box protein B2./FTId=PRO_000091805.
                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSFAC, T02442;
Ensembl; ENSMUSG00000056829; Mus musculus.
MGI; MGI:137468; Poxb2.
InterPro; IPR001766; TF Fork head.
InterPro; IPR011991; Wing hlx DNA bd.
Pfam; PF00220; Fork head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X92591; CAA63335.1; -; mRNA.
BRBL; X71942; CAA50744.1; -; Genomic_DNA.
PIR; D47746; D47746.
HSSP; Q63245; ZHDC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Poly-His.
Poly-His.
Poly-Pro.
Poly-Ala.
Poly-Ala.
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ProDom; PD000425; TF Fork head; 1.
SMART; SM00339; FH; 1.
                                                                                                                                                                                                                                              MEDLINE=93361500; PubMed=7689224;
                                                                                                                                                                                      in the central nervous system."; Mech. Dev. 55:221-230(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45170 MW;
                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE OF 4-114.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 92.3
nes 12; Conservative
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258
330
399
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153
162
172
                                                                   musculus (Mouse)
                                                                                                                                        NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         428 AA;
                                                                                                                 NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                      Schuetz G.;
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COMPBIAS
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COMPBIAS
SEQUENCE
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                                                                    Mus
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EWEL, ALSISSATY, CAH70683.1; -; Genomic_DNA.

REMEL, ALSISSATY, CAH70683.1; -; Genomic_DNA.

REMEL, ALSISSATY, CAH70683.1; -; Genomic_DNA.

REGO; GO:0005350; F:transcription factor activity; IEA.

RO; GO:0006355; P:transcription; IEA.

RO; GO:0006355; P:transcription; IEA.

RIGEPRO; IPR011991; Wing hlx_DNA_bd.

RIGEPRO; IPR011991; Wing hlx_DNA_bd.

REMER; PR00053; FORK_Head; 1.

RODOS; PR000425; TF Fork_head; 1.

RODOS; PR000425; FORK_HEAD 1; 1.

ROSITE; PS00655; FORK_HEAD 1; 1.

ROSITE; PS00656; FORK_HEAD 2; UNKNOWN_1.

ROSITE; PS00656; FORK_HEAD 2; UNKNOWN_1.

ROSITE; PS00659; FORK_HEAD 3; 1.

ROSITE; PS00659; FORK_HEAD 3; 1.
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                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haich F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-JUL-2004, integrated into UniProtKB/TrEMBL.
19-JUL-2004, sequence version 1.
19-JUL-2006, entry version 16.
SWI/SWF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1.
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92.3%; Pred. No. 1.2e+02;
ive 1; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                         Kimberley A.;
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
                                                   07-DEC-2004, integrated into UniProtKB/TrEMBL.
07-DEC-2004, sequence version 1.
07-EBB-2006, entry version 12.
OTTHUMP0000001510.
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PRT;
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Q6GLG1;
PRELIMINARY;
                                                                                                                                                                    ORFNames=RP11-159H20.4-001;
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221 AAVAAAAAAAAA 233
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Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                         [1]NUCLEOTIDE SEQUENCE.
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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Gaps

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1; Mismatches

Matches

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RESULT 13

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Query Match
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Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Hulyk S.W., Villalon D.K., Maclan A., Kodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.B., Schmutz J., Myers R.M., Schein J.B., Schmutz J., Myers R.M., Schein J.B., Schon J.B., Schart J.B., Schall J.B., Schein J.B., Sones S.J.M., Marra M.A., Schein J.B., Ones S.J.M., Marra M.A., Schein J.B., Ones S.J.M., Marra M.A.,
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R. L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Bueteow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S. I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Caranici P., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; BC074534; AAH74534.1; -; mRNA.
Ensembl; ENSXETG0000021355; Xenopus tropicalis.
GO; GO:0003577; F:DNA binding; LEA.
GO; GO:0005355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR00910; HMG 12_box.
Pfam; PF00555; HMG box; I.
SMART; SM00398; HMG; 1.
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92.5%; Score 49; DB 2; Length 435; 92.3%; Pred. No. 1.2e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Klein S., Gerhard D.S.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50118; HMG BOX 2; 1.
SEQUENCE 435 AA; 48441 MW; 6F227A5D387A9CA2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         458 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            318 AAVAAAAAAAA 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and mouse cDNA sequences."
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Matches 12, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QEPEC2_HUMAN
QEPEC2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=OFOXD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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OG PT OG 
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Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Erezyilmaz D.F., Riddiford L.M., Truman J.W.; "An ancestral role for a metamorphosis-determining factor in a direct-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92.5%; Score 49; DB 2; Length 458; 92.3%; Pred. No. 1.3e+02; ive 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                   Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, BC062339, AAH62339.1; -; mRNA.
Ensembl, ENSG0000091542; Home sapiens.
GO; GO:0005569; F:iron ion binding; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
InterPro; IPR053123; 20G-FeII Oase.
Pfam; PF03111; 20G-FeII Coxy; I.
Hypothetical protein; Iron; Oxidoreductase.
SEQUENCE 458 AA; 51409 MW; 88ACCDA9992B5AEB CRC64;
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G0; G0:0005634; C:nucleus; IEA.
G0; G0:0005576; F:nucleic acid binding; IEA.
G0; G0:0005515; F:protein binding; IEA.
G0; G0:0008270; F:zinc ion binding; IEA.
InterPro; IPR000210; BTB.
InterPro; IPR013069; BTB.PDZ.
InterPro; IPR013069; BTB.PDZ.
InterPro; IPR013069; BTB.PDZ.
INTERPRO; IPR017087; Znf.C2H2.
PFam; PF00651; BTB; 1.
SMART; SM00225; BTB; 1.
SMART; SM00225; ZnF.C2H2; 2.
SMART; SM00255; ZnF.C2H2; 2.
PROSITE; PS50097; BTB; 1.
PROSITE; PS500157; ZINC_FINGER_C2H2_2; 2.
Metal-binding; Nuclear protein; Zinc; Zinc-finger.
                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-OCT-2005, integrated into UniProtKB/TrEMBL 11-OCT-2005, sequence version 1. 21-FEB-2006, entry version 7. 10-OCT-2005 entry version 7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q3S2W8 ACHDO PRELIMINARY; PRT;
Q3S2W8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Acheta domesticus (House cricket).
                                                                                                                                                                                       mouse cDNA sequences."
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                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
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Matches 12; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBL_TaxID=6997;
                                                                                                                                                                                                                                                                                                                                                          NIH MGC Project;
                                                                                                                                                                                                                                                                                                                    TISSUE=Brain;
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COMPBIAS
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ZN_FING
ZN_FING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                             Gaps
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Human chromosome 1 international sequencing consortium;
Humar chromosome 1 international sequencing consortium;
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
                                                 Length 506;
                                                                                           Indels
  F4FCCA9BE6415EC0 CRC64;
                                                                                                                                                                                                                                                                                             ZBTBB HUMAN STANDARD; PRT; 512 AA. 080ABB; 05YREs; 26.ARE-2004, integrated into UniProtKB/Swiss-Prot. 01-0CT-2002, sequence version 1. 07-MAR-2006, entry version 25. Zinc finger and BTB domain-containing protein 8. Name=ZBTB8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i - SUBCELLULAR LOCATION: Nucleus (Potential).
-i - SIMILARITY: Contains 1 BTB (POZ) domain.
-i - SIMILARITY: Contains 2 C2H2-type zinc fingers.
                                              Score 49; DB 2; Ler
Pred. No. 1.4e+02;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
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    54175 MW;
                                              92.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nat. Genet. 36:40-45(2004)
                                                                                                                                                                                 218 AAVAAAAAAAA 230
                                                                                                                                       1 AAMAAAAAAAA 13
                                       Query Match
Best Local Similarity 92.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
  506 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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SEQUENCE
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Culicidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50097, BTB; 1.
PROSITE; PS50097, ZINC_FINGER_C2H2_1; 1.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 2.
DNA-binding; Metal-binding; Nuclear protein; Repeat; Transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transcription regulation, Zinc, Zinc-finger.
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BB970D200B60CC9F CRC64;
EMBL; AL356986; CAH73365.1; -; Genomic_DNA.
EMBL; AL033529; CAH73365.1; JOINED; Genomic_DNA.
EMBL; AL033529; CAT20022.1; -; Genomic_DNA.
EMBL; AL033629; CAI20022.1; JOINED; Genomic_DNA.
EMBL; AL0356986; CAI20022.1; JOINED; Genomic_DNA.
ENSembl; ENSG0000185718; Homo sapiens.
InterPro; IPR000210; BTB.
InterPro; IPR000210; BTB.
InterPro; IPR000210; BTB.
From PF00651; BTB.
From PF006525; BTB.
From PF00655; ZFCC2H2; INTERPROTORER FROM PF006035; ZFCCCH2; INTERPROTORER FR
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GO; GO:0003676; F:nucleat acid binding; IEA.
GO; GO:0000166; F:nucleatide binding; IEA.
InterPro; IPR012677; a_b_plait_nuc_bd.
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C2H2-type 2.
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341 363 C22
369 392 C21
132 153 PO.
512 AA; 55562 MW; I
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Q7PPSO;
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136 AAVAAAAAAAAA 148
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NCBI_TaxID=180454;
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Query Match
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Birren B.W., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,
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Ustilaginomycetidae, Ustilaginales, Ustilaginaceae, Ustilago.
                                                                                                                                                                 92.5%; Score 49; DB 2; Length 521; 92.3%; Pred. No. 1.4e+02; ive 1; Mismatches 0; Indels
                                                          Pfam; PF00076; RRM 1; 3.
SMART; SM00360; RRM; 3.
SMART; SM00361; RRM 1; 1.
TIGRFAMs; TTGR01645; half-pint; 1.
PROSITE; PS50102; RRM; 3.
SEQUENCE 521 AA; 55760 MW; 68A0C7DEA9FE24DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                         19-JUL-2005, integrated into UniProtKB/TrEMBL
InterPro; IPR006532; PolyU bd.
InterPro; IPR000504; RNP1 RNA bd.
InterPro; IPR003954; RRM 1.
PANTHER; PTR10432:SF141; PolyU half_pint; 2.
                                                                                                                                                                                                                                                                                                                                           529 AA.
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Q4P290;
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OFFEB-2006, entry version 4.
Hypothetical protein.
ORFNames=UM05773.1,
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                                                                                                                                                                                      Local Similarity 92.3
les 12; Conservative
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MEDLINE-20156006; Pubmed-10731132; DOI=10.1126/science.287.5461.2185; Addams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D., Adams M.D., Scherer S.E., Holf R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P. W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Prannkoch C., Baldwin D., Abril J.F., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Beson K.Y., Benos P.V., Berman B.P., Brandari D., Bolshakov S., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Abrils R.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Abolson R., Douley S., Dahlke C., Davenport L.B., Davies P., Abderry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Abderry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Abderry J.M., Evangelista C.C., Ferraz C., Ferriera S., Pleischmann W., Burbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Posler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
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                                                                                                                                                                                                                                                         Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
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in
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GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0003700; F:transcription of transcription, DNA-dependent; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR000679; Znf_GATA.
Pfam; PF00320; GATA; 1.
PROSITE; PS50114; GATA ZN_FINGER_2; 1.
Hypothetical protein.
SEQUENCE 529 AA; 53820 MW; D5ABC2C8EA96E06D CRC64;
                                "The genome sequence of Ustilago maydis.";
Submitted (FBE-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Canton-5; TISSUB-Embryo;
MEDLINE=97032935; PubMed=8878683;
Hart M.C., Wang L., Coulter D.E.;
"Comparison of the structure and expression of odd-skipped and
related genes that encode a new family of zinc finger proteins
Drosophila.";
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01-MAY-2000, sequence version 1.
07-MAR-2006, entry version 30.
Protein sister of odd and bowel.
Name=sob; ORFNames-CG3242;
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Prerygota; Nooptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 49; DB 2; Length 529;
Pred. No. 1.4e+02;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AACP01000212; EAK86012.1; -; Genomic_DNA.
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Zimmer A., Zody M., Lander E.S.;
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92.3%;
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Matches 12; Conservative
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dlodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
Houstin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Jalali M., Kalush F., Karpen G.H., Re Z., Kennison J.A., Ketchum K.A.,
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
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Liu X., Mattei B. McIntosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Raiazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Spier E., Siden Kiamos I., Simpson M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
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Williams S.M., Woodage T., Weinstock G.M., Wang S., Zhoo Q., Zhong X.,
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Zhu X., Smith H.O.,
Chence 287:2185-2195(2000).
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Johansen K.A., Green R.B., Iwaki D.D., Hernandez J.B., Lengyel J.A.;
The Drm-Bowl-Lin relief-of-repression hierarchy controls fore- and morphogenesis.";
Thindgut patterning and morphogenesis.";
Mech. Dev. 120:1139-1151(2003).

-!-FUNCTION: Pair-rule protein that determines both the size and during embryogenesis. DNA-binding transcription factor that acts during embryogenesis. DNA-binding transcription factor that acts primarily as a transcriptional repressor but can also function as a transcriptional activator, depending on the stage of development and spatial restrictions (By similarity). May function redundantly with odd and drm in leg joint formation during the larval stages, acting downstream of Nocch activation.

-!- SUBCELLULAR LOCATION: Nucleus (Probable).

-!- TISSUE SPECIFICITY: Has two temporally distinct modes of expression during early embryogenesis; expressed in a non-periodic domain at the blastcoderm stage. Also expressed in a non-periodic domain at the anterior of the embryo. During gastrulation, the seven primary stripes that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Berkeley; TISSUE=Embryo;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R.A., Gonzalez M., Glarin H., Kronmiller B., Li P.W., Liao G.,
Miranda A., Mungall C.J., Nunoo J., Pacleb J.M., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K.H., Yu C., Lewis S.E., Rubin G.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               systematic review.";
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ribsembl; CG1242; Drosophila melanogaster.

RelyBase; FBG0004892; sob.

GG; GG: 0005654; Cinucleus; ISS.

GG; GG: 0005654; Firanscriptional activator activity; ISS.

GG; GG: 0005654; Firanscriptional activator activity; ISS.

GG; GG: 0007569; Firanscriptional repressor activity; ISS.

GG; GG: 0007350; Firanscription activate; ISS.

GG; GG: 0007366; Firanscription of transcription from R. .; ISS.

Repressor IPRO070687; ZIC C2H2.

Repressor IPRO070687; ZIC C2H2.

Repressor IPRO07069; ZIC C2H2.

Repressor ZIC CANDER C2H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . .; ISS.
                                                                                                                                                                                                                                                                                                                                         Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
               each of the 14 segments in the extended germ band. Expression is relatively weak at the blastoderm stage, gaining in intensity at gastrulation. Expressed in the invaginating stomedeum and proctcodeum of the embryonic gut. By stage 13, expressed in the region that will form the proventriculus and in a wide ring at the most posterior portion of the midgut. Expression continues in the gut through the remainder of embryogenesis. Expressed in the proximal Malphighian tubules, brain and pharyngeal muscles during late embryogenesis. Expressed weakly in a segmentally repeated pattern in the leg disk at the distal edge of each presumptive leg segment except in tarsal segments 1 to 4.

SIMILARITY: Contains 5 C2H2-type zinc fingers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Metal-binding; Nuclear procein; Pair-rule protein; Repeat; Repressor;
Transcription; Transcription regulation; Zinc; Zinc-finger.
CHAIN 1 578 Protein sister of odd and bowel.
FFTId=PRO 0000046928.
ZN_FING 395 417 C2H2-type-1.
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                                                                                                                                                                                                                                                                                                                                                                  Distributed under the Creative Commons Attribution-NoDerivs License
in alternate segments. This results in the labelling
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Pred. No. 1.56+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0F600954CFA7D8D0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SS -> G (in Ref. 1)
P -> L (in Ref. 1)
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01-0CT-2002, sequence version 2.
1-FEB-2006, entry version 39.
CG32105-PB (RE70810p).
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                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE003579; AAF51087.1; -; Genomic_DNA.
EMBL; BT002205; AAC24960.1; -; mRNA.
PIR; S72227; S72227.
HSSP; P07248; ZADR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C2H2-type 2.
C2H2-type 3.
C2H2-type 4.
C2H2-type 5.
Ala-rich.
Ser-rich.
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                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U62004; AAC47282.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58455 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             274 AAVAAAAAAAA 286
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COMPBIAS
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STRAIN=Berkeley;
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Q9NVRO;
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                                                                       Lewis S.E.
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                                                                                                                 MEDINE-ZOIDE SEQUENCE.

RAM NUCLECTIDE SEQUENCE.

RAM Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

Randon R.C., Rogers Y.-H.C., Blazej R.G., Change M., Pichifer B.D.,

RAM R.H., Doyle C., Baxter E.G., Helt G., Nalson C.R., Miklos G.L.G.,

RA Beeson K.Y., Baros P.V., Berman B.P., Bhandari D., Belahakov S.,

Rokova D., Bocchan M.R., Buxellal J., Baytaktaroll. Belahakov S.,

RAM C.C., Busam D.A., Butler H., Cadieu E., Center A., Chadra I.,

RAM C.C., Busam D.A., Dahlke C., Davenport L.B., Davies P., Andonon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RAM C., Bushellist C.C., Ferraz C., Ferriar S., Pleistchmann W.,

RAM C., Cabrielian A.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

RAM Godon K., Mouse M., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,

RAM Goder R., Gong F., Gorrell J.H., Gu Z., Kennison J.A., Ketchu K.A.,

RAM C., Ralush F., Karpen G.H., Ke.Z., Kennison J.A., Ketchu K.A.,

Liu X., Matteria B., Karlen C.D., Kraff C., Kravitz S., Kulp D., Lai Z.,

Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,

Reland S., Moy M., Murphy B., Murphy L., Murshy L., Murshy C., Morris J., Mosheefi A.,

Relanct S.M., Moy M., Murphy B., Nurshern D.R., Pacleb J.M.,

Ranct S., Siden-Kiamos II. Simpson M., Strong R., Shen H.,

Shen B.C., Siden-Kamos II. Simpson M., Strong S., Yao, O.A.,

Ray Shreka R., Tector C., Truner R., Venter E., Wang X.,

Wang Z.-Y. Wassarman D.A., Weinsteck M., Weissenbed J.,

Wang Z.-Y. Wassarman D.A., Weinsteck M., Weissenbed J.,

Ray Hilliams S.M., Woodey T., Worley K.C., Wu D., Yang S., Zhon Y.,

Ray C., Shork S., Shork S.M., Wooley S., Shork W., Weinsteck S., Shork W.,

Ray Shreka R., Zhong F.W., Shork W
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MEDLINE=22436065; PubMed=12537568;
Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Patel B. J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Weinskas R., Tabor P.E., Wan K., Stapleron M., Sutton G.G., Venter C., Weinstrock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; Finishing a whole-genome shotgun: release 3 of the Drosophila melanogaster euchromatic genome sequence.;
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E
ORFNames=CG12105, Dmel CG32105;
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Haxapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome Biol. 3: RESEARCH0084.1-RESEARCH0084.20(2002).
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Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P., Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stapleton M., Carlson J., Chavez C., Frise E., George R., Pacleb J., Park S., Wan K., Yu C., Celniker S.; Submitted (Aug-2005) to the EMBL/Genbank/DDBJ databases.
-: SUBCELLULAR LOCATION: Nuclear (By similarity).
-: SIMILARITY: Contains 2 LIM zinc-binding domains.
                                                                                                                                                                                                                                                                                                                 Berkeley Drosophila Genome Project;
Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
Yu C., Rubin G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                    'Annotation of the Drosophila melanogaster euchromatic genome:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92.5%; Score 49; DB 2; Length 640; 92.3%; Pred. No. 1.6e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00478; LIM_DOWAIN_1; 2.
PROSITE; PS00428; LIM_DOWAIN_2; 2.
PROSITE; PS01359; ZF_PHD_1; ÜNKNOWN_1.
DNA-binding; Developmental protein; Homeobox; LIM domain; Metal-binding; Nuclear protein; Transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JAN-2006) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Drosophila melanogaster release 4 sequence.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
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640 AA; 67760 MW; AIAI0F826018C98E CRC64;
                                                                                                                                                                                                             systematic review.";
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002)
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EMBL; BT003467; AAO39470.1; -; mRNA.
HSSP; P50480; 1BW5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Flyase; FBGD052105; CG32105.

GO; GO:0005515; F:protein binding; IPI.

InterPro; IPR011356; Homeobox.

InterPro; IPR012287; Homeodomain-rel.

InterPro; IPR007107; LIM homeo.

InterPro; IPR001781; LIM Zn bd.

InterPro; IPR001965; Znf-PHD.

Pfam; PF00465; Homeobox; 1.
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Best Local Similarity 92.3
Matches 12; Conservative
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SMART; SM00132; LIM; 2.
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Pubbed-14702039; DOI=10.1038/ng1285;

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Non H., Yada T., Nakamura N., Ohara O., Isogai T., Sugano S.,

Nakai W., Yada T., Nakamura N., Ohara O., Isogai T., Sugano S.,

Non H., Sano B., None R., Hata H., Watanabe H., Nakai W., Yada T., Nakamura N., Ohara O., Isogai T., Sugano S.,

Nakai W., Yada T., Nakamura N., Ohara O., Isog
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A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Mang J., Heish F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
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Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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01-OCT-2000, integrated into UniProtKB/TrEMBL.
01-OCT-2000, sequence version 1.
07-MAR-2006, entry version 27.
Hypothetical protein FLJ10572 (Kelch-like 11).
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                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                           Name=KLHL11;
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NUCLEOTIDE SEQUENCE.

TISSUE=Testis

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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentía; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carnino: P., Hayashizaki Y.;
"High-efficiency full-lengh cDNA cloning.";
Methods Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11brary, clone:B230201M16 product:Mi-2 autoantigen 240 kDa protein homolog (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adult male corpora quadrigemina cDNA, RIKEN full-length enriched
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                                                                                                                                                                                                                                                                                                                                                                                                                                 92.5%; Score 49; DB 2; Length 708; 92.3%; Pred. No. 1.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                     708 AA; 80148 MW; 38733CE875172E12 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                       Ensembl; ENSG00000178502; Homo sapiens. HGNC; HGNC:19008; KLHL11. GO; GO:0005515; F:protein binding; IEA. InterPro; IPR011705; BACK. InterPro; IPR010210; BTB. InterPro; IPR013069; BTB. POZ.
                                                                 EMBL; AK001434; BAA91689.1; -; mRNA.
EMBL; BC034470; AAH34470.1; -; mRNA.
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07-FEB-2006, entry version 21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                              Pfam; PF01344; Kelch 1; 3.
SMART; SM00225; BTB; 1.
PROSITE; PS50097; BTB; 1.
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4 AAVAAAAAAAA 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 92.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                    Pfam; PF07707; BACK; 1.
Pfam; PF00651; BTB; 1.
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Motteadd H., Wastensans S., Wikk H., Wikkonor F., Wakwuchil H., Wo P., Wortead H., Wastensans S., Wikking S., Watting S., Watt

Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License ANCLIDED SQUENCE.
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Ensembl; ENSMUGG0000018474; Mus musculus.

Ensembl; ENSMUGG0000018474; Mus musculus.

MGI; MGI:1344395; Chd3.

GO; GO:0016581; C:hurb complex; IDA.

GO; GO:0016581; C:hurb complex; IDA.

GO; GO:0005315; F:protein binding; IPI.

GO; GO:0005313; P:chromatin assembly or disassembly; IDA.

InterPro; IPR010953; Chromo. EMBL; AK045449; BAC32375.1; -; mRNA. InterPro; IPR001965; Znf\_PHD. Pfam; PF08073; CHDNT; 1. Pfam; PF00385; Chromo; 1. Pfam; PF00628; PHD; 2. SMART; SM00298; CHROMO; 2. SMART; SM00249; PHD; 2. Nature 409:685-690(2001). NUCLEOTIDE SEQUENCE. NUCLEOTIDE SEQUENCE. NUCLEOTIDE SEQUENCE Q14839; 1MM2 HSSP; 

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2003, integrated into UniProtKB/TrEMBL.
01-MAR-2003, sequence version 1.
07-FEB-2006, entry version 20.
10 days neonate skin cDNA, RIKEN full-length enriched library,
clone:4732491L07 product:hypothetical BTB/POZ domain|Kelch repeat|Type
1 antifreeze|Alanine-rich region containing protein, full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/67; TISSUE=Skin;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                        Length 708;
                                                                                                                                                                                                  Score 49; DB 2; Lengtn /v. Pred. No. 1.88+02;
                                                                                                                                                                      708 AA; 80411 MW; A9CE144CE3310CBB CRC64;
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PubMed=16141072; DOI=10.1126/science.1112014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Methods Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                709 AA.
                                                                                                                                                                                                                                                                                                         1; Mismatches
PS00598; CHROMO 1; UNKNOWN 1.
PSS0013; CHROMO 2; 2.
PSS0016; ZF_PHD 2; 2.
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Best Local Similarity
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                                                                                                           Nuclear protein.
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Qecess;
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Pubmed=15496914; DOI=10.1038/nature03025;

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A Mauceli E., Bouneau L., Fischer C., Ozouf-Cozlaz C., Bernot A.,

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"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
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                        19-JUL-2005, sequence version 1.
07-MAR-2006, entry version 8.
Chromosome 16 SCAF14537, whole genome shotgun sequence. (Fragment)
ORFNames-GSTENG00014837001;
                                                                                                                               Tetraodon nigroviridis (Green puffer).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Crinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetraodontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           preliminary data.
-!- FUNCTION: Binds calmodulin in a calcium dependent manner. Mafunction as scaffolding or signaling protein (By similarity)
-!- SUBCELLULAR LOCATION: Cytoplasmic and membrane-bound (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genoscope; Whitehead Institute Centre for Genome Research; Submitted (FBS-2004) to the EMBL/GenBank/DDB databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBU whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        805 AA; 87779 MW; FEC67F3387228E7F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92.5%; Score 49; DB 2; Le
100.0%; Pred. No. 1.9e+02;
ive 0; Mismatches 0;
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InterPro; IPR001680; WD40.
Pfam; PF00400; WD40; 6.
PRINTS; PR00320; GPRCTEINBRPT.
ProDom; PD000018; WD40; 3.
SMART; SM00320; WD40; 5.
19-JUL-2005, integrated into UniProtKB/TrEMBL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the early vertebrate proto-karyotype.";
Nature 431:946-957(2004).
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PROSITE; PS50082; WD REPEATS 2; 4.
PROSITE; PS50294; WD REPEATS REGION; 1.
Calmodulin-binding; WD repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adachi J. Alzawa K., Akimura T., Arakawa T., Bono H., Carninci P., Adachi J., Alzawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kaukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Sanato M., Sano H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yawunishi A., Muramatsu M., Hayashizaki Y.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                            STRAIN=C57BL/6J; TISSUB=Skin;
MEDLINE=20499374; Dubmed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Wnormalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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                                                                                                                                                                                                                                                                                                                                          MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibata K., Ttoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata Y., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
        'Functional annotation of a full-length mouse cDNA collection.";
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709 Aa; 80429 MW; BA3DB8D4CA6FEB7A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ensembl; ENSMUSCONOCOSSI; Mus musculus.
MGI; MGI:2388648; Klhl11.
GO; GO:0005151; F:protein binding; IEA.
InterPro; IPRO11705; BACK.
InterPro; IPRO13069; BTB.
InterPro; IPRO13069; BTB.
Fam; PFO7707; BACK; 1.
Pfam; PFO0651; BTB; 1.
Pfam; PFO0651; BTB; 1.
Pfam; PFO0651; BTB; 1.
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PROSITE; PS50097; BTB; 1.
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nes 12; Conservative
                                     Nature 409:685-690(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
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                                                                                         NUCLEOTIDE SEQUENCE
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Gaps

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0

19-SEP-2002, integrated into UniProtKB/Swiss-Prot.

01-MAY-2000, sequence version 1. 21-FEB-2006, entry version 39.

805 AA.

PRT;

Q4SPHO\_TETNG PRELIMINARY; Q4SPHO;

TETNG

RESULT 25 Q4SPH0 ID Q4 AC Q4

Matches

8 g

Length 805; Indels

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Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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AC Q3U
DT 11-
DT 11-
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RX Adams M.D., Celniker S. E., Holt R.A., Evans C.A., Gocayne J.D.,

Adams M.D., Celniker S. E., Holt R.A., Evans C.A., Gocayne J.D.,

Adams M.D., Celniker S. E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S. E., Holt R.A., Evans C.A., Gocayne J.D.,

B. George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

Brandon R.C., Rogers Y.-H.C., Blazel, R.G., Champe M., Pfeiffer B.D.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

Ballew R.M., Banns P.V., Berman B.P., Bandari D., Bolharkov S.,

Borkova D., Botchen M.R., Bouck J., Broketein P., Brothier P.,

RA Borkova D., Botchen M.R., Bouck J., Broketein P., Brothier P.,

RA Borkova D., Botcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

A Borkova D., Botcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

A Borkova D., Botcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Bordon K., Doup L.E., Downes M., Dugan-Rocha S., Pleischman W.,

RA Bordon K., Doup L.E., Downes M., Dugan-Rocha S., Pleischman W.,

RA Bordon K., Doup L.E., Downes M., Dugan-Rocha S., Pleischman W.,

RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,

A Jalai M., Kalush F., Katpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Ajalai M., Kalush F., Katpen G.H., Ke Z., Kannison J.A., Ketchum K.A.,

Ajalai M., Kalush F., Katpen G.H., Ke Z., Kulp D., Lai Z.,

Liu X., Mattei B., McIntosh T.C., McLeod M.P., McRotheria A.,

Rabon D.R., Puttman G.S., Pan S., Pollard J., Nosherson D.,

Rabon D.R., Nalson K.A., Nixon K., Nixon W. McRoth W., Relson D.L.,

Rabon D.R., Plattman G.S., Pan S., Pollard J., Waisen M.,

Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

Syriekas R., Moyon F.N., Worley K.C., Wu D., Yang S., Yao Q.A.,

Rabon R.R., Moyers E.W., Robin G.M., Waissenbech J.,

Rabon R.R., Moyers E.W., Robin G.W., Waissenbech J.,

Rabon R.R., Moyers E.W., Robin G.W., Waissenbech J.,

Rabon R.R., Zoder J., Stappson M., Stung S., Zhu X., Sm
                                                                                                                                                                              MEDLINE-21952490; PubMed=11955446; DOI=10.1016/S0092-8674(02)00679-7; Kramps T., Peter O., Brunner E., Nellen D., Froesch B., Chatterjee S., Murone M., Zuellig S., Basler K. K.; Millen B., Robert S., Murone M., Willen B., Stephens signaling requires BCL9/legless-mediated recruitment of pygopus to the nuclear beta-catenin-TCF complex.";
                                                                                                                                                                                                                                                                                                                                   MEDLINE=22010046; PubMed=12015286;
Parker D.S., Jemison J., Cadigan K.M.;
"Pygopus, a nuclear PHD-finger protein required for wingless signaling
in Drosophila.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22426069; PubMed=12537572;
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Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Protein pygopus (Gammy legs protein).
Name=pygo; Synonyms=gam; ORFNames=CG11518;
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Dittera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                      Development 129:2565-2576(2002)
                                                                                                                                                                                                                                                                 Cell 109:47-60(2002).
                                                                                                                                                                NUCLEOTIDE SEQUENCE.
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BioCyc; DMEL-XXX-02:DMEL-XXX-02-014325-MONOMER; -.
GO; GO:0005634; C:nucleus; NAS.
GO; GO:0005634; C:nucleus; NAS.
GO; GO:0035214; P:eye-antennal disc development; IMP.
GO; GO:0030177; P:postrive regulation of Wnt receptor signali. . .; IPI.
GO; GO:0003675; P:segment polarity determination; IMP.
GO; GO:00016655; P:Wnt receptor signaling pathway; IMP.
InterPro; IPR001965; Znf_PHD.
Ffam; PF00629; PHD; II.
SNGRY; RSN0249; PHD; II.
SNGRY; RSN0249; PHD; II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
                                                                                                           Complete protecme; Developmental protein; Metal-binding;
Nuclear protein; Segmentation polarity protein; Wnt signaling pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PHD-type. Nuclear localization signal (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Distributed under the Creative Commons Attribution-NoDerivs License
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                  'Annotation of the Drosophila melanogaster euchromatic genome:
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Pred. No. 2e+02;
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S -> P (in Ref. 1).
                                                       Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein pygopus.
/FIId=PRO_000097124.
                                                                                                                                                                                                                                                                                                                                                                                                   throughout development. -- -- SIMILARITY: Contains 1 PHD-type zinc finger.
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11-0CT-2005, sequence version 1.
07-FEB-2006, entry version 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AR457206; AAL91369.1; -; mRNA.
EMBL; AX075095; AAL79357.1; -; mRNA.
EMBL; AB003778; AAF57161.1; -; Genomic_DNA.
EMBL; AX058500; AAL13729.1; -; mRNA.
Ensembl; CG11518; Drosophila melanogaster.
Flybase; FBgn0043900; pygo.
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                                                                              [5]
NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS01359; ZF PHD 1; 1. PROSITE; PS50016; ZF_PHD_2; 1.
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92.3%;
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nes 12; Conservative
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Lewis S.E.;
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RC STRAIN-657BL/60;

Rubbed=1614072; DOI-10.1126/science.1112014;

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RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R., Chall Gatta G.,

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PubMed=16141073; DOI=10.1126/science.1112009;
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Bandai I.A., Schmaider C., Semple C.A., Secton M., Shimada K.,
Bandai I.A., Sandai M., Sakal M., Sakat L., Shibate K., Shibate K., Shimagawa A.,
Bandai I.A., Schmaider C., Semple C.A., Secton M., Sakatu M., Sak

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98151363; PubMed=9482736; DOI=10.1093/emboj/17.5.1395; Tapon N., Nagata K., Lamarche N., Hall A.; M. Naw acc target POSH is an SH3-containing scaffold protein involved in the JNK and NP-kappaB signalling pathways."; EMBO J. 17:1395-1404(1998).
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                                                                                                                                                                                        MGI, MGI.1913/; BARGASSO.1.1; -; MKNA.

MGI, MGI.1913/; BARGASSO.1.1; -; MKNA.

GO; GO:0005078; F:PMAP-Kinase scaffold activity; IDA.

GO; GO:0005518; F:PMAP-Kinase scaffold activity; IDA.

GO; GO:0005518; F:PROTEIN binding; IDA.

GO; GO:00046328; F:regulation of JNK cascade; IDA.

InterPro; IPR00108; Neu_cyt_fact_2.

InterPro; IPR00108; SH3 1; 3.

InterPro; IPR00184; Znf. RING.

Pfam; PF00018; SH3 1; 3.

Pfam; PF00019; FING.

PRINTS; PR00495; PG7PHOX.

PRINTS; PR00495; SH3 3.

PRODOM; PS000106; SH3; 3.

PROSITE; PS00018; ZF. RING 1; 1.

PROSITE; PS00018; ZF. RING 1; 1.

PROSITE; PS00018; ZF. RING 2; 1.
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HSSP; P19878; 1K4U.
MGI; MGI:1913066; Sh3md2.
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nes 12; Conservative
              NUCLEOTIDE SEQUENCE.
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,

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Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
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Name=CG15803; ORFNames=Dmel_CG15803;

Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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Pred. No. 2.1e+02;
L; Mismatches 0; Indels
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Ephydroidea, Drosophilidae, Drosophila.
R GO; GO:0030027; C:lamellipodium; IDA.

R GO; GO:0005078; F:MAP-kinase scaffold activity; IDA.

GO; GO:0005515; F:protein binding; IPI.

GO; GO:0046328; F:protein binding; IPI.

GO; GO:0046328; F:regulation of JMK cascade; IDA.

InterPro; IPR00108; New_cyt_fact_2.

R InterPro; IPR001841; Znf. RING.

R Pfam; PF00018; SH3 1; 4.

R Pfam; PF00097; Zf-C3HC4; 1.

R Pfam; PF00097; Zf-C3HC4; 1.

R PRINTS; PR00499; PG7PHOX.

R PRINTS; PR00499; PG7PHOX.

R PRINTS; PR00499; PG7PHOX.

R PRODOM; P000066; SH3; 4.

R RRART; SW00184; RING; 1.

R RROSITE; PS00018; ZF RING 1; 1.

R PROSITE; PS00018; ZF RING 2; 1.

R PROSITE; PS00018; ZF RING 2; 1.
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01-OCT-2002, sequence version 2.
21-FEB-2006, entry version 28.
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419 AAVAAAAAAAA 431
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897 AA; 94372 MW; 3A74789E08FD1A2F CRC64;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
MEDLINE=22446069; PubMed=12537572;
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Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.
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Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith
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"Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QOVBP2:CG5053; NbExp=1; IntAct=EBI-172540, EBI-202525; QOVQW7:ed; NbExp=1; IntAct=EBI-172540, EBI-85823; SIMILARITY: Contains 4 PDZ (DHR) domains.
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Submitted (JAN-2006) to the EMBL/GenBank/DDBJ databases.
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Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
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HSSP; Q64512; 10ZI.
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FlyBase; FBgn0038606; CG15803.
GO; G0:0005515; F:protein binding; IPI.
InterPro; IPR001478; PDZ.
Pfam; PF00595; PDZ; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
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PROSITE; PS50106; PDZ; 4.

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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Pred. No. 2.1e+02;
1; Mismatches 0; Indels
         Length 897;
                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              914 AA; 95963 MW; 0D3F7A4B4AD9E067 CRC64;
13-SEP-2004, integrated into UniprotKB/TrEMBL.
13-SEP-2004, sequence version 1.
07-FEB-2006, entry version 12.
MKIAAL194 protein (Fragment).
Mmame=Sh3md2: Synonyms=mKIAA1494;
Mus musculus (Mouse).
                                                                                                                                      914 AA.
                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AK173185; BAD32463.1; -; mRNA.
                                                                                                                                      PRT;
                                                                                                                                       PRELIMINARY;
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133 AAVAAAAAAAAA 145
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Matches 12; Conservative
                                                       1 AAMAAAAAAAA 13
                                  12; Conservative
                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE
                      Best Local Similarity
                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                     Q69ZII_MOUSE
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             Query Match
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RC STRAIN-GC7BL/G07 TISSUE-Medulla oblongata;
RX PUBMed=16141072; DOI=10.1126/science.1112014;
RA DAGE STRAIN-GC7BL/G07 TISSUE-Medulla oblongata;
RA DAGE STRAIN-GC7BL/G07 TISSUE-Medulla oblongata;
RA DAGE STRAIN-GC7BL/G07 TISSUE-MEDIAL S., Rolls C., Rodzius R., Shimokawa R., Ra Davis M.J., Wilnung L.G., Ajdrinis V., Allen J.E.,
RA Davis M.J., Wilnung L.G., Ajweiler R., Allen J.E.,
RA Davis M.J., Wilnung L.G., Ajweiler R., Allen J.E.,
RA Davis M.J., Dalla B. D., Dallay R. N., Bailey T.L.,
RA CHUK K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
Christoffels A., Clutterbuck D.R.,
R. Theome M.L., Dalla B. D., Davn T., Engstrom P., Fagiolini M., Faulkner G.,
RA Georgi: Hemming P. Gingers T.R., Golobori T.K., Hirokawa N.,
R. Hill D., Humhilecki L., Iacono M., Ikec K., Iwama A., Ishikawa T.,
RA Tano H., Kalabar G., Krishnan S.P., Kruger A., Kummerd G.,
RA Mataoda H., Mataoza G., Krishnan S.P., Kruger A., Kummerd S., Markin I.,
Rutono H., Walisag G., Krishnan S.P., Kruger A., Kummerd G.,
RA Mataoda H., Mataoza S., Miki H., Mignone F., Myake S., Morris K.,
Nowilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Nataoda H., Walisag S., Miki H., Mignone F., Myarke S., Morris K.,
RA Salzberg S.L., Larapug K.C., Sene S., Nori F., Obaran V.,
Schonbach C., Sekiguchi S., Nishikawa S., Nori F., Obara B.,
RA Shada Y., Shinada H., Shinada K., Silva D., Sinclair B.,
Shibata Y., Shinada H., Shinada K., Silva D., Sinclair B.,
Shibata Y., Shinada H., Shinada K., Silva D., Sinclair B.,
Ramoig K., Van Nimwegen E., Yougura K., Sene S., Taken J., Tack M.,
Ramanishi H., Zabarovsky E., Zhu S., Zhu S., Taken J., Kawashina N.,
Rawashina T., Kolima M., Kato T., Kawaji H., Kawagashira N.,
Rawashina T., Kolima M., Kato T., Kawaji H., Kawagashira N.,
Rawashina T., Kolima M., Rondo S., Hume D.A., Nai H., Nakana J.,
R., Mahleetedt C., Mattick J.S., Hume D.A., Nai H., Nakana J.,
R., Wasashina T., Kolima M., Roto S., Hume D. Sakriki D., Tacheman S.,
R., Hamong K., Ilua M., Kato T., Kawashina J., Naika J., Naika J., Suuki H.,
R., Wasashina T
                                                        11-OCT-2005, integrated into UniProtKB/TrEMBL.
11-OCT-2005, sequence version,1.
07-FEB-2006, entry version 3.
Adult male medulla oblongata cDNA, RIKEN full-length enriched library, clone:6330596E03 product:hypothetical Transforming protein Ski/SAND-like/Putative DNA binding containing protein, full insert sequence.
                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Methods Enzymol. 303:19-44(1999).
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PubMed=16141073; DOI=10.1126/science.1112009;
RIKEN Genome Exploration Research Group, and Genome Science Group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'The transcriptional landscape of the mammalian genome.";
                  PRT;
                                                                                                                                                                                                                                                                                            Muroidea; Muridae; Murinae; Mus.
                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                Q3UYA4_MOUSE
Q3UYA4;
                                                                                                                                                                                                     Name=Lbxcorl;
MOUSE
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RG (Genome Network Core Team) and the FNATMY Consectium;

RE Science 309:1564-1566(12005).

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Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                         STRAIN=C57BL/6J; TISSUB=Medulla oblongata;
Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
Muramatsu M., Hayashizaki Y.;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Mateumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yonada Y., Ishikawa T., Ozawa K., Tanaka T., Mateuura S., Kawai J., Yonada Y., Ishikawa T., Lono Y., Kira A., Hayashizaki Y., "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
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21-FEB-2006 entry version 31.
CG32466-PA, isoform A.
Name=rn; ORPNames=Dmel CG32466;
Drosophila melanogaster (Fruit fly).
Bukaryota; Merazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Proptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AK134840; BAE22308.1; -; mRNA.

MGI; MGI:2443473; Lbxcorl.
GO; GO:0005634; C:nucleus; RCA.
GO; GO:0005634; C:nucleus; IDA.
GO; GO:00056734; C:rranscription factor complex; IDA.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:000514; F:transcription corepressor activity; IDA.
GO; GO:0050875; P:cellular physiological process; RCA.
GO; GO:0016481; P:negative regulation of transcription; IDA.
InterPro; IPR003380; Transform_Ski.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92.5%; Score 49; DB 2; Length 935; 92.3%; Pred. No. 2.2e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l prote<sup>I</sup>n.
935 AA; 96933 MW; A9C2953F4A77E367 CRC64;
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Q9V193;
                                                                                                                                                                                                                          Genome Res. 10:1757-1771 (2000)
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Matches 12, Conservative
                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE
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Bottova D., Botchan M.R., Bouck J., Botokatein P., Bottova D., Botchan M.R., Bouck J., Botokatein P., Candrea I., Candrea J., Changer A., Changer A., Candrea J., Changer A., Candrea J., Candrea J., Changer A., Deng J., Date S.M., B. Doddon K., Dodg E., Delicher A., Deng J., Mays A.D., Dew J., Dietz S.M., B. Doddon K., Dodg E., Delicher A., Deng J., Mays A.D., Dew J., Dietz S.M., B. Doddon K., Dodg E., Calcater M., Deng J., Dew J., Dietz S.M., Dodg E., Delicher A., Deng J., Gaspa M. K., Glasser K., Dunn P., B. Dodgon K., Dong E., Gorgelia J., Gaspa M. K., Glasser K., Garaga M. S., Galbatt W. M., Glasser K., A. Martis M., Jares P., Martis M., Garaga M., Martis M.,
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VARSPLIC
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       NUCLECOTIDE SEQUENCE [LARGE SCALE MENA] (ISOFORMS 1 AND 3).

STRAIN-C57BL/6J; TISSUB-Cerebellum, and Testis;
PubMed-elf41072; DOI=10.1126/science.1112014;
Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., Anderden P., Kasukawa T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Bajic V.B., Brenner S.B., Batalov S., Forrest A.R., Zavolan M., Bajic V.B., Brinning L.G., Aidinis V., Allen J.E.,
Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
Crowe M.L., Dalla E., Dalrymple B.P., Ge Bono B., Della Gatta G.,
Ail Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
Aletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
Retcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
All D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
Jak M., Kanapin A., Katch M., Kawasawa Y., Kelso J., Kitamura H.,
Altano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.,
Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.,
Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
Libu J.,
Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
Libu J.,
Libu J
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                                                                                                                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
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TISSUE=Embryonic brain;

PubMed=15520197; DOI=10.1074/jbc.M411652200;

Mizuhara E., Nakatani T., Minaki Y., Sakamoto Y., Ono Y.;

"COrll, a novel neuronal lineage-specific transcriptional corepressor for the homeodomain transcription factor Lbx1.";

J. Biol. Chem. 280:3645-3655(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92.5%; Score 49; DB 2; Length 946; 92.3%; Pred. No. 2.2e+02; ive 1; Mismatches 0; Indels
                                    Submitted (JAN-2006) to the EMBL/GenBank/DDBJ databases.
                                                                 -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QBBX4E; QSWB12; QBC0T2;
21-JUN-2005, integrated into UniProtKB/Swiss-Prot.
01-WAR-2003, sequence version 1.
07-FEB-2006, entry version 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 2), FUNCTION,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             964 AA.
                                                                                                                                                                                                                                             EMBL; AE003672; AAF54032.3; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=Lbxcorl; Synonyms=Corll;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AAMAAAAAAAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 92.3
Matches 12, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
$ \frac{1}{2} \text{S} \text{C} \text{C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
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Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K., Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P., Nilson R., Nishikawa S., Nori F., Ohara O., A chazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G., Ra Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M., Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C., Sengalori K., Semple C.A., Seno S., Sessa L., Sheng Y., Schnbach C., Skimada H., Shimada K., Silva D., Sinclair B., Shimada H., Shimada K., Silva D., Sinclair B., Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Takenaka Y., Sultana R., Tegner J., Teichmann S.A., Berling S., Stupka E., Verafor M., Silva D., Sinclair B., Vamanoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A., A dead H.R., van Nimwegen E., Verafor M., S., Tegner J., Teichmann S.A., A ramanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C., A crimmond S.M., Tasadale R.D., Liu E.T., Brueic V., Quackenbush J., A Grimmond S., Kananori-Katayama M., Suzuki M., Azakawa T., Itoh M., Kato T., Kawaji H., Kawagashira N., Rawashima T., Kojima M., Kato T., Kawaji H., Kawagashira N., Maki M., Plessy C., Shibata K., Shiraki T., Suzuki S., Harashiraki Y., Suzuki Y., Suzuki Y., Matshiraki Y., Suzuki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isoid=Q8BX46-3; Sequence=VSP_014178, VSP_014180, VSP_014181; Note=No experimental confirmation available; TISSUE SPECIFICITY: Expressed in brain with higher levels in embryo than adult. Also expressed in adult testis. In embryonic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  brain, expressed in a subset of postmitotic neurons generated posterior to the midbrain-hindbrain border. In the developing spinal cord, selectively expressed in dorsal horn interneurons.-:- SIMILARITY: Belongs to the SKI family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro; IPR003380; Transform Ski.
Pfam; PF02437; Ski Sno; 1.
Alternative splicing; Coiled coil; Nuclear protein; Repressor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ladybird homeobox corepressor 1./FTId=PRO_000129391.
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Ensembl; BNSMUSG0000022245; Mus musculus.
MGI; MGI:443473; Lbxcott.
GO; GO:0005634; C:nucleus; IDA.
GO; GO:0005667; C:transcription factor complex; IDA.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0003144; F:transcription corepressor activity; IDA.
GO; GO:0016481; P:negative regulation of transcription; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The transcriptional landscape of the mammalian genome."; Science 309:1559-1563(2005).
-!- FUNCTION: Acts as a transcriptional corepressor of LBX1.
-!- SUBDNIT: Interacts with LBX1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9QVT4:- (xeno); NDEXp=1; IntAct=EBI-604451, EBI-60470
O88712:Ctbp1; NDExp=1; IntAct=EBI-604451, EBI-604547;
O09106:Hdac1; NDExp=1; IntAct=EBI-604451, EBI-301912;
P52955:Lbx1; NDExp=1; IntAct=EBI-604451, EBI-604594;
Q62440:Tle1; NDExp=1; IntAct=EBI-604451, EBI-604471;
SUBCELLULAR LOCATION: Nucleus.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Missing (in isoform 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /FTId=VSP 014178.
Missing (In isoform 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=Q8BX46-1; Sequence=Displayed;
Note=No experimental confirmation available;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=Q8BX46-2; Sequence=VSP_014179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transcription; Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FTIG=VSP
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EMBL, AKO29916; BAC26674.1; -; mRNA.
EMBL, AKO49035; BAC35520.1; -; mRNA.
HSSP; P12755; 1MR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143
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RYCLEAULINE SALVAMENE (LIANUS SCHEIG DENOVILE DATA).

RY CYLLANDEL SALVAMENE (LIANUS SCHEIG DENOVILE DATA).

RY DEMOGRAPISOTREE: DOTE-10.1038/nature002426;

RY Gibbs R.A. Weinstock G.M. Metaker M.L. Muzny D.M., Sodergren E.J.,

RY Gibbs R.A. Weinstock G.M. Metaker M.L. Muzny D.M., Sodergren E.J.,

RY Gerer S., Scott G., Steffen D., Worley K.C., Burch P.E., Okwuonu G.,

RA Morgan M., Hawes A., Gill R., Holt R.A., Adams M.D., Amanatides P.G.,

RA Baden-Tillson H. Barnstead M., Cini S., Evans C.A., Norlyen T.,

RA Baden-Tillson H. Barnstead M., Cini S., Evans C.A., Norlyen T.,

RA Foaler C., Glodek A., Gu. J. dennings D., Kraft C.L., Norlyen T.,

RA Frankoch C.M., Sitter C., Sutton G.G., Venter J.C., Woodage T.,

RA Brankoch M., Schein J., Bosdet I., Fiell C., Donng P.J., Osoegawa K.,

RA Dune J., Blakesley R.W., Bosdet I., Fiell C., Jones S.,

RA Kraywinski M., Mathewson C., Siddigui A., Wev N., McDherson J.,

RA Branko S., Praser C.M., Sitter J., Shatsman S., Geer K., Chen Y.,

RA Abramzon S., Nierman W.C., Havlak P.H., Chen R., Durbin K.J., Egan A.,

RA Ralfus K.J., McDecod M.P., Milosavijeric A., Vilk D., Volkov A.,

RA Ralfus K.J., McDecod M.P., Milosavijeric A., Vilk D., Volkov A.,

Wheeler D. A., Zhang Z., Balley J.A., Eichler E.B., Turun E.,

RA Briney B., Mongin E., Ureta-Vidal A., Moodwart C., Zdohorov B.,

RA Briney B., Suyama M., Torrente D., Gosele C., Hummel D., Kreitler T.,

RA Briney B., Wongin E., Ureta-Vidal A., Moodwart C., Zdohorov B.,

RA Briney B., Wongin E., Ureta-Vidal A., Woodwart C., Zdohorov B.,

RA Briney B., Wongin E., Ureta-Vidal A., Woodwart C., Zdohorov B.,

RA Briney B., Wongin R., Willer W., Woodwart C., Rummel D.,

RA Briney B., Wongin R., Willer W., Woodwart C., Rummel D.,

RA Briney B., Wongin E., Woodwart C., Rummel D., Gosele C., Hummel D.,

RA Briney B., Wong C., Basko D., Tonellake D., Twigger S.,

Roudews T.D., Caccamo M., Clamp M., Clarke D., Twigger S.,

Radecok M., Wolbe D., Warde S., Bourque G., Lobez Colin C., Patter E., Raber B. A.,

Rochwartz S., Taylor J., Wang S.,
                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buzrchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Rattus.
                                                                                                                                                                                                 Gaps
/FTId=VSP_014179.
LQGGGGGGA-> PARGRRRR (in isoform 3)
/FTId=VSP_014180.
                                                                                                                                                                                                 ö
                                                                                                                                                    Score 49; DB 1; Length 964;
Pred. No. 2.2e+02;
1; Mismatches 0; Indels
                                                                                           961 961 0 -> P (in Ref. 1).
964 AA; 100276 MW; B1ECDB443D789E2C CRC64;
                                                    Missing (in isoform 3)./FTId=VSP_014181.
                                                                                                                                                                                                                                                                                                                                                                                                                21-JUN-2005, integrated into UniProtKB/Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
                                                                                                                                                                                                                                                                                                                                                                             964 AA.
                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUN-2005, sequence version 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-MAR-2006, entry version 8.
Ladybird homeobox corepressor 1.
                                                                                                                                                          92.5%;
                                                                                                                                                                              92.3%;
                                                                                                                                                                                                                                                                            512 AAVAAAAAAAA 524
                                                                                                                                                                                                                                       1 AAMAAAAAAAA 13
                                                                                                                                                                          Local Similarity 92.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                    290
                                                            964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10116;
                                                            291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=Lbxcorl;
                                                                                                                                                                                                                                                                                                                                                                               LBXCO RAT
                                                                                                                       SEQUENCE
                                                                                                                                                              Query Match
                      VARSPLIC
                                                            VARSPLIC
                                                                                               CONFLICT
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                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                     Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
Kent W.J., Rosenbloom K.R., Trumbower H., Weirauch M., Cooper D.N.,
                Stenson P.D., Ma B., Brent M., Arumugam M., Shteynberg D., Copley R.R., Taylor M.S., Riethman H., Mudunuri U., Peterson J., Guyer M., Felsenfeld A., Old S., Mockrin S., Collins F.; Genome sequence of the Brown Norway rat yields insights into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human chromosome 15 international sequencing consortium;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases
-!- FUNCTION: Acts as a transcriptional corepressor of LBX1 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                             Nature 428:493-521(2004).
-!- FUNCTION: Acts as a transcriptional corepressor of LBX1 (By
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                                                                                                                                                                                                                                                                                                              Ladybird homeobox corepressor/FTId=PRO_0000129392.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92.5%; Score 49; DB 1; Length 965; 92.3%; Pred. No. 2.2e+02; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                             Score 49; DB 1; Length 964;
Pred. No. 2.2e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AC009292; -; NOT ANNOTATED_CDS; Genomic_DNA.
HGNC; HGNC:21326; LBXCOR1.
Coiled coil; Nuclear protein; Repressor; Transcription;
                                                                                                                                                                                                                                                   EMBL, AABR03062264; -; NOT_ANNOTATED_CDS; Genomic_DNA. RGD; 1307687; RGD1307687.
                                                                                                                                                                                                                                                                                                                                                                 78D1B922CAB29B7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99831 MW; 313E95B0430A979B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBUNIT: Interacts with LBX1 (By similarity). -!- SUBCELLULAR LOCATION: Nucleus (By similarity). -!- SIMILARITY: Belongs to the SKI family.
                                                                                                                                        -!- SUBUNIT: Interacts with LBX1 (By similarity).
-!- SUBCELLULAR LOCATION: Nucleus (By similarity).
-!- SIMILARITY: Belongs to the SKI family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUN-2005, integrated into UniProtKB/Swiss-Prot.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              965 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUN-2005, sequence version 1. 07-MAR-2006, entry version 6. Ladybird homeobox corepressor 1.
                                                                                                                                                                                                                                                                                                                                                                    964 AA; 100234 MW;
                                                                                                                                                                                                                                                                                                                                                                                                 92.5%;
92.3%;
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                                                                                                                                                                                                                                                                                                       Transcription regulation.
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                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 92.3
es 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                mammalian evolution."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
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965 AA;
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                                                                                                                                similarity).
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Ephydroidea;
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PubMed=15496914; DOI=10.1038/nature03025;
A Jailon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
A Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
A Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Blemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
A cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
Rellis M., Volff J.-N., Guigo R., Zody M.C., Meskrov J.,
Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
II. Nature 431:946-957(2004).
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                                                                                                                                                                                   Tetraodon nigroviridis (Green puffer).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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07-FBB-2006, entry version 19.
CG1770-PB, isoform B
Name=HDAC4; ORFNames=Dmel CG1770;
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 49; DB 2; Length 1065;
Pred. No. 2.4e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genoscope, Whitehead Institute Centre for Genome Research, Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; CAAE01014537; CAF97427.1; -; Genomic DNA.
SEQUENCE 1065 AA; 118021 MW; EDDB6A851F655E0F CRC64;
                                                                                                                                  19-JUL-2005, sequence version 1.
07-FEB-2006, entry version 3.
Chromosome 16 SCAF14537, whole genome shotgun sequence.
ORFNames=GSTENG00014784001,
                                                                                                                       19-JUL-2005, integrated into UniProtKB/TrEMBL
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                                                                                                PRT; 1065 AA
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                                                                                               PRELIMINARY;
                                   515 AAVAAAAAAAA 527
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           1 AAMAAAAAAAA 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        preliminary data.
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Best Local Similarity
                                                                                                                                                                                                                                               NCBI_TaxID=99883;
                                                                                               Q4SPK5_TETNG
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QBIR69;
                                                                        36
TETNG
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1D : Q8
AC : Q8
DT : Q1
DT : Q1
DT : Q1
DE : CC
GN : Nc
OS : D1
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Components, Endopmenyodia, Dipmers Brachycers, Muscomorpha;

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EMBL; AE003492; AAX52490.1; -; Genomic_DNA.
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 MEDLINE=20196006; Pubbled=10731132; DOI=10.1126/science.287.5461.2185; Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., A Gutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Ragers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., A Brandon R.C., Ragers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., A Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Bernan B.P., Bhandari D., Blashakov S., Benson K.Y., Bernan B.P., Bhandari D., Bolshakov S., Burtis K.C., Busam D.A., Burler H., Cadleu B., Center A., Chandra I., Ab Burtis K.C., Busam D.A., Butler H., Cadleu B., Center A., Chandra I., Ab Ballew B., Delcher A., Dang Z., Mays A.D., Dew I., Dietz S.M., Ab Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Plunkov B.C., Dunn P., Burbin K.J., Evangelista C.C., Ferriera S., Fleischmann W., Rosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
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                                                                                                     Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R. Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith
             Lewis S.E.; Annotation of the Drosophila melanogaster euchromatic genome: a
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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26-APR-2005, sequence version 1.
26-APR-2005, sequence version 1.
26-APR-2005, entry version 5.
CG1770-PC, isoform C.
Name=HDAC4; ORFNames=Dmel_CG1770;
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Boptera; Endoptera; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                              Score 49; DB 2; Length 1181;
Pred. No. 2.6e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                           FlyBase; FBGN0041210; HDAC4.

InterPro; IPR000286; His deacetylse.

InterPro; IPR01220; Lectin legB.

PANTHER; PTHR10625; His deacetylse; 3.

Pfam; PF00850; Hist deacetyls; 1.

PRNTS; PR01270; HDASUPER.

PRNTS; PS0037; LECTIN LEGUME BETA; UNKNOWN 1.

SEQUENCE 1181 AA; 126044 MW; AD451B406E8719B1 CRC64;
                                                                                                                                               "Drosophila melanogaster release 4 sequence.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                             Submitted (JAN-2006) to the EMBL/GenBank/DDBJ databases
                                                    Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1199 AA.
                                                                                                                                                                                                                                                                               EMBL; AE003492; AAN09318.1; -; Genomic_DNA.
                                                                                          Berkeley Drosophila Genome Project;
                                                                                                                                                                                                                                                                                                                                                                                                                 92.5%;
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423 AAVAAAAAAAAA 435
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Best Local Similarity 92.3'
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                                                                            NUCLEOTIDE SEQUENCE.
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                                          review
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Q59E49;
                                         systematic
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Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeeyam C.,
A Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
A Lusko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Lasko P., Mishina N.V., Moberty C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Palazzolo M. Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
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Shue B.C., Siden-Kiamos I., Simpson M., Stupski M.P., Smith T.,
RA Shee E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,
RA Shies R., Wassarman D.A., Weinstock G.M., Weissenbach J.,
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Rel Yel, Yeh R.-F., Zaveri J.S., Zhan M., Zhong G., Zhao Q., Zheng H.,
Railiams S.M., Myers E.W., Rubin G.M., Venter J.C.;
R. Thhe genome sequence of Incosphila melanogaster.";
R. Frience 2872185-2195 (2000)
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MEDIJNE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R., Raminker J.S., Bergman C.M., Lewis S.E., Rubin G.M., Partel S., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
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Berkeley Drosophila Genome Project;
Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
Calliss R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
Yu C., Rubin G.;
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MEDLINE=2245069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Misra S., Crosby M.A., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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Calniker 2.2426065; PubMed=12537568;

Calniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgon A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Facilter B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; Finishing a Whole-genome shotgun: release 3 of the Drosophila melanogaster euchromatic genome sequence.";

Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JAN-2006) to the EMBL/GenBank/DDBJ databases.
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
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Ephydroidea; Drosophilidae; Drosophila
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22368461; PubMed=12481296; DOI=10.1002/gene.10159; Zeremski M., Stricker J.R., Fischer D., Zusman S.B., Cohen D.; "Histone deacetylase dHDAC4 is involved in segmentation of the Drosophila embryo and is regulated by gap and pair-rule genes.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=HDAC4; Synonyms=HDAC4; ORFUNE a.
Drosophila melanogaser (Fruit fly)
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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07-FEB-2006, entry version 26.
CG1770-PA, isoform A.
Name-HDAC4; ORFNames-Dmel CG1770;
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazaa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92.5%; Score 49; DB 2; Length 1203; 92.3%; Pred. No. 2.6e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                    DB 2; Length 1199;
InterPro; IPR000286; His deacetylse.
InterPro; IPR001220; Lectin_legB.
PANTHER; PTHA10625; His deacetylse; 3.
PRIM; PR00850; Hist deacetyl; 1.
PRINTS; PR01270; HDA5UPER.
PROSITE; PS00307; LECTIN LEGUME BETA; UNKNOWN 1.
SEQUENCE 1199 AA; 128125 MW; 40C97AD33F86169C CRC64;
                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PSO0307; LECTIN LEGUME BETA; UNKNOWN 1.
SEQUENCE 1203 AA; 128666 MW; 04B5D0B12088979F CRC64;
                                                                                                                                                                      Score 49; DB 2; I
Pred. No. 2.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2003, integrated into UniProtKB/TrEMBL.
01-MAR-2003, sequence version 1.
07-FEB-2006, entry version 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000, integrated into UniProtKB/TrEMBL
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                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1203 AA.
                                                                                                                                                                                                               1; Mismatches
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InterPro; IPR001220; Lectin_legB.
PANTHER; PTHR10625; His_deacetylse; 3.
Pfam; PF00850; His_deacetyl; 1.
PRINTS; PR01270; HDASUPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Histone deacetylase dHDAC4 isoform a.
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                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                      92.5%;
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tes 12; Conservative
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Best Local Similarity
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C081947 DRO
ID 01-MA
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DT 01-MA
DT 07-FE
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CN Nome
CN Nome
CN Noby
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Q9VYF3 DRO
Q9VYF4
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DT 01-OC
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RANGLEOTIDE SEQUENCE.

RAY MUCLEOTIDE SEQUENCE.

RAY MADIAINS-1016016; PubMed=10731132; DOI=10.1126/science.287.5461.2185; Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewisi S.E., Li P.W., Hoskins R.A., Galle R.F., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Ray Baradon R.C., Ragaers Y.-H.C., Halt G., Malson C.R., Miklos G.L.G., Wan K.H., Doyle C., Barker E.G., Helt G., Melson C.R., Miklos G.L.G., Ray Baradon R.C., Ragaers Y.-H.C., Halt G., Melson C.R., Miklos G.L.G., Ray Baradon R.C., Ray Raman B.P., Bhandari D., Bolshakov S., Ballew R.M., Basu A., Baradon R.P., Bhandari D., Bolshakov S., Burtis K.C., Busam D.A., Barandal B.P., Bhandari D., Bolshakov S., Burtis K.C., Busam D.A., Barandal R.C., Baranshoch C., Baldwin D., Bottevar A., Change P., Donne P., Brotter A., Change P., Bhandari D., Bolshakov S., Borterry J.M., Cawley S., Dahlor R., Deng Z., Mays A.D., Dew I., Dietz S.M., de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Acherry J.M., Cawley S., Delcher A., Heiman T.J., Hernandez J.R., Houck J., Ray Bosler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K., Adalsi M., Kalush F., Korraz C., Kernison J.A., Recthum K.J., Burtis M., Heiman T.J., Hernandez J.R., Houck J., Barkon M., Harris N.L., Harvey D.A., Heiman T.J., Mernel B.E., Kodira C.D., Kraft C., Kravitz S., Kilp D., Lai Z., Lians M., Matchi B.E., Kodira C.D., Kraft C., Kravitz S., Kilp D., Lai Z., Lians C., Mourts G., Mishina N.V., Mobarry C., Morris J., Mosherei A., Mount S.M., Wount S.M., Wow M., Whyen B., Murzhby L., Muzny D.M., Nather E., Shen H., Ray Balazzolo M., Pittman G.S., Pan S., Pollar G., Kravitz S., Scheler F., Shen H., Ray Balazzolo M., Pittman G.S., Pan S., Pollar G., Scheler F., Shen H., Spier E., Spradling A.C., Stapheron M., Stups R., Shen B., Spier E., Spradling A.C., Stapheron M., Stups R., Sheng K.M., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Wang S., Yao O., Zheng L., Schence 287:2185-2195(2
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MEDIANE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
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Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                     NUCLEOTIDE SEQUENCE.

Berkeley Drosophila Genome Project;

Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
"U., Rubin G.;
"Drosophila melanogaster release 4 sequence.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                           -!- INTERACTION:
P29310-2:14-3-3-zeta; NbExp=1; IntAct=EBI-149766, EBI-198120;
Lewis S.E.; "Annotation of the Drosophila melanogaster euchromatic genome: a
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92.5%; Score 49; DB 2; Length 1248;
Best Local Similarity 92.3%; Pred. No. 2.7e+02;
Matches 12; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    Intact; Q9VYF3; -.
Flybase; FBGn0041210; HDAC4.
GO, GO:0005515; F:protein binding; IPI.
InterPro; IPR001220; LecTin legB.
InterPro; IPR001220; LecTin legB.
PANTHER; PTHR10625; His deacetylse; 3.
PERM; PR01270; HDASUPER.
PR01270; HDASUPER.
PROSITE; PS00307; LECTIN LEGUME BETA; UNKNOWN 1.
SEQUENCE 1248 AA; 133650 MW; D300C8523CA2C311 CRC64;
                                                                                                                                                                                                                                                                       Submitted (JAN-2006) to the EMBL/GenBank/DDBJ databases.
                                     systematic review.";
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
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Search completed: September 9, 2006, 23:00:20 Job time : 125.139 secs

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Perfect score:

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Scoring table:

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Abp52286 HLA-DR2 m
Abp52212 HLA-DR2 m
Abp52214 HLA-DR2 m
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Adj57547 Cop-1 rel
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Adj59500 Copolymer
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Adg1227 Copolymer
Adw86539 Ordered c
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Ads2520 Copolymer
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Aef02689 R
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Aef0761 A
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Ab058367 H
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Ab0583774 H
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ADD57531
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ADD69500
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Adw35215 HLA-DR2
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               GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Gapop 10.0 , Gapext 0.5
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score greater than or equal to
and is derived by analysis of
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Maximum Match 100%
Listing first 100 s
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                                                                    protein search, using
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seq length: 200000000
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Human gen Novel hum

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Aay99164 Aay99163 Aay99245

Score

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Gaps

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The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to hard.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human leukocyte antigen, HLA, major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition;
100.0%; Score 54; DB 8; Length 13
100.0%; Pred. No. 0.14;
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                                              0; Indels
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                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    anti-tumour necrosis factor agent.
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                                                                                                                                                                                                                                                                  ABP52215 standard; peptide; 15 AA.
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                                                   13; Conservative
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                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strominger JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200259143-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
  Query Match
Best Local S:
Matches 13;
                                                                                                                                                                                                                                                                                                                    ABP52215;
                                                                                                                                                                                                                        RESULT 2
                                                                                                                                                                                                                                                 ABP52215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes an isolated MHC class II compound (I) comprising: (a) an MHC class II component comprising at least a portion of an MHC class II alpha chain and at least a portion of an MHC class II beta beta chain, such that the MHC class II alpha chain and MHC class II beta chain form a peptide binding groove; (b) a spaceholder Molecule; and (c) an effector component, where the effector component is linked to the MHC class II component. Also described: (I) a pharmaceutical composition comprising the MHC class II molecule and a carrier; (2) a method of producing an MHC class II compound; (3) a method of directly identifying an antigen-specific T cell; (4) a method of regulating an immune response in a subject; (5) a method of treating an immune disorder in a subject; (7) a method of treating an immune disorder in a subject; (1) has virucide, antibacterial, antiparasitic, cytostatic and immunosuppressive activities, and can be used in gene therapy. The MHC class II compound (I) can be used for preparing a composition for treating immune cativities, and can be used in gene therapy. The MHC class II compound confections, neoplastic disease, autoimmunity or toxicity. The present sequence represents a spaceholder molecule peptide, which can be used in the present invention.
       Adw35620 HLA bindi
Adw34387 HLA bindi
Adn64988 HLA bindi
Adv78640 Cell atta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antibacterial, antiparasitic, cytostatic, immunosuppressive;
gene therapy, viral infections, bacterial infection, parasitic infection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MHC class II compound; MHC class II component; MHC class II alpha chain; MHC class II beta chain; peptide binding groove; spaceholder molecule; effector component; immune response; immune disorder; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New MHC class II compound, useful for preparing a composition for treating immune disorders e.g. viral infections, bacterial infections, parasitic infections, neoplastic disease, autoimmunity or toxicity.
                                                                                                                                                                                                                                                                                                                                                                                                                 Human MHC class II compound spaceholder molecule SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neoplastic disease; autoimmunity; toxicity; human.
                                                                                                                                                      ALIGNMENTS
                                ADW34387
ADN64988
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            ADW35620
                                                                              ADV78640
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                                                                                                                                                                                                                                                                          ADI29008 standard; peptide; 13 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-JUL-2003; 2003WO-US021767.
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2002US-0397893P.
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12-JUL-2002; 22-JUL-2002;

RESULT 1

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15-APR-2004

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Sequence 13 AA

ADW35574;

RESULT 3 ADW355

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The invention relates to a composition comprising at least one peptide having an isolated, prepared epitope selected from any of the sequences from 30 lists given in the specification. Also disclosed is a method for inducting a cytotoxic T cell response against a pre-selected antigen in a patient expressing a specific MHC class I allele by contacting cytotoxic C T cells from the patient with the composition cited above. The composition comprises an epitope that is joined by an amino acid linker. The epitope is admixed or joined to a CTL or HTL epitope. The epitope is bound to an HLA molecule on the antigen-presenting cell, where when an A2 restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL binds to a complex of the HLA molecule and the epitope. Specifically claimed are peptides having allele-specific binding motifs for HLA. The compositions and methods are useful for preventing, treating or diagnostic agents for evaluating immune responses, for making antibodies and for evaluating efficacy of a vaccine. Sequences given in ADW29251.

ADW37745 represent epitopes of the invention as given in Tables 2-31.
                                                                                                               Virucide, cytostatic, gene therapy, vaccine, epitope, cytotoxic T cell, MHC class I; CTL, HTL, A2-restricted cytotoxic lymphocyte, HLA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New composition comprising at least one peptide having allele-specific binding motifs for HLA, useful for preventing, treating or diagnosing viral diseases and cancer.
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Pred. No. 0.71;
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20-APR-2001; 2001US-0285624P.
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                                                                   HLA binding epitope #5091.
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                                                                                                                                                             viral disease; cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sette A, Sidney J,
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                                                                                                                                                                                                           Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      having an isolated, prepared epitope selected from any of the sequences from 30 lists given in the specification. Also disclosed is a method for inducing a cytotoxic T cell response against a pre-selected antigen in a patient expressing a specific MHC class I allele by contacting cytotoxic T cells from the patient with the composition cited above. The composition comprises an epitope that is joined by an amino acid linker. The epitope is admixed or joined to a HTL epitope. The epitope is bound to an HLA molecule on the antigen-presenting cell, where when an A2 restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL binds to a complex of the HLA molecule and the epitope. Specifically claimed are peptides having allele-specific binding motifs for HLA. The compositions and methods are useful for preventing, treating or diagnostic agents for evaluating immune responses, for making antibodies and for evaluating efficacy of a vaccine. Sequences given in ADW32251-ADW37745 represent epitopes of the invention as given in Tables 2-31.
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                                                                                                                                                                                                                                                                          Virucide, cytostatic, gene therapy, vaccine, epitope, cytotoxic T cell, MHC class I; CTL, HTL, A2-restricted cytotoxic lymphocyte, HLA, viral disease, cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a composition comprising at least one peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 52-379; 382pp; English.
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                                                                                    ADW35574 standard; peptide; 13 AA
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20-APR-2001; 2001US-0285624P.
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                                                                                                                                                                                                                              HLA binding epitope #6324.
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                                                                                                                                                                                                                                                                                                                                                                      Unidentified
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Sette A,

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7; Length 13; 1; Indels Virucide, cytostatic, gene therapy; vaccine, epitope; cytotoxic T cell; MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;

ADW34341;

RESULT 4 ADW34341

Query Match Matches

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23-MAR-2000; 2000US-0191637P.
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Best Local Similarity
Matches 12; Conser
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                                                                                                                              Sette A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a composition comprising at least one peptide having an isolated, prepared epitope selected from any of the sequences from 30 lists given in the specification. Also disclosed is a method for inducing a cytotoxic T cell response against a pre-selected antigen in a patient expressing a specific MHC class I allele by contacting cytotoxic T cells from the patient with the composition cited above. The composition comprises an epitope that is joined by an amino acid linker. The epitope is admixed or joined to a CTL or HTL epitope. The epitope is composition of the mission of the composition of the CTL binds to a complex of the HLA molecule and the epitope. Specifically claimed are peptides having allele-specific binding motifs for HLA. The compositions and methods are useful for preventing, treating or compositions and methods are useful for preventing, treating or diagnostic agents for evaluating immune responses, for making antibodies and for evaluating efficacy of a vaccine. Sequences given in ADM29251-
ADM37745 represent epitopes of the invention as given in Tables 2-31.
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                                                                                                                                                                                                                                                                                                           New composition comprising at least one peptide having allele-specific binding motifs for HLA, useful for preventing, treating or diagnosing viral diseases and cancer.
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20-APR-2001; 2001US-0285624P.
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Matches 12; Conservative
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   viral disease; cancer
                                                                                                                                                                                                                    (EPIM-) EPIMMUNE INC
                                                                                                                                                                                                                                                    Sette A, Sidney J,
                                                                                                                                                                                                                                                                                   WPI; 2003-441519/41
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                                                                  WO2003040165-A2
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                                                                                               15-MAY-2003
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Query Match

RESULT 6 ADW34519

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The invention relates to a composition comprising at least one peptide chaving an isolated, prepared epitope selected from any of the sequences from 30 lists given in the specification. Also disclosed is a method for inducing a cytotoxic reall response against a pre-selected antigen in a parient expressing a specific MiG class I allele by contacting cytotoxic composition comprises an epitope that is joined by an amino acid linker. The composition comprises an epitope that is joined by an amino acid linker. The composition comprises an epitope that is joined by an amino acid linker. The bound to an HLA molecule on the antigen-presenting cell, where when an A2 resprict cytotoxic lymphocyte (CTD) is present, a receptor of the CTD binds to a complex of the HLA molecule and the epitope. Specifically claimed are peptides having allele-specific binding motifs for HLA. The compositions and methods are useful for preventing, treating or captuages and ancer. The peptide epitopes are useful as diagnostic agents for evaluating immune responses, for making antibodies and for evaluating efficacy of a vaccine. Sequences given in ADM29251-

MAN37745 represent epitopes of the invention as given in Tables 2-31.
                                                                                                                                                                                                                                                                                                                                                                                                                              New composition comprising at least one peptide having allele-specific binding motifs for HLA, useful for preventing, treating or diagnosing viral diseases and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                              Southwood S;
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18-OCT-2001; 2001WO-US051650.
                                                                         19-OCT-2000; 2000US-0242350P.
20-APR-2001; 2001US-0285624P.
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                                                                                                                                                                                                     (EPIM-) EPIMMUNE INC.
                                                                                                                                                                                                                                                                              Sidney J,
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90.7%;
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                                                                                                                                                                                                     1 AAFAAAAAAAA 13
                                                                                                                                                                                  12; Conservative
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                                                                                                                                                                        Local Similarity
                                                                                                                                          Sequence 465 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
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                                                                                                                                                               Query Match
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ADI29007
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                                                                                                        The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to newly discovered cancer markers associated with the cancerous state of prostate cells. Also disclosed is a method of
                                               isolated nucleic acid detection reagent for detecting 1000 or more as from Drosophila and for elucidating cell signaling and cell-cell
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Anderson D;
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                                                                                      Disclosure; SEQ ID NO 38724; 21pp + Sequence Listing; English.
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Pred. No. 17;
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Glatt K, Zhao X,
                                                                                                                                                                                                                                                                                                                                                                                                                                           Prostate; cancer; cytostatic; gene therapy; marker.
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                                                                                                                                                                                                                                                                  0; Mismatches
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Myers EW;
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PWD,
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12-DEC-2001; 2001US-0341746P.
05-MAR-2002; 2002US-0362158P.
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Matches 12; Conservative
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Adams M,
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                    WPI; 2001-656860/75
                            N-PSDB; ABL14747
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                                                                     interactions.
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Venter JC,
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Hoersh S,
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assessing whether a patient is afflicted with prostate cancer. The method of the invention involves assessing whether a patient is afflicted with prostate cancer by comparing the level of expression of a marker in a patient sample and the normal level of expression of the marker in a control non-prostate cancer sample, where a significant increase in the level of expression of the marker in the patient sample and the normal level indicates that the patient is afflicted with prostate cancer. Nucleic acids of the invention are useful for diagnosing or treating prostate cancer, and may be useful in gene therapy. Sequences given in ABPS1777-ABDS531 represent marker CDNA and proteins. Note: The sequence data for this patent did not form part of the printed specification, but thouse, int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADI29007 standard; peptide; 13 AA
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22-JUL-2002; 2002US-0397893P.
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comprising the MHC class II molecule and a carrier; (2) a method of producing an MHC class II compound; (3) a method of directly identifying an antigen-specific T cell; (4) a method of regulating an immune response in a subject; (5) a method of treating an immune disorder in a subject; (6) a method of treating an immune disorder ex vivo in a subject; and (7) a method of treating an immune disorder ex vivo in a subject; and circuide, antibacterial, antiparasitic, cytostatic and immunosuppressive activities, and can be used in gene therapy. The MHC class II compound (I) can be used for preparing a composition for treating immune disorders, e.g., viral infections, bacterial infections, parasitic infections, and can be used in appared by the MHC class II compound from the present invention.
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                                                                                                                                                                                                                                                                                                                                          Gaps
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Pred. No. 1;
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06-DEC-2002; 2002US-0431510P.
06-DEC-2002; 2002US-0431516P.
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92.3%;
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                                                                                                                                                                                                                                                                     Sequence 13 AA;
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polypeptide of the invention, gene therapy, production of transgenic animals and production of engineered lung tissue for treatment and research. Lung specific genes (LSGs) were identified by a systematic analysis of gene expression data in the LIFESEQ Gold database using the data mining software package candidate lead automatic search program (CLASP). Genes were grouped into gene bins where each bin is a cluster of sequences grouped together where they share a common contig.

Since a spressed tissue specific genes were selected based on the Differentially expressed tissue-specific genes were selected based on the expression levels for each gene in libraries of normal tissues or non-tumour tissues from cancer patients were compared with the expression levels in tissue associated with tumour or disease. This sequence represents a protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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11-JUL-2000; 2000US-00614150.
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polypeptide that
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C ignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance;
                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield;
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                                                         DB 4; Length 285;
                                                                                                                  1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plant full length insert polypeptide segid 65028.
                                                                                                                     0; Mismatches
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                                                         Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                              ADY09213 standard; protein; 646 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-APR-2003; 2003US-00425114.
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05-NOV-2001; 2001US-00985678.
                                                         88.9%;
92.3%;
                        Query Match
Best Local Similarity 92.30,
Conservative
                                                                                                                                                                                                                                 189 AAIAAAAAAAA 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                           1 AAFAAAAAAA 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KOVALIC D K.
SCREEN S E.
TABASKA J E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-180133/17.
Sequence 285 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US2004034888-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIU J.
ZHOU Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-APR-2005
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(SCRE/)
(TABA/)
(CAOY/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ZHOU/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (rin1/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liu J,
                                                                                                                                                                                                                                                                                                                        RESULT 12
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XX A ADY0

ADY
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, aligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed cativity of (II) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders of supplement protein expression or biological activity. The involving aberrant protein expression or biological activity. The colypeptide and polymoraleotide sequences have applications in a polymoraleotide sequences not produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG3037, represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in
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or for modifying seed oil or protein yield and/or
the amino acid sequence of a plant full length insert
can be used in the recombinant DNA construct of the
                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                         8; Length 646;
                                                                                                                                                                             Indels
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                                                                                                                                       Score 48; DB 8
Pred. No. 36;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human diagnostic protein #15658.
                                                                                                                                                                                                                                                                                                                                                     ABG15667 standard; protein; 1444 AA
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                                                                                                                                       88.9%;
92.3%;
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                                                                                                                                                                                                                  1 AAFAAAAAAAA 13
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                                                                                                                                                                             12; Conservative
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                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                   Sequence 646 AA;
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                                                            invention.
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03-FEB-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                         AAY58972;
                                                                                                                                                         Matches
                                                                                                                                                                                                                                 RESULT 15
                                                                                                                                                                                                                                          AAY58972
                                                                                                                                                                                                                                                              886666666688888
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                                                                                                                                                                                                                                                  Copeptide; copolymer 1; autoimmune disease; multiple sclerosis; autoimmune haemolytic anaemia; autoimmune oophoritis; autoimmune thyroiditis; autoimmune uveoretinitis; chromic immune thrombocytopenic purpura; colitis; contact sensitivity disease; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; Hashimoto's disease; idiopathic myxedema; myaschenia gravis; psoriasis; pemphigus vulgaris; rheumatcid arthritis; systemic lupus erythematchsus; immunosuppressant; neuroprotective; antianhyroid; antidiabetic; thyromimetic; antipsoriatic; antithyroid; dermatological; antiinflammatory; therapy; major histocompatibility complex; MHC class II; human lymphocyte antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a copeptide that can be used to treat autoimmune conditions. It is an example of copeptides of the invention that were designed to bind to the groove of human leukocyte antigen HLA-DR1 and HLA-DR4 molecules. The copeptides show a high affinity for major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acids randomly joined in a linear array where one is aromatic, one is aliphatic and the other is charged, used to treat autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   terpolymers, copeptides and copolymer 1 which contain three amino
                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fridkis-Hareli
                                                  Length 1444;
                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "may be substituted by Val or Phe"
                                                                        1; Indels
                                                                                                                                                                                                                                 Copeptide useful for treatment of autoimmune disease.
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                                                    DB
74;
                                                                         Mismatches
 electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                    88.9%; Score 48; 92.3%; Pred. No.
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                                                                                                                                                                      AAY58983 standard; peptide; 15 AA.
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98US-0101825P.
98US-0102960P.
98US-0108184P.
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                                                                                                                 782 AAIAAAAAAAA 794
                                                                                                                                                                                                               (first entry)
                                                                                              1 AAFAAAAAAAAA 13
                                                  Query Match 88.9
Best Local Similarity 92.3
Matches 12; Conservative
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(HARD ) HARVARD COLLEGE.
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                                Sequence 1444 AA;
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12-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
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autoimmune haemolytic autoimmune uveoretinitis;
autoimmune thyroiditis; autoimmune uveoretinitis;
chronic immune thrombocytopenic purpura; colitis;
contact sensitivity disease; diabetes mellitus; Graves disease;
duillain-Barre's syndrome; Hashimoto's disease; idiopathic myxedema;
myasthenia gravis; psoriasis; pemphigus vulgaris; rheumatoid arthritis;
systemic lupus erythemactosus; imunosuppressant; neuroprotective;
antianaemic; antithyroid; antidiabetic; thyromimetic; antipsoriatic;
antirheumatic; antiarthritic; dermatological; antinflammatory; therapy;
major histocompatibility complex; MHC class II; human lymphocyte antigen;
histocompatability complex (MHC) class II proteins associated with an autoimmune disease, especially HLA-DR1, HLA-DR2 or HLA-DR4, bind to antigen presenting cells, and inhibit T cell responses. They are especially used to treat multiple sclerosis, autoimmune haemolytic anaemia, autoimmune coophoritis, autoimmune thyroiditis, autoimmune thyroiditis, sucioimmune sensitivity disease, diabetes mellitus, Graves disease, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxedema, myasthania gravis, psoriasis, pemphigus vulgaris, rheumatoid arthritis and systemic lupus erythematosus (all claimed)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Copeptide; copolymer 1; autoimmune disease; multiple sclerosis;
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                                                                                                                                                                                                                                                                                                                                                                                                          Score 47; DB 3; Length 15;
Pred. No. 1.6;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Copeptide useful for treatment of autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ΣÌ
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98US-0101825P.
98US-0102960P.
98US-0108184P.
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                                                                                                                                                                                                                                                                                                                                                                                                                87.0%;
91.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-MAY-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Conservative
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Best Local Similarity
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(HARD ) HARVARD
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                                                                                                                                                                                                                                                                                                                                                         Sequence 15 AA;
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02-OCT-1998;
12-NOV-1998;
09-MAR-1999;
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Strominger JL,
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                                                                                          Strominger JL;
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                                                                        Aharoni R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY82075;
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                                                                                                                                                                                                                                                                               uveoretinitis, chronic immune thrombocytopenic purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxedema, myasthenia gravis, psoriasis, pemphigus vulgaris, rheumatoid arthritis and systemic lupus erythematosus (all claimed). The present peptide is a high level inhibitor of both HLA-DR-1 and -DR-4-restricted type II collagen-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chronic immune thrombocytopenic purpura; collitis; contact sensitivity disease; diabetes mellitus; Graves disease; duolitus; Guillain-Barre's syndrome; Hashimoto's disease; idiopathic myxedema; myasthenia gravis; psoriasis; pemphigus vulgaris; rheumatoid arthritis; systemic lupus erythematosus; imunosuppressant; neuroprotective; systemic luthyroid, antidabetic; thyromimetic; antipsorialisis, antithhroid; antidabetic; dermatological; antidiflammatory; therapy; major histocompatibility complex; MHC class II; human lymphocyte antigen;
                                                                                 The present sequence represents a copeptide that can be used to treat autoimmune conditions. It is an example of copeptides of the invention that were designed to bind to the groove of human leukcoyte antigen HIA-DR1 and HIA-DR4 molecules. The copeptides show a high affinity for major histocompatability complex (MHC) class II proteins associated with an autoimmune disease, especially HIA-DR1, HIA-DR2 or HIA-DR4, bind to antigen presenting cells, and inhibit T cell responses. They are especially used to treat multiple sclerosis, autoimmune haemolytic anaemia, autoimmune cophoritis, autoimmune thyroiditis, autoimmune
aliphatic and the other is charged, used to treat autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Copeptide; copolymer 1; autoimmune disease; multiple sclerosis; autoimmune haemolytic anaemia; autoimmune cophoritis; autoimmune thyroiditis; autoimmune uveoretinitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 47; DB 3; Length 15;
Pred. No. 1.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Copeptide useful for treatment of autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                          Claim 82; Page 88; 147pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY58985 standard; peptide; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0101825P.
98US-0102960P.
98US-0108184P.
99US-0123675P.
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91.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15 AA;
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02-OCT-1998
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09-MAR-1999
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The present sequence represents a copeptide that can be used to treat autoimmune conditions. It is an example of copeptides of the invention that were designed to bind to the groove of human leukocyte antigen HLA-DR1 and HLA-DR4 molecules. The copeptides show a high affinity for major histocompatability complex (MHC) class II proteins associated with an autoimmune disease, especially HLA-DR2, HLA-DR2 or HLA-DR2, The antigen presenting cells, and inhibit T cell responses. They are especially used to treat multiple sclerosis, autoimmune haemolytic anaemia, autoimmune cophoritis, autoimmune thyroidatis, autoimmune especiality, disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto of disease, idiopathic myxedema, myasthenia gravis, psomphigus vulgaris, rheumatoid arthritis and systemic lupus erythematosus (all claimed)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MHC class II; major histocompatibility complex; autoimmune disease; inflammatory disease; binding; rheumatoid arthritis; antiinflammatory; antiarthritic; multiple sclerosis.
                                                                                                                                                                                                                                                                     New terpolymers, copeptides and copolymer 1 which contain three amino acids randomly joined in a linear array where one is aromatic, one is aliphatic and the other is charged, used to treat autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                        Fridkis-Hareli M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 47; DB 3;
Pred. No. 1.6;
                                                                                                        Sela M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                     Teitelbaum D, Arnon R,
                                                                                                                                                                                                                                                                                                                                                                                                         Claim 137; Page 69; 147pp; English
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(YEDA ) YEDA RES & DEV CO LTD. (HARD ) HARVARD COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0093859P.
99US-0123675P.
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91.7%;
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                                                                                                                                                                                                      WPI; 2000-182641/16.
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Best Local Similarity
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The present invention describes synthetic peptides having an amino acid sequence comprising at least 3 residues selected from the group of amino acids consisting of aromatic acids, negatively charged amino acids, positively charged amino acids, and alighbatic amino acids, the synthetic peptides being at least 7 amino acid residues in length and capable of binding to a major histocompatibility complex (MHC) class II protein associated with an autorimmune disease. The synthetic peptides have anticinflammatory and anti-arthritic activities. They are used to treat inflammatory and demyelinating autoimmune diseases, especially rheumatoid arthritis and multiple sclerosis. The peptides are specific for particular MHC class II alleles. Purified, short and synthetic peptides should have fewer side effects than mixtures of random peptides; may include many repeats of the active sequence and/or contain amino acid analogues that improve stability (or other desired features). AAV82021 to AAV82044 represent specifically claimed epetide sequences which can be used as part of the synthetic peptides of the present invention; AAV82045 to AAV82061 represent specifically claimed examples of the synthetic peptides of the present invention; AAV82045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptides from the present invention; and AAY82064 to AAY82080 represent other peptides used in the exemplification of the present invention
                             Example 8; Page 32; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 15 AA;
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0; Indels Score 47; DB 3; Length 15 Pred. No. 1.6; , Mismatches 87.0**%**; 91.7**%**; Query Match
Best Local Similarity >\*.

Best 11; Conservative 2 AFAAAAAAAAA 13 3 AYAAAAAAAAA 14 셤 ð

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Gaps

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WHC class II protein binding peptide SEQ ID NO:33. AAY82061 standard; peptide; 15 AA. (first entry) 01-JUN-2000 AAY82061; RESULT 18 

MHC class II; major histocompatibility complex; autoimmune disease; inflammatory disease; binding; rheumatoid arthritis; antiinflammatory; antiarthritic; multiple sclerosis.

Synthetic

WO200005249-A2

03-FEB-2000.

99WO-US016617. 98US-0093859P 22-JUL-1999; 23-JUL-1998;

99US-0123675P. (HARD ) HARVARD COLLEGE 09-MAR-1999;

Fridkis-Hareli WPI; 2000-205374/18. Strominger JL,

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New synthetic peptide, useful for treating autoimmune disease, rheumatoid arthritis.

Claim 24; Page 41; 57pp; English.

The present invention describes synthetic peptides having an amino acid sequence comprising at least 3 residues selected from the group of amino acids consisting of aromatic acids, negatively charged amino acids,

positively charged amino acids, and aliphatic amino acids, the synthetic peptides being at least 7 amino acid residues in length and capable of binding to a major histocompatibility complex (MHC) class II protein associated with an autoimmune disease. The synthetic peptides have anti-inflammatory and anti-arthritic activities. They are used to treat inflammatory and demyelinating autoimmune diseases, especially rheumatoid arthritis and multiple sclerosis. The peptides are specific for particular MHC class II alleles. Purified, short and synthetic peptides should have fewer side effects than mixtures of random peptides; may include many repeats of the active sequence and/or contain amino acid analogues that improve stability (or other desired features). AAY82021 to AAY82044 represent specifically claimed peptide sequences which can be used as part of the synthetic peptides of the present invention; AAY82045 to AAY82063 represent present invention and AAY82060 represent present invention ö The present invention describes synthetic peptides having an amino acid sequence comprising at least 3 residues selected from the group of amino acids consisting of aromatic acids, negatively charged amino acids, positively charged amino acids, and aliphatic amino acids, the synthetic peptides being at least 7 amino acid residues in length and capable of binding to a major histocompatibility complex (MHC) class II procein associated with an autoimmune disease. The synthetic peptides have anti-inflammatory and anti-arthritic activities. They are used to treat inflammatory and demyelinating autoimmune diseases, especially rheumatoid MHC class II; major histocompatibility complex; autoimmune disease; inflammatory disease; binding; rheumatoid arthritis; antiinflammatory; antiarthritic; multiple sclerosis. Gaps New synthetic peptide, useful for treating autoimmune disease, e.g. rheumatoid arthritis. ;; 0 Length 15; 0; Indels MHC class II protein binding peptide SEQ ID NO:27. Score 47; DB 3; Pred. No. 1.6; 1; Mismatches ( Example 8; Page 32; 57pp; English. AAY82077 standard; peptide; 15 AA. Σ Fridkis-Hareli 98US-0093859P 99US-0123675P 87.0%; 91.7%; (first entry) 11; Conservative 2 AFAAAAAAAA 13 4 AYAAAAAAAAA 15 (HARD ) HARVARD COLLEGE WPI; 2000-205374/18. Local Similarity Sequence 15 AA; Strominger JL, WO200005249-A2. 22-JUL-1999; 23-JUL-1998; 09-MAR-1999; 01-JUN-2000 03-FEB-2000. Synthetic AAY82077; Query Match datches RESULT 19 AAY82077 8 g

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particular MHC Class II alleles. Purified, short and synthetic peptides should have fewer side effects than mixtures of random peptides; may include many repeats of the active sequence and/or contain amino acid analogues that improve stability (or other desired features). AAY82021 to AAY82044 represent specifically claimed peptide sequences which can be used as part of the synthetic peptides of the present invention, AAY82045 to AAY82063 represent specifically claimed examples of the synthetic peptides from the present invention; and AAY82064 to AAY82080 represent other peptides used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neuronal degeneration; nerve regeneration; injury; disease; T cell; copolymer 1, Cop 1, spinal cord injury; blunt trauma; trauma; haemorrhaqic stroke; ischeemic stroke; diabetic neuropathy; Bell's palsy; senile dementia; Alzheimer's disease; Parkinson's disease; glaucoma; senile demerve palsy; Huntington's chorea; amyotrophic lateral sclerosis; status epilepticus; non-arteritic optical neuropathy; vitamin deficiency; HIA-DR molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Promoting nerve regeneration or preventing, inhibiting or treating neuronal degeneration caused by injury or disease comprises administering T cells activated by copolymer 1 (Cop 1) or a Cop 1-related peptide or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The specification describes a method for preventing or inhibiting neuronal degeneration, or for promoting nerve regeneration, or treating neuronal degeneration caused by injury or disease. The method comprises administering activated T cells which have been activated by copolymer 1 (Cop 1) or a Cop 1-related peptide or polypeptide; or Cop 1 or a Cop related peptide. The method is used for preventing or inhibiting neuronal degeneration, or for promoting nerve regeneration, or
                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide which binds to peptide binding groove of HLA-DR molecules.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG63197 standard; peptide; 15 AA
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07-JUN-2000; 2000US-0209799P.
20-JUL-2000; 2000US-00620216.
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(MCIN/) MCINNIS
                                                                                                                                                                                                               Sequence 15 AA;
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treating neuronal degeneration caused by injury or disease comprising spinal cord injury, blunt trauma, penetrating trauma, haemorrhagic stroke, ischaemic stroke, diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea, amyotrophic lateral sclerosis, status epilepticus, non-arteritic optical neuropathy, or vitamin deficiency. Cop lor the Cop 1-related peptide or polypeptide is useful in the preparation of a medicament for preventing or inhibiting neuronal degeneration, or for promoting nerve regeneration. AAG63175-AAG63206 represent peptides which bind to the peptide binding groove of HIA-DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Promoting nerve regeneration or preventing, inhibiting or treating neuronal degeneration caused by injury or disease comprises administering T cells activated by copolymer 1 (Cop 1) or a Cop 1-related peptide or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        epilepticus; non-arteritic optical neuropathy; vitamin deficiency;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The specification describes a method for preventing or inhibiting neuronal degeneration, or for promoting nerve regeneration, or treating neuronal degeneration caused by injury or disease. The method comprises administering activated I cells which have been activated by copolymer 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neuronal degeneration; nerve regeneration; injury; disease; T cell; copolymer 1; Copolymer cord injury; blunt trauma; trauma; haemorrhagic stroke; ischaemic stroke; diabetic neuropathy; Bell's palsy senile dementia; Alzheimer's disease; Parkinson's disease; glaucoma; facial nerve palsy; Huntington's chorea; amyotrophic lateral sclerosis;
                                                                                                                                                                                   molecules. The peptides are homologous to the binding motifs of Cop 1, and have similar activities to Cop 1. As such, they may be used in the method of the invention
                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide which binds to peptide binding groove of HLA-DR molecules.
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                                                                                                                                                                                                                                                                                                 Length 15;
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                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                             Score 47; DB 4;
Pred. No. 1.6;
1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sela M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 32; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ä.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG63203 standard; peptide; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-JAN-2000; 2000US-00487793.
07-JUN-2000; 2000US-0209799P.
20-JUL-2000; 2000US-00620216.
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                                                                                                                                                                                                                                                                                               87.0%;
91.7%;
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                                                                                                                                                                                                                                                                                                                                     11; Conservative
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                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              status epileptic
HLA-DR molecule.
                                                                                                                                                                                                                                                             Sequence 15 AA;
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clop 1) or a Cop 1-related peptide or polypeptide; or Cop 1 or a Cop 1-
celated peptide or polypeptide. The method is used for preventing or
inhibiting neuronal degeneration, or for promoting nerve regeneration, or
treating neuronal degeneration, or for promoting nerve regeneration, or
spinal cord injury, blunt trauma, penetrating trauma, haemorrhagic
spinal cord injury, blunt trauma, penetrating trauma, haemorrhagic
stroke, ischaemic stroke, diabetic neuropathy, senile dementia,
Alzheimer's disease, Parkinson's disease, facial nerve (Bell's) palsy,
glaucoma, Huntington's chorea, amyotrophic lateral sclerosis, status
c pilepticus, non-arteritic optical neuropathy, or vitemin deficiency. Cop
cop 1-related peptide or polypeptide is useful in the
preparation of a medicament for preventing or inhibiting neuronal
c degeneration, or for promoting nerve regeneration. Add63175-Ad663206
represent peptides which bind to the peptide binding groove of HuA-DR
molecules. The peptides are homologous to the binding motifs of Cop 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                method of the invention
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Local Similarity 91.7 Les 11; Conservative Sequence 15 AA; Query Match Matches

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Gaps

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Score 47; DB 4; Length 15; Pred. No. 1.6; 1; Mismatches 0; Indels

87.0%; 91.7%;

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AAG63194 standard; peptide; 15 AA AAG63194 

(first entry) 01-OCT-2001 AAG63194;

Neuronal degeneration; nerve regeneration; injury; disease; T cell; copolymer 1; Cop 1; spinal cord injury; blunt trauma; trauma; haemorrhagic stroke; ischaemic stroke; diabetic neuropathy; Bell's palsy; senile dementia; Alzheimer's disease; Parkinson's disease; glaucoma; facial nerve palsy; Huntington's chorea; amyotrophic lateral sclerosis; status epilepticus; non-arteritic optical neuropathy; vitamin deficiency; HLA-DR molecule. Peptide which binds to peptide binding groove of HLA-DR molecules.

Synthetic

WO200152878-A2.

26-JUL-2001

22-JAN-2001; 2001WO-US002117.

20-JAN-2000; 2000US-00487793. 07-JUN-2000; 2000US-0209799P. 20-JUL-2000; 2000US-00620216.

RES & DEV CO LTD. MCINNIS P A. (YEDA ) YEDA (MCIN) Kipnis J; щ Yoles ΣÌ Sela Cohen IR, Eisenbach-Schwartz M,

WPI; 2001-476094/51.

Promoting nerve regeneration or preventing, inhibiting or treating neuronal degeneration caused by injury or disease comprises administering T cells activated by copolymer 1 (Cop 1) or a Cop 1-related peptide or

New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.

WPI; 2002-608439/65.

The present invention describes compositions (I) comprising a peptide

Example 1; Page 30; 54pp; English.

Disclosure; Page 32; 105pp; English

The specification describes a method for preventing or inhibiting

neuronal degeneration, or for promoting nerve regeneration, or treating neuronal degeneration caused by injury or disease. The method comprises administering activated T cells which have been activated by copolymer 1 (Cop 1) or a Cop 1-related peptide or polypeptide; or Cop 1 or a Cop 1-related peptide or polypeptide; or Cop 1 or a Cop 1-related peptide or polypeptide; or Cop 1 or a Cop 1-related peptide. The method is used for preventing or confinibiting neuronal degeneration, or for promoting nerve regeneration, or treating neuronal degeneration caused by injury or disease comprising spinal cord injury, blunt trauma, penetrating trauma, haemorrhagic stroke, ischaemic stroke, diabetic neuropathy, senile dementa, captacke, diabetic neuropathy, senile dementa, captacke, diabetic neuropathy, or vitamin deficiency. Cop cylepticus, non-arteritic optical neuropathy, or vitamin deficiency. Cop 1 or the Cop 1-related peptide or polypeptide is useful in the cop 1-related peptide or polypeptide is useful in the cordinates which bind to the peptide binding groove of HLA-DR collections. The peptides which bind to the binding groove of HLA-DR cancer and have similar activities to Cop 1. As such, they may be used in the ö Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; Gaps ;; 0 Length 15; 0; Indels Score 47; DB 4; Pred. No. 1.6; HLA-DR2 molecule binding peptide SEQ ID NO:10. 1; Mismatches anti-tumour necrosis factor agent. ABP52216 standard; peptide; 15 AA. Fridkis-Hareli M; 24-JAN-2002; 2002WO-US002071. 24-JAN-2001; 2001US-0263569P 87.0%; 91.7%; 16-OCT-2002 (first entry) Best Local Similarity 91.7 Matches 11; Conservative 2 AFAAAAAAAA 13 3 AYAAAAAAAAA 14 (HARD ) HARVARD COLLEGE method of the invention Strominger JL, Sequence 15 AA; WO200259143-A2. sapiens. 01-AUG-2002 Synthetic ABP52216; Query Match Ношо RESULT 23 ABP52216 0Š 셤

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with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility formplex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agents. The peptide further inhibits proliferation of autocantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to ABP52205 represent peptides used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                               invention
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Sequence 15 AA;

Gaps ö Score 47; DB 5; Length 15; Pred. No. 1.6; 0; Indels 1; Mismatches 87.0%; 91.7%; 11; Conservative Local Similarity Query Match Matches

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ABP52286 standard; peptide; 15 AA. RESULT 24

(first entry) 16-OCT-2002 ABP52286;

HLA-DR2 molecule binding peptide SEQ ID NO:80.

Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.

sapiens. Homo

Synthetic.

WO200259143-A2

01-AUG-2002

24-JAN-2002; 2002WO-US002071

24-JAN-2001; 2001US-0263569P.

(HARD ) HARVARD COLLEGE

Fridkis-Hareli M; Strominger JL,

WPI; 2002-608439/65.

New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.

Example 1; Page 34; 54pp; English.

with an amino acid sequence with tyrosine (Y), Iysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine present invention describes compositions (I) comprising a 

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demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
                                             ABP52305 represent peptides used in the exemplification of the present
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0
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                                                                                                                             Score 47; DB 5;
Pred. No. 1.6;
1; Mismatches
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91.7%;
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                                                                                                  Sequence 15 AA;
                                                                  invention
                                                                                                                               Query Match
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RESULT 25

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ABP52212 standard; peptide; 15 **ABP52212** 

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ABP52212;

(first entry) 16-OCT-2002 HLA-DR2 molecule binding peptide SEQ ID NO:6.

Human leukocyte antigen, HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; fimune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.

sapiens. Synthetic. WO200259143-A2.

01-AUG-2002

24-JAN-2002; 2002WO-US002071.

24-JAN-2001; 2001US-0263569P.

(HARD ) HARVARD COLLEGE

Fridkis-Hareli Strominger JL,

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WPI; 2002-608439/65

New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis. 

Example 1; Page 30; 54pp; English.

with an amino acid sequence with typesite. It is the properties of the peptide with a major histocompatibility complex of the peptide with a major histocompatibility complex (MHC) class II History protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to ABP52205 represent peptides used in the exemplification of the present present invention describes compositions (I) comprising a peptide invention

Sequence 15 AA;

4 AYAAAAAAAAA 15

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The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions compositions the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABPS5207 to ABPS5205 represent peptides used in the exemplification of the present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.
                                                                                                                                                                                                                                                                                                                          Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition;
                                   Gaps
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Pred. No. 1.6;
1; Mismatches 0; Indels
Length 15;
                                 0; Indels
 5;
                                                                                                                                                                                                                                                                                            HLA-DR2 molecule binding peptide SEQ ID NO:8.
DB 5
1.6;
                                   Mismatches
 Score 47;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 30; 54pp; English.
                                                                                                                                                                                          ABP52214 standard; peptide; 15 AA
                                                                                                                                                                                                                                                                                                                                                                                                                  anti-tumour necrosis factor agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fridkis-Hareli M;
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Best Local Similarity 91.7%;
Matches 11; Conservative
 87.0%;
91.7%;
                                                                                                                                                                                                                                                             (first entry)
                                   11; Conservative
                                                                     AFAAAAAAAAA 13
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 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        sapiens.
                                                                                                                                                                                                                                                             16-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
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                                   Matches
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with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted I cell clones. ABP52207 to ABP52305 represent peptides used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral
                                                                                                                                                         Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present invention describes compositions (I) comprising a peptide
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                                                                                                                         HLA-DR2 molecule binding peptide SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADJ57538 standard; peptide; 15 AA.
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               ABP52210 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fridkis-Hareli M;
                                                                                                                                                                                                                                                                                                                                                                                                                                        24-JAN-2002; 2002WO-US002071.
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                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                           WO200259143-A2
                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                          16-OCT-2002
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                                                                                                                                                                                                                                                                                                                          Synthetic.
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                                                     ABP52210;
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ADJ57538
ID ADJ57
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ADJ57538;

Synthetic

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The invention relates to a vaccine that comprises an active agent from Copolymer I (Cop-1), Cop-1 related peptide, Cop-1 related polypeptide or poly-Glu, Tyr. The vaccine comprises the active agent without adjuvant or is emulsified in an adjuvant. The vaccine is useful for reducing disease progression and/or protection of motor nerve degeneration and/or protection of motor neuron disease e.g. protection from glutamate toxicity in motor neuron disease e.g. muscular atrophic lateral sclerosis, primary lateral sclerosis, progressive muscular atrophy, progressive bulbar palsy (PBP or bulbar onset). It may be used in combination with another drug e.g. Riluzole for treating motor neuron disease. The non-pathogenic synthetic copolymers protects autoimmunity and thus reduces further injury-induced damage and protects central nervous system cells from glutamate toxicity; protects retinal cop-1 related-peptide.
                                                                                                                                                                                                                                                                    Vaccine useful in the treatment of motor neuron disease e.g. amyotrophic lateral sclerosis and progressive muscular atrophy, comprises copolymer-1 or related peptide or polypeptide, or poly-Glu, Tyr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cop-1; copolymer 1; vaccine; neuroprotective; glutamate toxicity; motor neuron disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADJ57541 standard; peptide; 15 AA.
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                                                                                                                                                                                    Yoles E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yoles E;
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                                                          05-DEC-2002; 2002WO-IL000979.
                                                                                                 06-DEC-2001; 2001US-0336139P.
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                                                                                                                                           (YEDA ) YEDA RES & DEV
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                                                                                                                                                                                    Eisenbach-Schwartz M,
                                                                                                                                                                                                                           WPI; 2003-569005/53.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 15 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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ADJ57541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a vaccine that comprises an active agent from Copolymer 1 (Cop-1), Cop-1 related peptide, Cop-1 related polypeptide or poly-Glu,Tyr. The vaccine comprises the active agent without adjuvant or is emulsified in an adjuvant. The vaccine is useful for reducing disease protection and/or protection of motor nerve degeneration and/or protection from glutamate toxicity in motor neuron disease e.g. amylotrophic lateral sclerosis, primary lateral sclerosis, progressive muscular atrophy, progressive bulbar palsy (PBP or bulbar onset). It may be used in combination with another drug e.g. Riluzole for treating motor neuron disease. The non-pathogenic synthetic copolymers protects central nervous system calls from glutamate toxicity; protects retinal ganglion cells from glutamate toxicity. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vaccine useful in the treatment of motor neuron disease e.g. amyotrophic lateral sclerosis and progressive muscular atrophy, comprises copolymer-1 or related peptide or polypeptide, or poly-Glu, Tyr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cop-1; copolymer 1; vaccine; neuroprotective; glutamate toxicity;
                                                                                                                     Cop-1; copolymer 1; vaccine; neuroprotective; glutamate toxicity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
0
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0
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 20; 49pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADJ57547 standard; peptide; 15 AA.
                                                                              Cop-1 related-peptide, SEQ ID 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cop-1 related-peptide, SEQ ID 29
                                                                                                                                                                                                                                                                                                                                                                                              (YEDA ) YEDA RES & DEV CO LTD
                                                                                                                                                                                                                                                                                                           05-DEC-2002; 2002WO-IL000979.
                                                                                                                                                                                                                                                                                                                                                     06-DEC-2001; 2001US-0336139P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87.0%;
                                  06-MAY-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Eisenbach-Schwartz M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cop-1 related-peptide
                                                                                                                                           motor neuron disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-569005/53.
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Best Local Similarity
                                                                                                                                                                                                                         WO2003047500-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15 AA;
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Synthetic

EXSXXXXXXXXXXXXXXXX

RESULT 29 ADJ57547

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Gaps

; 0

Score 47; DB 7; Length 15; Pred. No. 1.6; 1; Mismatches 0; Indels Copolymer 1-related peptide SEQ ID NO:23. ADQ59600 standard; peptide; 15 AA. 07-JAN-2003; 2003US-0438310P. D6-JAN-2004; 2004WO-IL000006 91.78; (first entry) 11; Conservative 2 AFAAAAAAAAA 13 3 AYAAAAAAAAA 14 Query Match Best Local Similarity WO2004060265-A2. Sequence 15 AA; 07-OCT-2004 22-JUL-2004. Synthetic. AD059600; Matches RESULT 31 ADQ59600 à 셤 

The invention relates to a vaccine that comprises an active agent from Copolymer 1 (Cop-1), Cop-1 related peptide, Cop-1 related polypeptide or poly-Glu, Tyr. The vaccine comprises the active agent without adjuvant or is emulaified in an adjuvant. The vaccine is useful for reducing disease progression and/or protection of motor nerve degeneration and/or protection of motor nerve degeneration and/or protection of motor nerve degeneration and/or protection from glutamate toxicity in motor neuron disease e.g. amylotrophic lateral sclerosis, primary lateral sclerosis, progressive muscular atrophy, progressive bulbar palsy (PBP or bulbar onset). It may be used in combination with another drug e.g. Riluzole for treating motor neuron disease. The non-pathogenic synthetic copolymers protects autoimmunity and thus reduces further injury-induced damage and protects central nervous system cells from glutamate toxicity; protects retinal ganglion cells from glutamate toxicity. The present sequence represents a Cop-1 related-peptide. Vaccine useful in the treatment of motor neuron disease e.g. amyotrophic lateral sclerosis and progressive muscular atrophy, comprises copolymer-1 or related peptide or polypeptide, or poly-Glu, Tyr. Disclosure; SEQ ID NO 23; 49pp; English.

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Gaps . 0

eye-drop vaccine; eye drop; vaccine; immunisation; Copolymer 1; Copolymer 1 related peptide; ophthalmological; neuroprotective; nootropic; antiparkinsonian; anticonvulsant; analgesic; antidabetic; hepatotropic; respiratory; osteopathic; neuronal degeneration; central nervous system; CNS; peripheral nervous system; PNS; glutamate toxicity; spinal cord injury; blunt trauma; haemorrhagic stroke; ischaemic stroke; senile dementia; haltoeimer's disease; parkinson's disease; motor neuron disease; amyotrophic lateral sclerosis; prion disease; Creutzfeldt-Jakob disease; vitamin deficiency; epilepsy; amnesia; anxiety; autoimmune disease; multiple sclerosis; peripheral neuropathy; retinal disorder; glaucoma.

(YEDA ) YEDA RES & DEV CO LTD

Bakalash S, Eisenbach-Schwartz M,

Fulga V;

WPI; 2004-543774/52

Eye-drop vaccine for the therapeutic immunization of a mammal against glaucoma and neuronal degeneration caused by a disease in the central or

1-related polypeptide. (1) has ophthalmological, neuroprotective, notropic, antiparkinsonian, anticonvulsant, analgesic antidiabetic, hopatotropic, respiratory and osteopathic activities. The eye-drop vaccine (1) can be used for treating or preventing neuronal degeneration in the central caused by an injury, disease of sorter or condition in the central nervous system (CNS) or peripheral nervous system (PNS), for preventing or inhibiting neuronal secondary degeneration which may otherwise follow or in the PNS after an injury, disease, disorder or condition or for protecting CNS and PNS cells from glutamate toxicity, where the injury is spinal cord injury, blunt traum, penetrating traum, brain coup or contrecoup, haemorrhagic stroke or ischemic stroke, and where the disease is a semile demental including Parkinson's disease, and where the injury is spinal cord injury, blunt traum, contraction stroke, and where the disease is a semile demental including Parkinson's disease, and where the injury is spinal cord injury, bluntington's chorea, a motor neuron disease including aparkinson's disease, and where the injury is appropriate polary disease, aparten disease, and where the injury is anytopic lateral sclerosis, a prion disease, including parkinson's disease, and disease, and dependence, and autoimmune disease including disease, status epilepticus, carpal tunnel syndrome, indury carbot disease, anytome, antoimmune disease, acute such as amyloid polymeuropathy, hypedyscamia, sjocyen-lateson syndrome, acute sensory neuropathy, diabetic neuropathy, uremic neuropathy, chronic ataxic neuropathy, uremic neuropathy, chronic ataxic neuropathy, billary cirrhosis, primary auch as alcohol or organophosphates, charcet Marie-Tooth disease, actinal control and alcendance and derendance, and autoimmune disease control and alcohol or organophosphates, charcet Marie-Tooth disease, actinal derendance and alcendance and derendance and elemental recordance and control and alcohol or organophosphates, charcet Marie-Tooth disease, acti The present invention describes an eye-drop vaccine (I) for the therapeutic immunisation of a mammal. (I) comprises an active agent selected from Copolymer 1, a Copolymer 1-related peptide, and a Copolymer 1-related polypeptide. (I) has ophthalmological, neuroprotective, peripheral nervous system (e.g. Alzheimer's disease), comprises Copolymer such as retinal degeneration, or a disease associated with 1y elevated intraocular pressure such as glaucoma. The present represents a copolymer 1 related peptide, which is given in the exemplification of the present invention. Disclosure; SEQ ID NO 23; 49pp; English abnormally elevated disorder 

Sequence 15 AA;

Gaps . Score 47; DB 8; Length 15; Pred. No. 1.6; 0; Indels Mismatches 87.0%; 91.7%; Local Similarity 91.7 Query Match fatches

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ADQ59606 standard; peptide; 15 AA. ADQ59606; ADQ59606 셤

Copolymer 1-related peptide SEQ ID NO:29. 

(first entry)

07-0CT-2004

eye-drop vaccine; eye drop; vaccine; immunisation; Copolymer 1; Copolymer 1-related peptide; ophthalmological; neuroprotective; nootropic; antiparkinsonian; anticonvulsant; analgesic; antidiabetic; hepatactropic; respiratory; osteopathic; neuronal degeneration; central nervous system; CNS; peripheral nervous system; PNS; dlutamate toxicity; spinal cord injury; blunt trauma; haemorrhagic stroke; ischaemic stroke; senile dementia;

Alzheimer's disease; Parkinson's disease; motor neuron disease; amyotrophic lateral sclerosis; prion disease; Creutzfeldt-Jakob disease; vitamin deficiency; epilepsy; amnesia; anxiety; autoimmune disease; multiple sclerosis; peripheral neuropathy; retinal disorder; glaucoma. Bakalash S, Fulga V; (YEDA ) YEDA RES & DEV CO LTD 06-JAN-2004; 2004WO-IL000006. 07-JAN-2003; 2003US-0438310P. Eisenbach-Schwartz M, WPI; 2004-543774/52. WO2004060265-A2 22-JUL-2004 Synthetic. 

Eye-drop vaccine for the therapeutic immunization of a mammal against glaucoma and neuronal degeneration caused by a disease in the central or peripheral nervous system (e.g. Alzheimer's disease), comprises Copolymer

Disclosure; SEQ ID NO 29; 49pp; English.

vaccine (1) can be used nor freating or preventing neuronal degeneration caused by an injury, disease, disorder or condition in the central nervous system (CNS) or peripheral nervous system (PNS), for preventing or inhibiting neuronal secondary degeneration which may otherwise follow a primary injury in the CNS, for promoting nerve regeneration in the CNS or in the PNS after an injury, disease, disorder or condition or for protecting CNS and PNS cells from glutamate toxicity, where the injury is spinal cord injury, blunt trauma, penetrating trauma, brain coup or contraccoup, hemorrhagic stroke or lschaemic stroke, and where the disease is a senile dementia including Alzheimer's disease, a contraccoup, hemorrhagic stroke or lschaemic stroke, and where the disease is a senile dementia including Alzheimer's disease, a motor neuron disease, a park inspection or for contraccoup, hemorrhagic stroke or lschaemic stroke, and where the disease, status spilepticus, carpal tunnel syndrome, intervertebral appropriate disease, cockaptne syndrome, intervertebral disc herniation, vitamin deficiency such as vitamin B deficiency, cord strokes, opiate tolerance and dependence, an autoimmune disease (e.g. multiple sclerosis), or a peripheral neuropathy, uremic neuropathy, cornic ataxic neuropathy sascoiated with a disease such as amyloidosis, obstructive lung diseases, acromegaly, malabsorption syndromes, polycythemia vera, igA and igG gammapathies, complications of such as alcohol or organophosphates, charcel-Marie-Tooth disease, ataxia celasoratic optic neuropathy, agreenomy adrenomyeloneuropathy, agreening such as alcohol or organophosphates, charcel-Marie-Tooth disease, ataxia celasoratic optic neuropathy, agreening accountant disease, ataxia disease associated with a retinal degeneration, or a disease, important on a multiple scenarion, a retinal disease, charced and course of intractors are in the course of the proportion of interventing disease, in the course of the proportion of the course of the course of the course of t The present invention describes an eye-drop vaccine (I) for the therapeutic immunisation of a mammal. (I) comprises an active agent selected from Copolymer 1, a Copolymer 1-related peptide, and a Copolymer 1-related polypeptide. (I) has ophthalmological, neuroprotective, nootropic, antiparkinsonian, anticonvulsant, analgesic, antidiabetic, hepatotropic, respiratory and osteopathic activities. The eye-drop vaccine (I) can be used for treating or preventing neuronal degeneration abnormally elevated intraocular pressure such as glaucoma. The present sequence represents a copolymer 1 related peptide, which is given in the exemplification of the present invention.

Sequence 15 AA;

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                      Gaps
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0
 Score 47; DB 8; Length 15;
Pred. No. 1.6;
                    Indels
                    ;
0
                   1; Mismatches
87.0%;
91.7%;
                    11; Conservative
          Best Local Similarity
 Query Match
                    Matches
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caused by an injury, disease, disorder or condition in the central nervous system (CNS) or peripheral nervous system (PNS), for preventing or inhibiting neuronal secondary degeneration which may otherwise follow a primary injury in the CNS, for promoting nerve regeneration in the CNS or in the PNS after an injury, disease, disorder or condition or for protecting CNS and PNS cells from glutamate toxicity, where the injury is spinal cord injury, blunt trauma, penetrating trauma, brain coup or contrecoup, haemorrhagic stroke or ischaemic stroke, and where the contrecoup, haemorrhagic stroke or ischaemic stroke, and where the contrecoup, haemorrhagic stroke or ischaemic stroke, and where the parkinsonian syndrome including Parkinson's disease, facial nerve (Bell's) palsy, Huntington's chorea, a motor neuron disease including amyotrophic lateral sclerosis, a prion disease including Creutifeldt. Jakob disease, Alper's disease, Batten disease, Cockayne syndrome, Lewy body disease, status epilepticus, carpal tunnel syndrome, intervertebral disc herniation, vitamin deficiency such as vitamin B deficiency,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eye-drop vaccine for the therapeutic immunization of a mammal against glaucoma and neuronal degeneration caused by a disease in the central or peripheral nervous system (e.g. Alzheimer's disease), comprises Copolymer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copolymer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              noctropic, antiparkinsonian, anticonvulsant, analgesic, antidiabetic, hepatotropic, respiratory and osteopathic activities. The eye-drop vaccine (I) can be used for treating or preventing neuronal degeneration
                                                                                                                                                                                                                                                                                                                                                                              Copolymer 1-related peptide, ophthalmological; neuroprotective; nootropic; antiparkinsonian; anticonvulsant; analgesic; antidabetic; hepatotropic; respiratory; osteopathic; nervonal degeneration; central nervous system; CNS; peripheral nervous system; PNS; all tamate toxicity; spinal cord injury; blunt trauma; haemorrhagic stroke; ischaemic stroke; senile dementia; Alzheimer's disease; Parkinson's disease; motor neuron disease; amyotrophic lateral sclerosis; prion disease; Creutzfeldt-Jakob disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vitamin deficiency; epilepsy; amnesia; anxiety; autoimmune disease; multiple sclerosis; peripheral neuropathy; retinal disorder; glaucoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            therapeutic immunisation of a mammal. (I) comprises an active agent selected from Copolymer 1, a Copolymer 1-related peptide, and a Copol-related polypeptide. (I) has ophthalmological, neuroprotective,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present invention describes an eye-drop vaccine (I) for the
                                                                                                                                                                                                                                                                                                                                                             eye-drop vaccine; eye drop; vaccine; immunisation; Copolymer 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fulga V;
                                                                                                                                                                                                                                                                                                           Copolymer 1-related peptide SEQ ID NO:20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 20; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bakalash S,
                                                                                                                                                                  ADQ59597 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RES & DEV CO LTD.
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                                                                                                                                                                                                                                                             07-OCT-2004 (first entry)
                           |:|||||||||
| AYAAAAAAAAA 15
2 AFAAAAAAAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eisenbach-Schwartz M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-543774/52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                ADQ59597;
                                                                                                                                            4DQ59597
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stress, opiate tolerance and dependence, an autoimmune disease (e.g. multiple sclerosis), or a peripheral neuropathy associated with a disease wuch as amyloid polymeuropathy, diabetic neuropathy uremic neuropathy, popplydemena, sologren-Larsson syndrome, acute sensory neuropathy, chronic ataxic neuropathy, biliary circhosis, primary syndromes, polycythemia vera, IgA and IgG ammapathies, complications of various drugs such as nitrofurantoin, metronidazole, isoniazid and toxins such as alcohol or organophosphates, Charcot-Marie-Tooth disease, ataxia telangiectasia, Friedreich's ataxia, adrenomyeloneuropathy, giant axonal neuropathy, Refsum's disease, Patry's disease, lipoproteinemia, non-arteritic optic neuropathy, age-related macular degeneration, a retinal disonater such as retinal degeneration, or a disease associated with abnormally elevated intraocular pressure such as glaucoma. The present sequence represents a copolymer I related peptide, which is given in the amnesia, anxiety, hyperalgesia, psychosis, seizures, oxidative exemplification of the present invention. %

Sequence 15 AA;

Gaps .. 0 Score 47; DB 8; Length 15; Pred. No. 1.6; 1; Mismatches 0; Indels 87.0%; 91.7%; 11; Conservative Local Similarity Query Match Matches

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2 AFAAAAAAAA 13 AYAAAAAAAA 14

ò 셤 RESULT 34 ADQ8122

ADQ81224 standard; peptide; 15 AA. (first entry) 21-OCT-2004 ADQ81224; 

pharmaceutical composition; copolymer 1; copolymer 1-related polypeptide; copolymer 1-related peptide; inflammatory bowel disease; antiinflammatory; antiulcer; gastrointestinal; regulatory T cell inducer; Crohn's disease; ulcerative colitis. Copolymer 1-related peptide SEQ ID NO:20.

Synthetic.

WO2004064717-A2.

05-AUG-2004

20-JAN-2004; 2004WO-IL000054.

21-JAN-2003; 2003US-0441136P.

(YEDA ) YEDA RES & DEV CO LTD.

Kayhan B; Aharoni R, Arnon R,

WPI; 2004-571593/55.

Composition useful for the treatment of a patient suffering from an inflammatory bowel disease comprises an active agent selected from copolymer 1, a copolymer 1-related polypeptide, and a copolymer 1-related

Kayhan B;

Aharoni R, Arnon R, WPI; 2004-571593/55.

(YEDA ) YEDA RES & DEV CO LTD.

20-JAN-2004; 2004WO-IL000054. 21-JAN-2003; 2003US-0441136P.

WO2004064717-A2.

05-AUG-2004.

Example 2; SEQ ID NO 29; 55pp; English.

peptide and a carrier

The present invention describes a pharmaceutical composition comprising an active agent selected from copolymer 1, a copolymer 1-related peptide and a carrier. Also described is an article of manufacture comprising packaging material and the pharmaceutical composition (preferably containing copolymer 1) contained within the packaging material. The packaging material includes a label that indicates that the agent is used for treating an inflammatory bowel disease. The pharmaceutical composition has antiinflammatory, antiulcer and gastrointestinal activities, and can be

Composition useful for the treatment of a patient suffering from an inflammatory bowel disease comprises an active agent selected from copolymer 1, a copolymer 1-related polypeptide, and a copolymer 1-related peptide and a carrier.

The present invention describes a pharmaceutical composition comprising an active agent selected from copolymer 1, a copolymer 1-related oblypeptide, and a copolymer 1-related peptide and a carrier. Also described is an article of manufacture comprising packaging material and the pharmaceutical composition (preferably containing copolymer 1) contained within the packaging material. The packaging material includes Example 2; SEQ ID NO 20; 55pp; English.

ö pharmaceutical composition; copolymer 1; copolymer 1-related polypeptide; copolymer 1-related peptide; inflammatory bowel disease; antiinflammatory; antiulcer; gastrointestinal; regulatory T cell inducer; Crohn's disease; ulcerative colitis. a label that indicates that the agent is used for treating an inflammatory bowel disease. The pharmaceutical composition has antiinflammatory, antiulder and gastrointestinal activities, and can be used as an inducer of regulatory T colls of the Th2 type. It can be used for the treatment of a patient suffering from an inflammatory bowel disease e.g. Crohn's disease and ulcerative colitis. The copolymer 1 binds promiscuously and with high affinity to various classes II MHC molecules of mouse and human origin, and can even displace antigens from the MHC antigen-binding groove. In this way, the presentation of other antigens and, consequently, the persistence of inflammatory process, are down regulated. In addition, Copolymer 1 is a potent inducer of regulatory T cells of the Th2 type. The present sequence represents a copolymer 1 related peptide which is used in the exemplification of the Gaps ö Score 47; DB 8; Length 15; Pred. No. 1.6; 0; Indels 1; Mismatches Copolymer 1-related peptide SEQ ID NO:29. ADQ81233 standard; peptide; 15 AA. 87.0%; 91.7%; 21-OCT-2004 (first entry) 11; Conservative 2 AFAAAAAAAA 13 14 3 AYAAAAAAAAA Local Similarity present invention. Sequence 15 AA; Synthetic. ADQ81233; Query Match Matches ADQ81233 ò g

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used as an inducer of regulatory T cells of the Th2 type. It can be used discase e.g. cron's disease and ulcerative colitis. The copolymer 1 binds promiscuously and with high affinity to various classes II MHC molecules of mouse and with high affinity to various classes II MHC molecules of mouse and human origin, and can even displace antigens from antigens and, consequently, the persistence of inflammatory process, are down regulated. In addition, Copolymer 1 is a potent inducer of regulatory T cells of the Th2 type. The present sequence represents a copolymer 1 related peptide which is used in the exemplification of the
                                                                                                                                                                                                                                                                                        present invention
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Sequence 15 AA;

Score 47; DB 8; Length 15; Pred. No. 1.6; Indels .; 0 Mismatches 87.0%; 91.7%; Conservative 13 AYAAAAAAAA 15 2 AFAAAAAAAA Query Match Best Local Similarity 11; Matches

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Gaps

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ADQ81227 standard; peptide; 15 (first entry) 21-OCT-2004 ADQ81227; RESULT 36 ADQ81227 

Ā

pharmaceutical composition; copolymer 1; copolymer 1-related polypeptide; copolymer 1-related peptide; inflammatory bowel disease; antiinflammatory; antiulcer; gastrointestinal; regulatory T cell inducer; crohn's disease; ulcerative colltis. Copolymer 1-related peptide SEQ ID NO:23.

Synthetic

WO2004064717-A2.

05-AUG-2004

20-JAN-2004; 2004WO-IL000054.

2003US-0441136P. 21-JAN-2003;

(YEDA ) YEDA RES & DEV CO LID.

Kayhan B; Aharoni R, Arnon R,

WPI; 2004-571593/55.

Composition useful for the treatment of a patient suffering from an infilammentory bowel disease comprises an active agent selected from copolymer 1, a copolymer 1-related polypeptide, and a copolymer 1-related peptide and a carrier.

Example 2; SEQ ID NO 23; 55pp; English.

an active agent selected from copolymer 1, a copolymer 1-related polypeptide, and a copolymer 1-related peptide and a carrier. Also described is an article of manufacture comprising packaging material and the pharmaceutical composition (preferably containing copolymer 1) contained within the packaging material. The packaging material includes inflammatory bowel disease. The pharmaceutical composition has antilnflammatory, antilucer and gastrointestinal activities, and can be used as an inducer of regulatory T cells of the Th2 type. It can be used for the treatment of a patient suffering from an inflammatory bowel The present invention describes a pharmaceutical composition comprising disease e.g. Crohn's disease and ulcerative colitis. The copolymer 1

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This invention relates to a novel method for treating or preventing graft rejection. Specifically, it refers to administering at least one copolymer 1 or its related heteropolymer with at least one immunosuppressive drug. The present invention describes the copolymer as containing at least three different amino acids each selected from at least three of the following groups: lysine and arginine; glutamic acid and appartic acid; alamine, glycine and alamine; and tyrosine, tryptophan and phenylalanine. In addition, the immunosuppressive drug is an antiprofilerative drug, inhibitor of lymphocyte activation, steroid, purine antimetabolite, antibody or immunosuppressive activation, steroid, purine antimetabolite, antibody or immunoadulator. Accordingly, these immunosuppressive compositions can be used for treating or preventing or graft rejection associated with transplantation of cells, tissue or organs (HiA-matched or mismatched) selected from hematopoietic cells, tend the cells, heart, lung, kidney, liver or skin. The copolymer lor its related heteropolymer in combined the accordance of the copolymer in combined to the cells, and articles the copolymer in combined to the copolymer or its accordance of the copolymer in combined to the copolymer in copolymer in
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binds promiscuously and with high affinity to various classes II MHC molecules of mouse and human origin, and can even displace antigens from the MHC antigen-binding groove. In this way, the presentation of other antigens and, consequently, the persistence of inflammatory process, are down regulated. In addition, Copolymer I is a potent inducer of regulatory T cells of the TAZ type. The present sequence represents a copolymer 1-related peptide which is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ordered copolymer peptide used to treat graft versus host disease Seq 29
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                                                                                                                                                                                                                                                                                                                    Length 15,
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                                                                                                                                                                                                                                                                                                                    89
                                                                                                                                                                                                                                                                                                                    Score 47; DB 8
Pred. No. 1.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADW86548 standard; peptide; 15 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2005-152159/16.
                                                                                                                                                                                                        present invention.
                                                                                                                                                                                                                                                          Sequence 15 AA;
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This invention relates to a novel method for treating or preventing graft rejection. Specifically, it refers to administering at least one copolymer 1 or its related heteropolymer with at least one copolymer 1 or its related heteropolymer with at least one containing at least three different amino acids each selected from at containing at least three different amino acids each selected from at class three of the following groups: lysine and arginine; glutamic acid and aspartic acid; alanine, glycine and alanine; and tyrosine, tryptophan antimerabolite, antibody or immunosuppressive drug is an cantiporoliferative drug, inhibitor of lymphocyte activation, steroid, purine antimetabolite, antibody or immunomodulator. Accordingly, these immunosuppressive compositions can be used for treating or preventing graft rejection associated with transplantation of cells, tissue or cramated heteropolymer in combination which other immunosuppressive drugs in combination with other immunosuppressive drugs in the content immunosuppressive drugs in the content immunosuppressive froms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treating or preventing graft rejection associated with transplantation of cells, tissue or organs comprises administering combination comprising copolymer 1 or its related heteropolymer with immunosuppressive drug for.
                                                                                                                                                                                                                                                                                                                                                                                                   Ordered copolymer peptide used to treat graft versus host disease Seg 23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         increases the effectiveness of the drugs at lower dosages, reducing side effects such that they are useful for host-versus-graft (HVG) response, as well as graft-versus-host disease (GVHD). This peptide sequence is an ordered copolymer of the invention.
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Pred. No. 1.6;
1; Mismatches 0; Indels
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  Pred. No. 1.6; ; Mismatches
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                                                                                                                                                                                                                                                           ADW86542 standard; peptide; 15 AA.
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L Similarity 91.7%;
11; Conservative
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Best Local Similarity 91.7
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention relates to a novel method for treating or preventing graft rejection. Specifically, it refers to administering at least one cooplymer or its related heteropolymer with at least one immunosuppressive drug. The present invention describes the copolymer as containing at least three different amino acids each selected from at least three of the following groups: lysine and arginine; glutamic acid and aspartic acid; alanine, glycine and alanine; and tyrosine, tryptophan and phenylalanine. In addition, the immunosuppressive drug is an addition, the immunosuppressive drug is an addition.
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     response, as well as graft-versus-host disease (GVHD). This peptide sequence is an ordered copolymer of the invention.
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                                                                                                                                        Length 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          graft rejection; immunosuppressive; immunomodulator;
                                                                                                                                   Score 47; DB 9;
Pred. No. 1.6;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                           ADW86539 standard; peptide; 15 AA.
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                                                                                                                                        87.0%;
91.7%;
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                                                                                      Sequence 15 AA;
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RESULT 38
ADM86539
ID ADM86539
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XX WO200
XX WO

Synthetic

ADW86539;

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Gaps

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Query Match

lower dosages, reducing toxic

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Mon Sep 11 15:00:11 2006
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This peptide represents a peptide derived from Cop 1 (Copolymer 1). This peptide was tested for binding to the peptide binding groove of HLA-DR. The method of the invention for treating a neurodegenerative disorder or disease in which there is accumulation of misfolded and/or aggregated proteins, excluding prion-related diseases, comprises administering to an individual an agent selected from Copolymer 1, a Copolymer 1-related polypeptide, and T cells activated with the invention also includes methods for: reducing disease them. The invention also includes methods for: reducing disease protection from glutamate toxicity in a patient suffering from a neurodegenerative disease or disorder selected from Huntington's disease, Alzheimer's disease or disease or disease or disease and parkinson's disease, Alzheimer's disease, Alzheimer's disease or Parkinson's disease. Specifically, treating a patient suffering from a neurodegenerative disease immunizing the patient with a vaccine comprises in membral disease progression or for protection from neurodegeneration in the patient. A pharmaceutical composition as administered in the method above, is useful for reducing disease procression, and/or for protection from neurodegeneration in the patient. A pharmaceutical composition as protection from glutamate toxicity in a patient suffering from the neurodegeneration in the method above, is useful for reducing disease procression, and/or for protection from neurodegeneration, and/or for protection from enurodegeneration, and/or in patient suffering from the neurodegeneration in the neurodegeneration, and/or in the method above, is useful for reducing disease procression, and/or for protection from enurodegeneration, and/or dor protection from enurodegeneration or disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alzheimer's disease or Parkinson's disease. The active agent is useful for manufacturing a medicament for treatment of neurodegenerative disorder or disease in which there is accumulation of misfolded and/or aggregated proteins, excluding prion-related diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Treating a neurodegenerative disorder or disease where there is accumulation of misfolded and/or aggregated proteins e.g. Parkinson's disease comprises using an agent e.g. Copolymer 1 or a Copolymer 1-related peptide.
                                                                                                                                                                                                                  Anticonvulsant; Nootropic; Neuroprotective; Antiparkinsonian; Cop 1; Copolymer 1; HLA-DR; neurodegenerative disease; glutamate toxicity; Huntingtons disease; Alzheimers disease; Parkinsons disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 20; 63pp; English.
                  AEA35261 standard; peptide; 15 AA.
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                                                                                                                     28-JUL-2005 (first entry)
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Search completed: September 9, 2006, 22:48:09 Job time : 99.4177 secs

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                                                                                           1.; Search time 13.6709 Seconds (without alignments) 84.457 Million cell updates/sec
GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd
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ALIGNMENTS

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A;Accession: T03285
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule: 1-94 <LEE5
A;Cross-references: UNIPROT:Q40629; UNIPARC:UPI00000A8A96; EMBL:U12171; NID:g607894; PID
A;Experimental source: strain IR54
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A;Residues: 1-299,'L',301-376 <FRA>
A;Cross-references: UNIPARC:UPI0000124746; GB:X05138; NID:97957; PIDN:CAA28784.1; PID:97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-376 <MAC>
A;Cross-references: UNIPROT:P06602; UNIPARC:UP1000016BBE4; GB:M14767; NID:g157386; PIDN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cispecies: Drosophila melanogaster
Cipate: 25-Oct-1917 #sequence revision 25-Oct-1987 #text_change 31-Dec-2004
Cipate: 25-Oct-1917 #sequence revision 25-Oct-1987 #text_change 31-Dec-2004
Cipate: 25-Oct-1917 #sequence revision 25-Oct-1987 #text_change 31-Dec-2004
Cipate 17 721-734, 1986
Arithe: Isolation, structure, and expression of even-skipped: a second pair-rule gene Arieference number: A26066; MuID:87051744; PMID:2877745
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A,Residues: 32-268;279-376 <MA2>
A,Cross-references: UNIPARC:UP1000017A27C; UNIPARC:UP1000017A27D; GB:M14767
A;Cross-references: UNIPARC:UP1000017A27C; UNIPARC:UP100017A27D; GB:M14767
B;Frasch, M.; Hoey, T.; Rushlow, C.; Doyle, H.; Levine, M.
BMBO J. 6, 749-759, 1987
A;Title: Characterization and localization of the even-skipped protein of Drosophila.
A;Reference number: A26636; MUID:87218536; PMID:2884106
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C;Species: Oryza sativa (rice)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
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C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;71-127/Domain: homeobox homology <HOX>
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                                     CyAccession: T03285
RyLee, J.Y.K.; Hodges, T.K.
submitted to the EMBL Data Library, July 1994
A;Description: Genomic DNA sequence of a rice anther-specific gene.
A;Reference number: Z14882
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Pred. No. 79;
1; Mismatches
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Matches 10; Conservative
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Matches 10; Conserv
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A;Gene: RTS2
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                                                                                                                         hypothetical protein Vng1530h [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Baccies: Halobacterium sp. NRC-1
C;Baccession: F84306
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablc Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
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A;Molecule type: mRNA
A;Residues: 143-158,'P',160-218 <STE2>
A;Cross-references: UNIPARC:UPI0000071C8Ç; EMBL:X71137; NID:g468793; PIDN:CAA50467.1; PI
C;Genetics:
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A;Residues: 1-443 <STE1>
A;Cross-references: UNIPROT:P41225; UNIPARC:UPI000003F546; EMBL:X71135; NID:9468790; PID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-85 <STO>
A;Cross-references: UNIPROT:Q9HPP9; UNIPARC:UPI0000638F2; GB:AE004437; NID:g10581018;
C;Genetics:
A;Gene: VNG1530H
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NyAlternate names: SRY (sex determining region Y)-box 3
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sext_change 09-Jul-2004
C;Accession: 138239; 138242; $67816
R;Stevanovic, M.; Lovell-Badge, R.; Collignon, J.; Goodfellow, P.N.
R;Stevanovic, M.; Lovell-Badge, R.; Collignon, J.; Goodfellow, P.N.
A;Reference number: 138239; MUID:94154672; PMID:8111369
A;Accession: 138239
A;Status: preliminary; translated from GB/EMBL/DDBJ
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Score 41; DB 2 Pred. No. 18;

82.0%;

Query Match 82.0 Best Local Similarity 100. Matches 10; Conservative

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100.0%; Prec. ...

A;Gene: GDB:SOX3; SOX-3; SOXB
A;Cross-references: GDB:250376; OMIM:313430
A;Map position: XG2-Kq27
C;Superfamily: human SOX3 protein; HWG box homology
F;136-211/Domain: HMG box homology <HMG>

82.0%; Score 41; DB 83.3%; Pred. No. 66; iive 1; Mismatches

Best Local Similarity 83.3 Matches 10; Conservative

Query Match

anther-specific protein - rice

RESULT 3

352 AAAAAAAAAMS 363

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engrailed homeodomain-containing protein En-1 - mouse
N;Alternate names: homeotic protein En-1
C;Species: Mus musculus (house mouse)
C;Date: 01-06c-1993 #sequence revision 18-Nov-1994 #text_change 31-Dec-2004
C;Accession: A48423; 813009; A24778
R;Logan, C.; Hanks, M.C.; Noble-Topham, S.; Nallainathan, D.; Provart, N.J.; Joyner, A.J.A;Title: Cloning and sequence comparison of the mouse, human, and chicken engrailed gen A;Reference number: A48423; MUID:93185339; PMID:1363401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:P09065; UNIPARC:UPI00000299A1
A;Experimental source: CD-1, embryo
A;Note: sequence extracted from NCBI backbone (NCBIP:126620)
R;Holland, P.W.H.; Williams, N.A.
FEBS Lett. 277, 250-252, 1990
A;Title: Conservation of engrailed-like homeobox sequences during vertebrate evolution.
A;Reference number: S13009; MUID:91099509; PMID:1980115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genes Dev. 1, 29-38, 1987
Affille: Bn.1 and Bn-2, two mouse genes with sequence homology to the Drosophila engrai.
A;Reference number: A91620; MUID:88112776; PMID:2892757
A;Accession: A26629
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A;Residues: 278-401 <JOY>
A;Cross-references: UNIPARC:UPI000016CA7C; GB:Y00201; GB:M11987; NID:g49587; PIDN:CAA68
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Mol. Cell. Biol. 12, 3967-3977, 1992
A;Title: Sequence analysis reveals homology between two proteins of the flagellar radia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RiJoyner, A.L.; Kornberg, T.; Coleman, K.G.; Cox, D.R.; Martin, G.R.
Cell 43, 29-37, 1985
A;Title: Expression during embryogenesis of a mouse gene with sequence homology to the
A;Reference number: A24778; WUID:86079501; PMID:2416459
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C;Species: Chlamydomonas reinhardtii
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 05-Oct-2004
C;Accession: B44498
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C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
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Pred. No. 83;
1; Mismatches
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A;Molecule type: mucleic acid
A;Residues: 321-380 <40L.>
A;Cross-references: UNIPARC:UPI000017A2AF
R;JOyner, A.L.; Martin, G.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 311-401 <JO2>
A;Cross-references: UNIPARC:UP1000017A2B0
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| Similarity 83.3%;
| 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-401 <LOG>
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C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 05-Oct-2004
C;Accession: B48423
R;Logan, C.; Hanks, M.C.; Noble-Topham, S.; Nallainathan, D.; Provart, N.J.; Joyner, A.I.
Dev. Genet. 13, 345-358, 1992
A;Title: Cloning and sequence comparison of the mouse, human, and chicken engrailed gene
A;Reference number: A48423; MUID:93185339; PMID:1363401
A;Accession: B48423
A;Status: preliminary; not compared with conceptual translation
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C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 02-Jul-1998
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 02-Jul-1998
C;Accession: A44443
Mol. Cell. Biol. 12, 2475-2483, 1992
A;Title: Point mutations in the Drosophila hairy gene demonstrate in vivo requirements A;Reference number: A44443; MUID:92269819; PMID:1588951
A;Accession: A44443
A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
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basic helix-loop-helix transcription repressor H - fruit fly (Drosophila virilis)
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A;Note: sequence extracted from NCBI backbone (NCBIN:102964, NCBIP:102966)
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C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;304-360/Domain: homeobox homology <HOX>
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submitted to the Protein Sequence Database, March 1999
A;Reference number: Z15261
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F;60-155/Domain: HSF DNA-binding domain homology <HSF>
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83.3%; Pred. No. 79;
iive 1; Mismatches
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A;Cross-references: UNIPARC:UPI000017BEF1
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A;Gene: FlyBase:Dvir/h
A;Cross-references: FlyBase:FBgn0013115
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Matches 10; Conservative
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Best Local Similarity
Matches 10; Conserva
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A; Residues: 1-392 < LOG>
                                                         A, Accession: T04213
A, Molecule type: DNA
A, Residues: 1-377 <BEV>
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Biochem. Biophys. Res. Commun. 226, 801-809, 1996
A;Title: Members of the MAZ family: A novel cDNA clone for MAZ from human pancreatic isl
A;Reference number: JC5076; WUID:96428591; PMID:8831693
                                                                                                                                                                                                A, Experimental source: pancreatic islet
C, Comment: This protein plays a role in the control of transcriptional initiation of gen
and between the introns of the mouse gene for immunoglobulin M-D.
C; Keywords: phosphoprotein; zinc finger
F;146,204,480/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status pre
F;349/Binding site: phosphate (Tyr) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Kania, M.A.; Bonner, A.S.; Duffy, J.B.; Gergen, J.P.
Genes Dev. 4, 1701-1713, 1990
A;Title: The Drosophila segmentation gene runt encodes a novel nuclear regulatory protei
A;Reference number: A36392; MUID:91065517; PMID:2249771
A;Accession: A36392
A;Status: preliminary
A;Molecule type: DNA
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A;Cross-references: UNIPARC:UP1000016A09A; EMBL:U08379; NID:9761717; PIDN:AAC50228.1; Pl
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C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 05-Nov-1999
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 05-Nov-1999
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 05-Nov-1999
R;Ge, O: Nilasena, D.S.; O'Brien, C.A.; Frank, M.B.; Targoff, I.N.
J;Clin. Invest. 96, 1730-1737, 1995
J;Title: Molecular analysis of a major antigenic region of the 240-kD protein of Mi-2-A;Reference number: I38558; MUID:96013633; PMID:7560064
A;Reference number: I38558
                                                                                                                                              A;Residues: 1-497 <TSU>
A;Cross-references: UNIPARC:UP10000163B39; DDBJ:D85131; NID:g1752741; PIDN:BAA12728.1;
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C,Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 09-Jul-2004
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C;Species: Homo sapiens (man)
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226, 801-809, 1996
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98;
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C;Superfamily: transcription factor CBF alpha 2
C;Keywords: transcription regulation
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Matches 10; Conservative
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Biochemistry 31, 4102-4110, 1992
A.Title: Isolation of a novel cDNA encoding a zinc-finger protein that binds to two site A.Title: Isolation of a novel cDNA encoding a zinc-finger protein that binds to two site A.Title: Isolation of A.M. MUID: 92232709; PMID: 1567856
A.Accession: A42170
A.Status: not compared with conceptual translation
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A, Residues: 1-494 < PVR.
A, Cross-references: UNIPROT. P56270; UNIPARC: UPI000017C427; GB:J05371
A, Note: it is uncertain whether Met-18 is the initiator or whether translation is initia
R, Bossone, S.A.; Asselin, C.; Patel, A.J.; Marcu, K.B.
R, Proc. Natl. Acad. Sci. U.S.A. 89, 7452-7456, 1992
A, Title: MAZ, a zinc finger protein, binds to c-MYC and C2 gene sequences regulating tra
A, Reference number: A46153; MUID:92366479; PMID:1502157
                                                                                                                                                    A;Cross-references: UNIPROT:Q01657; UNIPARC:UP1000013521B; GB:M87526; NID:g167435; PIDN:
A;Note: sequence extracted from NCBI backbone (NCBIN:111696, NCBIP:111698)
C;Superfamily: flagellar radial spoke protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          zinc finger protein MAZ - human (fragment)
N;Alternate names: MYC-associated zinc finger protein MAZ; zinc finger protein ZF87
C;Species: Homo sapiens (man)
C;Dacte: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 09-Jul-2004
C;Accession: AAZ170; AAG153
R;Pyrc, J.J.; Moberg, K.H.; Hall, D.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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C;Species: Homo sapiens (man)
C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 05-Nov-1999
C;Accession: JC5076
R;Tsutsui, H.; Sakatsume, O.; Itakura, K.; Yokoyama, K.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 18-417,'L',419-494 <BOS>
A;Cross-references: UNIPARC:UPI000012ECF8; GB:M94046
A;Experimental source: Hela cells
A;Note: sequence extracted from NCBI backbone (NCBIN:110666, NCBIP:110667)
C;Keywords: DNA binding; zinc finger
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                                                                                                                                                                                                                                                                                                                                            1; Indels
            A; Reference number: A44498; MUID: 92375065; PMID: 1508197
                                                                                                                                                                                                                                                                              Score 40; DB 2
Pred. No. 92;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
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Pred. No.
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                                                                                                                                                                                                                                                                                    80.0%;
83.3%;
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F;296-318/Region: zinc finger
F;324-346/Region: zinc finger
F;373-405/Region: zinc finger
F;409-430/Region: zinc finger
F;452-468/Region: alanine-rich
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116 AAAAAAAAA 127
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F,174-183/Region: alanine-rich
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Best Local Similarity 83.3
Matches 10; Conservative
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                                                                                                                                  A;Residues: 1-459 <CUR>
                                           A;Accession: B44498
A;Status: preliminary
A;Molecule type: DNA
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Matches

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A;Title: The Drosophila gene Hairless encodes a novel basic protein that controls alter:
A;Reference number: A44067; MUID:92387549; PMID:1516831
A;Accession: A44067
                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNA
A;Residues: 1-107 < PRE>
A;Cross-references: UNIPARC:UPI000012C93C; EMBL:X67239; GB:S49642; NID:g578331; PID:g578
R;Maier, D.; Stumm, G.; Kuhn, K.; Preiss, A.
R;Maier, D.; Stumm, G.; Kuhn, K.; Preiss, A.
R;Maier, D.; Stumm, G.; Kuhn, K.; Preiss, A.
A;Title: Hairless, a Drosophila gene involved in neural development, encodes a novel, scherence number: S33412; MUID:93041287; PMID:1419850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         abdominal segment formation protein pumilio - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Species: Ja-Sep-1993 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: A46221; S22026
B;Barker, D.D.; Wang, C.; Moore, J.; Dickinson, L.K.; Lehmann, R.
Genes Dev. 6, 2112-2336, 1992
A;Title: Pumilio is essential for function but not for distribution of the Drosophila all A;Reference number: A46221; MUID:93093466; PMID:1459455
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Ajacus: preliminary
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Ajaccession: BARA
Ajaccessides: 1-1533 cBARA
Ajaccession: S22026
Ajaccession: S22026
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A, Cross-references: UNIPARC:UP100001329FD; EMBL:X62589; NID:98393; PID:98394
                                                                                                                  A;Molecule type: DNA
A;Residues: 19-1077 cBAN>
A;Cross-references: UNIPROT:Q02308; UNIPARC:UPI000002AB24; GB:M95192; NID:g157621; PID:
A;Note: sequence extracted from NCBI backbone (NCBIN:112622, NCBIP:112623)
                                                                                                                                                                                                                                                               R;Preiss, A. suche EMBL Data Library, May 1994
A;Description: Hairless, a Drosophila gene involved in neural development, encodes a A;Reference number: A58929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: mRNA
A;Residues: 1-150,'A',152-701,'LL',704-890,'R',892-963,'RLLP',968-973,975-1077 <MAI>
A;Cross-references: UNIPARC:UP1000017BED1; EMBL:X67239
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Pred. No. 1.8e+02;
1; Mismatches 1; Indels
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83.3%; Pred. No. 2.46+02;
Live 1; Mismatches 1; Indels
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A,Cross-references: FlyBase:FBgn0003165
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1050 AAVAAAAAAAA 1061
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Best Local Similarity 83.3
Matches 10; Conservative
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Matches 10; Conservative
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                                                                                                                                                                                                                                                finger protein sob - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Spate: 04-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C;Accession: S72227
R;Hart, M.C.; Wang, L.; Coulter, D.E.
Genetics 144, 171-182, 1996
A;File: Comparison of the structure and expression of odd-skipped and two related genes
A;Reference number: S72277
A;Reference number: S72277
A;Accession: S7227
A;
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A;Note: activates JNK/SAPK cascade; Rac-binding protein
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serine-rich protein hairless - fruit fly (Drosophila melanogaster)

serine-rich protein hairless - fruit fly (Drosophila melanogaster)

N;Alternate names: 109K basic protein H

C;Species: Drosophila melanogaster

C;Date: 10-Jun-1993 #sequence revision 26-Feb-1999 #text_change 09-Jul-2004

C;Accession: A44067; A59804509; $33412; $24639

G;Accession: A452-1769, 1992
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C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T09071
R;Tapon, N.; Nagata, K.; Lamarche, N.; Hall, A.
EMBO J. 17, 1395-1404, 1998
A;Reference number: Z16552; MUID:98151363; PMID:9482736
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40; DB 2; Length 577
Pred. No. 1.1e+02;
1; Mismatches 1; Indels
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SH3 domains-containing protein POSH - mouse
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C,Keywords: signal transduction
F;8-58/Domain: RING finger homology <RRN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Genetics:
A;Gene: sob
A;Cross-references: FlyBase:FBgn0004892
C;Keywords: zinc finger
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419 AAVAAAAAAAA 430
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Best Local Similarity 83.3
Matches 10; Conservative
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273 AAVAAAAAAAA 284
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Matches 10; Conservative
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87 AAVAAAAAAA 98
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Rianonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Reference number: A75000; MUID:99065613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Accession: D88395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C, Accession: B96740

R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 200

A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. A; Authors: Hunter, J.L.; Y.; Lin, X.; Lin, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A; Wu, D.; Yu, G.; Praser, C.M.; Venter, J.C.; Davis, R.W.

A; Wu, D.; Yu, G.; Praser, C.M.; Venter, J.C.; Davis, R.W.

A; Mu, D.; Yu, G.; Praser, C.M.; Venter, J.C.; Davis, R.W.

A; Reference number: A66141; MUID:21016719; PMID:11130712
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A;Cross-references: UNIPROT:Q05196; UNIPARC:UPI00001311AE; GB:AE005173; NID:97239504; PI
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C.Species: Drosophila melanogaster
C.Date: 07-Sep-1990 #sequence revision 07-Sep-1990 #text_change 09-Jul-2004
C.Accession: A36391; A33106; Sl3514
R.Smoller, D.; Friedel, C.; Schmid, A.; Bettler, D.; Lam, L.; Yedvobnick, B.
Genes Bov. 4, 1688-1700, 1990
A.Title: The Drosophila neurogenic locus mastermind encodes a nuclear protein unusually
A.Reference number: A36391; MUID:91065516; PMID:1701150
                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-451 <STO>
A;Cross-references: UNIPROT:017222; UNIPARC:UPI000017A5BC; GB:chr_III; PIDN:AAB70991.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein F14023.15 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
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Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 39; DB 2; 1
Pred. No. 1.2e+02;
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83.3%;
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Best Local Similarity 83.3
Matches 10; Conservative
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| AAVAAAAAAEA 38
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                                             D88395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: F53A3.6
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                                                                                                                                    N.Alternate names: membrane protein fsh, 205K
N;Contains: female sterile homeotic protein, 110K
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 31-Dec-2004
C;Accession: A43742; B43742
R;Haynes, S.R.; Mozer, B.A.; Bhatia-Dey, N.; Dawid, I.B.
Dev. Biol. 134, 246-257, 1989
A;Title: The Drosophila fsh locus, a maternal effect homeotic gene, encodes apparent mem A;Teference number: A43742; MUID:89276730; PMID:2567251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
*Kesidues: 1-2038 -HAY>
A;Cross-references: UNIPROT:P13709; UNIPARC:UPI000012AC6C; EMBL:M23221; NID:g157452; PID
A;Accession: B43742
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A;Cross-references: UNIPROT:O69985; UNIPARC:UPI0000DACOB; EMBL:AL022268; PIDN:CAA18345.
A;Experimental source: strain A3(2)
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C;Species: Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Accession: T35129
R;Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, March 1998
A;Reference number: Z21568
A;Reference number: Z21568
A;Accession: T35129
A;Steuts: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                 female sterile homeotic protein, 205K - fruit fly (Drosophila melanogaster)
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C;Keywords: alternative splicing; transmembrane protein
F;1-2038/Product: female sterile homeotic protein, 205K #status predicted
F;1-1106/Product: female sterile homeotic protein, 110K #status predicted
F;59-116/Domain: bromodomain homology <BRO1>
F;503-560/Domain: bromodomain homology <BRO2>
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Pred. No. 3e+02;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1106 <HA2>
A;Csoss-references: UNIPARC:UPI000017A10F; EMBL:M23222
C;Genetics:
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Pred. No. 90;
1; Mismatches
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A,Gene: SCOEDB:SC4H2.30
C,Superfamily: ADP-ribosylglycohydrolase
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81.8%;
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Best Local Similarity 83.3%;
Matches 10; Conservative
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Matches 9; Conservative
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165 AMAVAAAAALA 175
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A;Molecule type: mRNA
A;Residues: 1-91 - GGUJ-
A;Cross-references: UNIPROT:P07835; UNIPARC:UPI0000125B4B; GB:M10148; NID:g213579; PIDN
R;Gauthier, S.; Wu, Y.; Davies, P.L.
                                                                                                                                                          homeotic protein ultrabithorax homolog - Junonia coenia (fragment)
NyAlternate names: ultrabithorax homeodomain protein
C;Species: Junonia coenia
C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 05-Oct-2004
C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 05-Oct-2004
C;Accession: 58883
R;Warren, R.W.; Nagy, L.; Selegue, J.; Gates, J.; Carroll, S.
Nature 372, 458-461, 1994
A;Title: Evolution of homeotic gene regulation and function in flies and butterflies.
A;Reference number: $58850; MUID:95075456; PMID:7840822
A;Accession: $58853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antifreeze protein 4 precursor - winter flounder ("Species: Pseudopleuronectes americanus (winter flounder) ("Species: Pseudopleuronectes americanus (winter flounder) ("C.) and ("C.) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: mucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-40 - WARR>
A;Cross-references: UNIPROT:Q25210; UNIPARC:UPI000017A2FE; EMBL:L42137
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1995
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
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R;Gourlie, B.; Lin, Y.; Price, J.; De Vries, A.L.; Powers, D.; Huang, R.C.C. J. Biol. Chem. 259, 14960-14965, 1984
A;Title: Winter flounder antifreeze proteins: a multigene family.
A;Reference number: A22592; MUID:85054993; PMID:6548752
A;Accession: A22592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antifreeze protein IIA7 precursor - winter flounder
C;Species: Pseudopleuronectes americanus (winter flounder)
C;Date: 05-0ct-1988 #sequence_revision 05-0ct-1988 #text_change 09-Jul-2004
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C;Superfamily: antifreeze protein
C;Keywords: antifreeze
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-85/Product: antifreeze protein 4 #status predicted <MAT>
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Pred. No. 45;
0; Mismatches
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83.3%;
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Best Local Similarity 83.3.
Best Local Similarity 83.3.
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 AAAAAAAAAA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AAMAAAAAAMA 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-85 <LIN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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A;Accession: A36391
A;Status: preliminary
A;Moleus: L1596 «SMO»
A;Residues: 1.1596 «SMO»
A;Cross-references: UNIPROT:P21519; UNIPARC:UPI000012EB74; GB:X54251; NID:g8203; PIDN:CA
A;Mote: strain Canton S
A;Mote: strain Canton S
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics: PlyBase:FBgn0002643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene mastermind protein - fruit fly (Drosophila virilis)
C;Species: Drosophila virilis
C;Species: Drosophila virilis
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T13998
R;Newfeld, S.J.; Tachida, H.; Yedvobnick, B.
J, Mol. Evol. 38, 637-641, 1994
A;Title: Drive-selection equilibrium: homopolymer evolution in the Drosophila gene maste
A;Reference number: Z17850; MUID:94365848; PMID:8083889
A;Accession: T13998
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Cispecies: Drosophila melanogaster

Cispecies: Drosophila melanogaster

Cispecies: Drosophila melanogaster

Cispacies: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000

Ciscossion: T13748

Risinclair, D.A.R.; Milne, T.A.; Hodgson, J.W.; Shellard, J.; Salinas, C.A.; Kyba, M.; R

Aititle: The Additional sex combs gene of Drosophila encodes a chromatin protein that bit Aix accession: T13748

Aix cession: T13748
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C;Genetics:
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A;Cross-references: UNIPARC:UPI0000760FA; EMBL:AJ001164; NID:g3292938; PIDN:CAA04568.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1596;
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                                                                                                                                                                                                                                                                                                                                                                                       Score 39; DB 2; 1
Pred. No. 3.3e+02;
0; Mismatches 2
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A;Molecule type: DNA
A;Residues: 1-1655 <NEW>
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C, Function:
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Best Local Similarity 83.3%;
Matches 10; Conservative
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es 10; Conserv
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Best Local $
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R;Tanaka, M.; Tanaka, T.; Harata, M.; Suzuki, T.; Mitsui, Y.
Biochem. Biophys. Res. Commun. 243, 531-537, 1998
A;Title: Triplet repeat-containing ribosomal protein L14 gene in immortalized human endo
A;Reference number: JC5954; MUID:98153799; PMID:9480843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-231 <AMO>
A;Cross-references: UNIPROT:Q02067; UNIPARC:UPI000000BE1; GB:M95603; NID:g193875; PIDN:
C;Keywords: DNA binding
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: 811563
R;Johnson, J.E.; Birren, S.J.; Anderson, D.J.
Nature 346, 858 861, 1990
A;Title: Two rat homologues of Drosophila achaete-scute specifically expressed in neuror A;Reference number: 811562; MUID:90363294; PMID:2392153
A;Accession: 811563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Cross-references: UNIPARC:UPI000004E622; DDBJ:D87735; NID:g1620021; PIDN:BAA13443.1; C;Superfamily: rat ribosomal protein L14
                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 02-Sep-2000
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99;
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Pred. No.
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83.3%;
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Best Local Similarity 83.3
Matches 10; Conservative
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Matches 10; Conservative
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                           1 AAMAAAAAAMA 12
                                                                                                                                                                                                                                                           ribosomal protein L14 - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-220 <TAN>
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A;Status: preliminary
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                                                                                                                             A,Molecule type: DNA
A;Residues: 1-63,'V',65-91 <GAU>
A;Cross-references: UNIPARC:UP10000001382; EMBL:X53718; NID:g64213; PIDN:CAA37754.1; PID
C;Genetics:
A;Introns: 19/2
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A;Residues: 1-172 <TUC>
A;Cross-references: UNIPROT:Q60586; UNIPARC:UPI00000E671C; GB:L29542; NID:g496161; PIDN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sex-determining protein Sry - multimammate rat (Mastomys hildebrantii)
C;Species: Mastomys hildebrantii
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 05-Oct-2004
C;Accession: S35568
R;Tucker, P.K.; Lundrigan, B.L.
Nature 364, 715-717, 1993
A;Title: Rapid evolution of the sex determining locus in Old World mice and rats.
A;Reference number: S35565; MUID:93361118; PMID:8355784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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R;Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, June 1999
A;Reference number: Z17528
A;Reference number: Z17528
A;Reference number: A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein DKFZp586E1621.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
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A,Experimental source: adult uterus; clone DKFZp586E1621
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                           A;Title: Nucleotide sequence of a variant antifreeze protein gene. A;Reference number: S12604; MUID:90384854; PMID:2402466
                                                                                                                                                                                                                                                                                                                     C;Keywords: antifreeze; tandem repeat
C;Keywords: antifreeze; tandem repeat
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-91/Product: antifreeze protein IIA7 #status predicted <MAT>
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Pred. No. 48;
0; Mismatches 2; Indels
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Pred. No. 70;
0; Mismatches
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C,Keywords: DNA binding
F;2-77/Domain: HMG box homology <HMG1>
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83.3%;
                                                                                                                                                                                                                                                                                             Superfamily: antifreeze protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76.0%;
83.3%;
Acids Res. 18, 5303, 1990
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Best Local Similarity 83.3
Matches 10; Conservative
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Best Local Similarity
Matches 10; Conserva
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A;Note: DKFZp586E1621.1
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Mech. Dev. 50, 177-186, 1995

A;Title: Gsh-2, a murine homeobox gene expressed in the developing brain.
A;Reference number: IS7039; MUID:95344993; PMID:7619729
A;Reference number: IS7039
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-305 <RES>
A;Cross-references: UNIPARC:UPI0000024E69; GB:S79041; NID:g1042008; PIDN:AAB34947.1; PII
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R. Yokoyama, M.; Nishi, Y.; Yoshii, J.; Okubo, K.; Matsubara, K.
DNA Res. 3, 311-320, 1996
A;Title: Identification and cloning of neuroblastoma-specific and nerve tissue-specific A;Reference number: JC5272; MUID:97191543; PMID:9039501
A;Contents: neuroblastma cell
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A,Residues: 1-314 <YOK>
A,Cross-references: UNIPROT:Q99453; UNIPARC:UPI0000131D16; DDBJ:D82344; NID:g1841337; P.
C,Comment: This protein is a transcriptional repressor involved in regulating gene expr.
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;99-155/Domain: homeobox homology <HOX>
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C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Oct-2004
C;Dates: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Oct-2004
C;Cacession: SIGS18, 840403; S57443
R;Izpisua-Belmonte, J.C.; Falkenstein, H.; Dolle, P.; Renucci, A.; Duboule, D.
EMBO J. 10, 2279-2289, 1991
A;Title: Murine genes related to the Drosophila AbdB homeotic gene are sequentially expi
A;Reference number: SIG317; MUID:91293104; PMID:1676674
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A;Residues: 1-323 <122>
A;Crossidues: 1-323 <122>
A;Gersard, M.; Duboule, D.; Zakany, J.
EMBO J. 12, 3539-3550, 1993
A;Title: Structure and activity of regulatory elements involved in the activation of the
A;Reference number: $40403; MUID:94074553; PMID:7902810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           paired type homeobox protein, NBP - human
C;Species: Homo sapiens (man)
C;Date: 16-Apr-1997 #sequence_revision 09-May-1997 #text_change 05-Oct-2004
C;Accession: JC5273
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C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;204-260/Domain: homeobox homology <HOX>
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Pred. No. 1.3e+02;
0; Mismatches 2; Indels
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Pred. No. 1.2e+02;
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N;Alternate names: homeotic protein Hoxd-11
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A,Status: nucleic acid sequence not shown
A,Molecule type: mRNA
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83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 83.3
Matches 10; Conservative
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Best Local Similarity 83.3
Matches 10; Conservative
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C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 09-Jul-2004
C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 09-Jul-2004
C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 09-Jul-2004
R;Izpisua-Belmonte, J.C.; Dolle, P.; Renucci, A.; Zappavigna, V.; Falkenstein, H.; Dubou Development 110, 733-745, 1990
A;Title: Primary structure and embryonic expression pattern of the mouse Hox-4.3 homeobc A;Title: Primary structure and embryonic expression pattern of the mouse Hox-4.3 homeobc A;Reference number: A43562; MUID:91209232; PMID:1982431
A;Accession: A43562
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
   A;Cross-references: UNIPROT:P19359; UNIPARC:UP10000047567; EMBL:X53725; NID:956630; PIDN
C;Keywords: DNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Ball, D.W.; Azzoli, C.G.; Baylin, S.B.; Chi, D.; Dou, S.; Donis-Keller, H.; Cumaraswam Proc. Natl. Acad. Sci. U.S.A. 90, 5648-5652, 1993
Proc. Natl. Acad. Sci. U.S.A. 90, 5648-5652, 1993
A;Title: Identification of a human achaete-scute homolog highly expressed in neuroendocr A;Reference number: A48279; MUID:93296195; PMID:8390674
A;Accession: A48279
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C;Species: Mus sp. (mouse)
C;Date: O2Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Oct-2004
C;Accession: I57039
R;Hsieh-Li, H.M.; Witte, D.P.; Szucsik, J.C.; Weinstein, M.; Li, H.; Potter, S.S.
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C;Species: 31-May-1996 #sequence_revision 31-May-1996 #text_change 09-Jul-2004
C;Accession: A48279
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A,Residues: 1-289 - KIZP-
A,Cross-references: UNIPROT: P23463; UNIPARC: UPI0000177DA6
C,Superfamily: homeotic protein Hox A7; homeobox homology
C,Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;196-252/Domain: homeobox homology <HOX>
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                                                                                                    Score 38; DB 2; Length 233;
Pred. No. 1e+02;
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                                                                                                                                                                    2; Indels
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                                                                                             Query Match 76.0%;
Best Local Similarity 83.3%;
Matches 10; Conservative
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homeotic protein Hox D8 - mouse
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Matches 10; Conservative
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achaete scute protein - human
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A; Residues: 1-238 <RES>
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Length 331;

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C;Accession: A39065
R;D'Esposito, M.; Morelli, F.; Acampora, D.; Migliaccio, E.; Simeone, A.; Boncinelli, E. Genomics 10, 43-50, 1991
A;Title: EVXZ, a human homeobox gene homologous to the even-skipped segmentation gene, i A;Reference number: A39065; MUID:91257849; PMID:1675198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Homo sapiens (man)
C;Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 31-Dec-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: 2q24.3-2q31
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;46-102/Domain: homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; not compared with conceptual translation A;Molecule type: DNA
A;Residues: 1-333 <DAE>
                                                                                           A;Note: sequence extracted from NCBI backbone (NCBIP:119832)
                                                                                                                                                        DB 2; L
1.3e+02;
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Pred. No. 1.3e+02;
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                                                                                                                                                           Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Gene: GDB:EVX2
A,Cross-references: GDB:127528; OMIM:142991
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83.3%;
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Matches 10; Conservative
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hypothetical protein lin2792 [imported] - Listeria innocua (strain Clip11262)

c;Species: Listeria innocua

c;Species: Listeria innocua

c;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

C;Accession: ABI781

R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker

J; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.

D; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A;Authors: Kreft, J; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
A;Authors: Kreft, J; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species

A;Reference number: ABI077; MUID:21537279; PMID:11679669

A;Status: preliminary

A;Status: preliminary
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B47236
Zinc-finger protein Pur-1 - golden hamster
Zinc-finger protein Pur-1 - golden hamster)
C;Species: Mesocricetus auratus (golden hamster)
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 05-Apr-1995
C;Accession: B47236
R;Kennedy, G.C.; Rutter, W.J.
A;Rennedy, G.C.; Rutter, W.J.
A;Title: Pur-1, a zinc-finger protein that binds to purine-rich sequences, transactivate
A;Reference number: A47236
A;Title: Pur-1, a zinc-finger protein that binds to purine-rich sequences, transactivate
A;Reference number: A47236
A;Accession: B47236
A;Accession: B47236
A;Residues: 1-331 < KEN>
A;Residues: 1-331 < KEN>
A;Coss-references: UniPARC:UPI000017C615
A;Experimental source: insulinoma cell line T
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C;Genetics:
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A,Residues: 'MNDFDEGGBSAAS',1-323 <TAK>
A;Cross-references: UNIPARC:UP1000026A38; EMBL:X60395; NID:g871427; PIDN:CAA42943.1; PI
C;Genetics:
A.Cross-references: UNIPARC:UDI000029F10; EMBL:X71422; NID:g397508; PIDN:CAA50553.1; R.Takada, S.; Cook, M.; Kramlauf, R.; McMahon, A.P. submitted to the EMBL Data Library, May 1991
A,Description: Genomic sequence of mouse Hox-4.6.
A,Reference number: S57443
A;Moleculo.
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A;Introns: 246/1
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;252-308/Domain: homeobox homology <HOX>
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Pred. No. 1.3e+02;
2; Mismatches 1; Indels
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Pred. No. 1.3e+02;
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A; Residues: 1-328 <GLA>
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07SBT2_TETNG

07SBT2_TETNG

07SBT3_RAFTH

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Q7PV80_A
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MEDLINE=2239456; PubMed=12504569; DOI=10.1006/viro.2002.1696;
Lin S.T., Chang Y.S., Wang H.C., Tzeng H.F., Chang Z.F., Lin J.Y.,
Wang C.H., Lo C.F., Kou G.H.;
"Ribonucleotide reductase of shrimp white spot syndrome virus (WSSV):
expression and enzymatic activity in a baculovirus/insect cell system
and WSSV-infected shrimp.";
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MEDLINE=20517548; PubMed=11062040; DOI=10.1006/viro.2000.0597;
Tsai M.F., Yu H.T., Tzeng H.F., Leu J.H., Chou C.M., Huang C.J.,
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"Identification and characterization of a shrimp white spot syndrome
virus (WSSV) gene that encodes a novel chimeric polypeptide of
cellular-type thymidine kinase and thymidylate kinase.";
Virology 277:100-110(2000).
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                                                                                                                                                                                                     White spot syndrome virus (WSSV).
Viruses; dsDNA viruses, no RNA stage; Nimaviridae; Whispovirus.
NCBI_TaxID=92652;
                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
MEDLINE=21548311; PubMed=11689662;
DOI=10.1128/VU.75.23.11811-11820.2001;
Yang F., He J., Lin X., Li Q., Pan D., Zhang X., Xu X.;
"Complete genome sequence of the shrimp white spot bacilliform
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PubMed=15452257; DOI=10.1128/JVI.78.20.11360-11370.2004;
                                                                                                                  UniProtKB/TrEMBL.
                                                                       82 AA.
                                                                       PRT;
                                                                                                 QBVALD, OQVALD, OQVALD, OQVALD, OQVARD, OQVAR, Sequence version 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Virol. 75:11811-11820(2001).
                                                                       PRELIMINARY;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Musinae; Mus
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STRAIN-CS7BH/6J; TISSUE=Thymus;
PubMed=16141072; DOI=10.1126/science.1112014;
PubMed=16141072; DOI=10.1126/science.1112014;
Carninol P., Ksaukawa T., Katayama S., Gough J., Frith M.C., Maeda N. Oyama R., Barasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Ambesi-Impiombato A., Apweiler R., Allen J.E.,
Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M., Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R., Crowe M.L., Dalla B., Dalrymple B.P., de Bono B., Della Gatta G., di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
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MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
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                                                                                                                                                                                                                                                                                                                                                        "The unique stacked rings in the nucleocapsid of the white spot
syndrome virus virion are formed by the major structural protein
VP664, the largest viral structural protein ever found.";
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PubNed=15596810; DOI=10.1128/JVI.79.1.140-149.2005;
Leu J.H., Tsai J.M., Wang H.C., Wang A.H., Wang C.H., Kou G.H.,
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J.M., Wang H.C., Leu J.H., Hsiao H.H., Wang A.H., Kou G.H.
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Pred. No. 35;
1; Mismatches 0; Indels
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF7E4C81AAF27D44 CRC64;
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Methods Enzymol. 303:19-44(1999).
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EMBL; AF440570; AAL89228.1; -; Genomic_DNA.
SEQUENCE 82 AA; 8635 MW; AF7E4C81AAF27D
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Q3UUSS;
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RC STRAIN-C57BL/61; TISSUB=Thymus;

RA MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

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RA Andarati R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Schriml L.M., Kanapin A., Marsuda H., Baralov S., Beisel K.W.,

RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.B., Cousins S.,

RA Gasteriand T., Gariboldi M., Gissi C., Godzik A., Gough J.,

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RA Kanaj A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

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RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RA Magashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pescol G.,

RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

Sultana R., Takenaka Y., Taylor M. S., Teasdale R.D., Tomita M.,

Kaltana R., Takenaka Y., Taylor M. S., Teasdale R.D., Tomita M.,

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Norabhia-seyi V. Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License STRAIN=C57BL/6J; TISSUE=Thymus; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Nuramatsu M., Hayashizaki Y.; Nuramatsu and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000). Gaps STRAIN=CSTBL/6J; TISSUE=Thymus;
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NUCLEOTIDE SEQUENCE.

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11-OCT-2005, sequence version 1.
07-FEB-2006, entry version 5.
17B-55 BB88 cDNA, RIKEN full-length enriched library, clone:1730024Dl4 product:HBV pX associated protein 8 large isoform homolog (Fragment).
Name=Hbxap;
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Bammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhang W.,
                                                                                                                                                                                                                                          Oryza sativa (japonicá cultivar-group).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae; BEP clade,
Bhrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                       MUCLEOTIDE SEQUENCE.

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Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X.,
Lu J., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
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GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPRO1471; TF_ERF.
Pfam; PF00847; AP2; 1.
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SEQUENCE 233 AA; 25434 MW; 90B3BF38A3A4A419 CRC64;
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                                                233 AA.
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HSSP; 080337; 1GCC.
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                                                PRELIMINARY; PRT;
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ProDom; PD001423; TF ERF; 1.
SMART; SM00380; AP2; 1.
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QJUK64;
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Thoron Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
The SIMILARITY: Contains 1 BTB (POZ) domain.
The SIMILARITY: Contains 2 CZHZ-type zinc fingers.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus
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                                                                                                                                                                        Length 309;
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                                                                                                                              309 AA; 34639 MW; 8099A6CAA99549E4 CRC64;
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                                                                                                                                                                      Score 44; DB 2; I
Pred. No. 1.9e+02;
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Ensembl; ENSWUSG0000048485; Mus musculus.
MGI:2387181; Zbtb8.
InterPro; IPR000210; BTB.
InterPro; IPR0100010; BTB.
InterPro; IPR010087; Znf_C2H2.
Pfam; PF00651; BTB; 1.
Prodom; PF000609; zf_C2H2; 2.
Prodom; PF000009; zf_C2H2; 1.
SMART; SM00225; BTB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                              484 AA.
                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1]
NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
                                                                EMBL; AK146154; BAE26938.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2003, sequence version 1. 07-MAR-2006, entry version 22.
                                                                                                                                                                        88.0%;
91.7%;
                                                                                                                                                                                                                  Matches 11, Conservative
                                                                                    MGI; MGI:2682305; Hbxap.
                                                                                                                                                                                                                                                          1 AAMAAAAAAMA 12
                                                                                                                                                                                                                                                                                                 7 AAAAAAAAAAA 18
                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=FVB/N;
                                                                                                                                                                                                                                                                                                                                                                                                              MOUSE
                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                            ZBTB8 M
                                                                                                                                                                                                                                                                                                                                                                                          MOUSE
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SSSERES
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Carrainci P. N. Katayama S., Goodh J., Frith M.C., Maeda N., Carrainci P., Kasukawa T., Katayama S., Goodh J., Frith M.C., Maeda N., Cyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Adanis V., Aldnis V., Allen J.E., Baralov S., Forrest A.R., Zavolan M., Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Ambesi-Impiombato A., Apweller R., Aturaliya R.N., Balley T.L., Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M., Crowe M.L., Dalla E., Dalrymple B.P., Ge Bono B., Della Gatta G., Aldinis V., Christoffels A., Clutterbock D.R., Aldinardo D., Down T., Engstrom P., Fagiolini M., Faulkner G., Aletcher C.F., Fukushima T., Furuno M., Fucaki S., Garibodidi M., Fletcher C.F., Fukushima T., Furuno M., Ikeok K., Hirokawa N., Alli D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T., Alat M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H., Attano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K., Kurochkin I.V., Laerau L.F., Lazarevic D., Lipovich L., Liu J., Alli J., Madan Babu M., Madera M., Marchioni L., Rabarsawa S., Miki H., Mignone F., Miyake S., Morris K., Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K., Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P., Matsuda S., Miki H., Matsuda H., Matsuda S., Miki H., Matsuda H., Nakauchi H., Naka
                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                  11-OCT-2005, integrated into UniProtKB/TrEMBL.
11-OCT-2005, sequence version 1.
21-FEB-2006, entry version 7.
21-FEB-2006, entry version 7.
11 days embryo head cDNA, RIKEN full-length enriched library, clone:cli30068L6 product:zinc finger and BTB domain containing 8, full insert sequence (0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:c230068H07 product:zinc finger and BTB domain containing 8, full insert sequence) (14, 17 days embryo head cDNA, RIKEN full-length enriched library, clone:3222401B20 product:zinc finger and BTB domain containing 8, full insert sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6J; TISSUB=Cerebellum, and Head;
STRAIN=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
MEDLINES 9927958hizaki Y.;
High-efficiency full-length cDNA cloning.";
Methods Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                 Gaps
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                Score 44; DB 1; Length 484; Pred. No. 2.8e+02;
                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                     B4FF082555B0CA1A CRC64;
                                                                                                        protein 8.
/FTId=PRO_000047722
                                                                                                                                                                                                                                                                                                                                                                                                          484 AA.
                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                      C2H2-type 1.
C2H2-type 2.
Ala-rich.
                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                     53387 MW;
 SM00355; ZnF_C2H2; 2.
                                                                                                                                                                                                                                   88.0%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                              136 AAMAAAAAAAA 147
                                                                                                                                                                                                                                                                 11; Conservative
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                                                                                                                                        92
353
382
149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                     484 AA;
                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                          Q3US18 MOUSE
Q3US18;
                                                                                                                                                      ZN_FING
ZN_FING
COMPBIAS
SEQUENCE
                                                                                                                                                                                                                                   Query Match
Best Local
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                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                   Matches
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Participant R. Nighlightonis S., Norie, P., Obers D., Ober D., Cannelland, D., Schnight B., School D., Ober D., Mann Y., Salbarges S.L., Sandalin A., Schnight B., School D., Shindalin B., School D., Shindalin B., School D., Shindalin B., School D., Ober D., Shindal B., School D., Ober D., Shindalin B., School D., Shindalin B., School D., Shindalin B., School D., Shindalin B., School D., Shindalin B., Sandalin B., School D., Shindalin B., Sandalin B., Shindalin B., Sandalin B., School D., Shindalin B., Sandalin B., Sandalin B., Shindalin B., Sandalin B., Shindalin B., Sandalin B., Shindalin B., Sandalin B., Sandalin B., Sandalin B., Shindalin B., Sandalin B., Sandalin B., Shindalin B., Shindali
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                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6J; TISSUE=Cerebellum, and Head; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA lbraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujite M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wanshima-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=CS7BL/63; TISSUB=Cerebellum; Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K., Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S., Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N., Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D., Shibata K., Shizaki T., Tagami M., Tagami Y., Waki K., Watahiki A., Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-CSTBL/6J; TISSUE-Cerebellum, and Head;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Yagaoka S., Sasaki N., Carninci P.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumioto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwake S., Inoue K., Togawa W., Izawa M., Ohara E., Watshika M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Rokazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RIKEN integrated sequence analysis (RISA) system-384-format
Sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=CS7BL/6J; TISSUB=Head;
Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
Shibata K., Shizaki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
Muramatsu M., Hayashizaki Y.,
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                               Haysahizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AK140914; BAE24519.1; -; mRNA.
EMBL; AK132152; BAE20599.1; -; mRNA.
EMBL; AK132152; BAE20999.1; -; mRNA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0008270; F:zinc ion binding; IEA.
GO; GO:0008270; F:zinc ion binding; IEA.
InterPro; IPR000210; BTB.
InterPro; IPR000210; BTB.
InterPro; IPR00051; Znf_C2H2.
InterPro; IPR00051; Znf_C2H2.
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                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE
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REAL STEADLY SEQUENCE.

REAL STEADLY STEADLY STEADLY STEADLY SEQUENCE. 1112014;

RA CATRINGLY P. Kasukawa T. Katayama S., Gough J., Frith M.C., Maeda N., RA Cyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., RA Gyama R., Ravasi T. Lenhard B., Wells C., Kodzius R., Shimokawa K., RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Rayle M., Milming L.G., Aldinis V., Allen J.E.,

RA Ambesi-Impiombato A., Apweiler R. Aturaliya R.N., Bailey T.L.,

RA Ambesi-Impiombato A., Apweiler R. W., Bersano T., Bono H., Chalk A.M.,

RA Ambesi-Impiombato A., Apweiler R. Aturaliya R.N., Bailey T.L.,

RA Growe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,

RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,

RA Crowe M.L., Dalla E., Dalrymple B.P., Regiolini M., Faulkner G.,

RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,

RA Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,

RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,

Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,

RA Attano H., Matsuzawa S., Madan Babu M., Madera M., Marchionni L.,

RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,

RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,

RA Milsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,

RA Schonbach C., Sekfguchi K., Sandelin A., Schosa L., Sheng Y.,

RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,

Schonbach C., Sekfguchi K., Sandelin A., Sessa L., Sheng Y.,

RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegener J., Teichmann S.A.,

RA Tammoja K., Tan S.L., Tang S., Zhurer A., Hide W., Bult C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ful1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=CS7BL/6J; TISSUE=Stomach;
MEDLINE=99279255; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninio: P., Hayashizaki Y.;
"High-efficiency fill-langh Cloning.";
Methods Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-OCT-2005, sequence version 1.
07-FEB-2006, entry version 5.
17 days embryo stomach cDNA, RIKEN full-length enriched library, clone:1920040M16 product.hepatitis B virus x associated protein,
                                                                                                                                                                                                                   ;
                                  PROSITE; PS50097, BTB; 1.
PROSITE; PS50097, BTB; 1.
PROSITE; PS001928; ZINC FINGER C2H2 1; 1.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 2.
Metal-binding; Nuclear protein; Repeat; Zinc; Zinc-finger.
SEQUENCE 484 AA; 53414 MW; ACA81D5402A2E7F4 CRC64;
                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                       Score 44; DB 2; I
Pred. No. 2.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-OCT-2005, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                            998 AA.
                                                                                                                                                                                                                 0; Mismatches
SMART; SM00225; BTB; 1.
SMART; SM00355; ZnF_C2H2; 2.
                                                                                                                                                                       88.0%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         insert sequence. (Fragment)
Name=Hbxap;
                                                                                                                                                                                                                                                                                                 136 AAMAAAAAAAA 147
                                                                                                                                                                                                                 11; Conservative
                                                                                                                                                                                                                                                        1 AAMAAAAAAMA 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE
                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                       Q3UJ04_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
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An Carimonod S.M., Teasdale R.D., Liu E.T., Erusic V., Quackenbush J.,
Ashalhstead C., Martick, 12. Hume D.M., Mai A.O., Sanah Rasan Taru Y.,
An Indua S. Tanaman K.L. KEDYMR, Nato T.M. Kawashina T., Sanah Rasan T. S.
Tidada S. T., Martick, 12. Hume D.M., Marka M.M., Manamalian genome.";
An Hagami M., Waki K., Mathiki A., Okamura-Oho Y., Suruki H., Kawasi J.,
Hagami M., Waki K., Mathiki A., Okamura-Oho Y., Suruki H., Kawasi J.,
Hayabilakaki Y.;
Tragami M., Waki K., Mathiki A., Okamura-Oho Y., Suruki H., Kawasi J.,
Hayabilakaki Y.;
Eschero 109:1529-15312005).
Mai M. Marki K., Mathiki A., Okamura-Oho Y., Suruki H., Kawasi J.,
Hayabilakaki Y.;
Manamalaki Y.;
Man

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                                                                                                                                                                                                                 Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Nibata Y., Muramatsu M., Hayashizaki Y.; Itoh M., Genome Res. 10:1617-1630(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600; MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibata K., Nacawa K., Nagaoka S., Sasaki N., Carninci P., Sumi N., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Mateumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; Riki integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
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MOI; MOI:2682305; Hbxap.

GO; GO:0005515; F:protein binding; IEA.

GO; GO:00063519; P:rainc ion binding; IEA.

GO; GO:0006352; P:rainc ion binding; IEA.

GO; GO:0006355; P:rainc ion binding; IEA.

InterPro; IPR001965; Znf_PHD.

SMART; SM00249; PHD; 1.

PROSITE; PS01359; ZF_PHD 1;

PROSITE; PS01359; ZF_PHD 1;

PROSITE; PS01359; ZF_PHD 2;

PROSITE; PS01359; ZF_PHD 2;

PROSITE; PS01359; ZF_PHD 2;
"Functional annotation of a full-length mouse cDNA collection.", Nature 409:685-690(2001).
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Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88.0%; Score 44; DB 2; Length 998; 91.7%; Pred. No. 5e+02;
                                                                                                                                                         STRAIN=C57BL/6J; TISSUE=Stomach; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AK146675; BAE27351.1; -; mRNA.
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QBIGNG_DROME PRELIMINARY; PRT;
QBIGNG;
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Best Local Similarity 91.7
Matches 11; Conservative
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                                                                                                                       SEQUENCE
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Q8IGN6_DR
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                                                                                                                                                                                                                                                                                    Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                  STRAIN-Berkeley;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Stapleton M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae, Chlorophyta; Prasinophyceae, Mamiellales; Mamiellaceae, Ostreococcus.
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Cell Cycle 3:513-518(2004).
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GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
GO; GO:0000087; P:protein tyrosine phosphatase activity; IEA.
GO; GO:000087; P:protein amino acid dephosphorylation; IEA.
InterPro; IPR000751; MPI Phosphatase.
InterPro; IPR001763; Rhodanese-like.
PANTHER; PTHR10828; MPI_Phosphatase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             86.0%; Score 43; DB 2; Length 235; 83.3%; Pred. No. 2.1e+02; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                         Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                  EMBL; BT001688; AAN71443.1; -; mRNA.
FlyBase; FBgn0038592; CG18599.
SEQUENCE 235 AA; 24886 MW; A88629B97C919948 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00450; RHOD; 1.
PROSITE; PS50206; RHODANESE 3; 1.
SEQUENCE 395 AA; 43146 MM; BAEA2E381C122C9E CRC64;
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Ephydroidea; Drosophilidae; Drosophila.
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QGVRGS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2004, sequence version 1.
07-FEB-2006, entry version 9.
Dual specificity phosphatase Cdc25.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 83.3
ses 10; Conservative
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                                                             NUCLEOTIDE SEQUENCE.
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tes 10; Conserv
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                      NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=cdc25;
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106 VRGS OS
106 OS - Q
107 - F
107 - 
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RR DWCEGOTIDE SEQUENCE.

RA MEDLINE-20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; Adams M.D. Celniker S.E., Hill P. W., Hoskins R.A., Galle R.F., Garle R.A., Levis S.E., Ii P. W., Hoskins R.A., Galle R.F., Garle G.G., Scherer S.E., Ii P.W., Hoskins R.A., Galle R.F., Garle G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X., Miklos G.L.G., Randon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D., Randon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D., Randon R.C., Rogers Y.-H.C., Blazel R.G., Madrows-Frankoch C. Bladwin D., Randon R.G., Bence P.V., Bernan B.P., Bandario D., Bolahakov S., Bence P.V., Bernan B.P., Bandario D., Bolahakov S., Borkova D., Bochen M.R., Bouck J., Brokstein P., Brottier P., Cherry J.W., Cawley S., Dalkov D., Davies P., Cherry J.W., Cawley S., Dalkov D., Dew I.D., Dow I.C., Ferraz C., Center A., Chanfra I., R. Doubn B., Bulhake C., Davemport L.B., Davies P., Horson M., P. Addie R., Gong F., Gorrell J.H., Gulber C., Ferraz C., Ferraz C., Perrice S., Plasser K., A. Houston K.J., Evanglista C.C., Ferraz C., Ferraz C., Perrice S., Plasser K., A. Houston K.J., Malush R., Kalush F., Kalpen G.H., Ke Z., Galbar W.M., Glasser K., A. Jalali M., Kalush F., Karpen G.H., Ke Z., Galbar W., Idesser K., Alali M., Kalush F., Karpen G.H., Ke Z., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J.H., Murny D.M., Nelson D.L., Nerlucon R.M., Moy M., Nurly B., Murny D.M., Nelson D.L., Nerlucon K.A., Nakorn K., Narny C., Mortis J., Morther B., Reinert K., Periners R., Vollac C., Staplecon M., Stupski M.P., Smith T., Spier E., Sprading A.C., Staplecon M., Stupski M.P., Smith H.O., Rishes R., Woodser T., Warsserman D.A., Weissenbach J., Mail Jame S., Warsserman D.A., Weissenbach J., Shing G.M., Warsserman D.A., Warsser
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MEDLINE=2242605; PubMed=12537568;
MEDLINE=2242605; PubMed=12537568;
Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Patel S.D., Peiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; Finishing a whole-genome shotgun: releases 3 of the Drosophila melanogaster euchromatic genome sequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name-CG18599; ORFNames-Dmel_CG18599;
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                     01-MAY-2000, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                 475 AA.
                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                          01-OCT-2002, sequence version 2.
21-FEB-2006, entry version 32.
CG18599-PA.
                                                                                                                                                                                                                            PRELIMINARY;
117 AAMAAAAASAM 127
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NUCLEOTIDE SEQUENCE
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NUCLEOTIDE SEQUENCE

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RAW TOUCLEOTIDE SEQUENCE.

RAY MUCLEOTIDE SEQUENCE.

RAY ENDIANCE-1018 PLANEd=10731132, DOI=10.1126/science.287.5461.2185;

RADARMS-12046006; PubMed=10731132, DOI=10.1126/science.287.5461.2185;

RAY Adama M.D., Cellikers S.E., 19 PW. H. Gokins R.A., Galle R.F.,

RAY Sutton G.G., Worthman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RAY Brandon R.C., Rogers Y.-H.C., Halt G., Chang C., Relifer B.D.,

RAY Brandon R.C., Rogers Y.-H.C., Halt G., Chang C., Relifer B.D.,

RAY Brandon R.C., Rogers Y.-H.C., Halt G., Chen L.X., Miklos G.L.G.,

RAY Brandon R.C., Rogers Y.-H.C., Halt G., Chen L.X., Baldwin D.,

Ballew R.M., Baeu A., Baxendale J., Bayrakkaroglu L., Beasley E.M.,

Ballew R.M., Cawley B.C., Buller H., Caddeu E., Center A., Challer P., Brottler P., Helman T.J., Hernandez J.R., Houck J., Roldek P., Gorrell J.H., Guz. S., Gelbart W.M., Glodek P., Gorrell J.H., Guz. S., Gelbart W.M., Gong F., Gorrell J.H., Guz. S., Gelbart W.M., Gong F., Rolling P., Laistler P., Lei Y., Leiteky A.A., Li J.H., Li J., Li J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Centrer S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeifer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Mar K., Stapleton M., Sutton G.G., Venter Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; Finishing a whole-genome shotgun: release 3 of the Drosophila melanogaster euchromatic genome sequence.", Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.,
"The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall G.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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MEDLINE=22426065; PubMed=12537568;
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NUCLEOTIDE SEQUENCE.
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                                  Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R., Patel S., Frise B., Mheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E., "The transposable elements of the Drosophila melanogaster euchromatin: "The transposable elements of the Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO:0005634; C:nucleus; IEA.
GO:0003700; F:transcription factor activity; IEA.
GO:0007275; P:devolopment; IEA.
GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Berkeley Drosophila Genome Project;
Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.
Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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PROSITE; PS50071; HOMECBOX 2; 1.
DNA-binding; Developmental protein; Homeobox; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86.0%; Score 43; DB 2; Length 475;
83.3%; Pred. No. 3.7e+02;
ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Drosophila melanogaster release 4 sequence.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JAN-2006) to the EMBL/GenBank/DDBJ databases -! - SUBCELLULAR LOCATION: Nuclear (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transcription; Transcription regulation.
SEQUENCE 475 AA; 50950 MW; 7DAC89752B1FA99D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
                                                                                                                                                       a genomics perspective.";
Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE003721; AAF55524.2; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001356; Homeobox.
InterPro; IPR012287; Homeodomain-rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY; PRT;
           MEDLINE=22426070; PubMed=12537573;
                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
MEDLINE=22426069; PubMed=12537572;
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ORFNames=CG31422, Dmel_CG31422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P06601; 1FJL.
FlyBase; FBgn0038592; CG18599.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00046; Homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00024; HOMEOBOX.
SMART; SM00389; HOX; 1.
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54 AALAAAAAAVA 65
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FlyBase;

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8888

Query Match

Best Local

Matches

DROME QBIMU7;

RESULT 11
Q81MU7 DRC
ID Q81MU
DAC Q81MU
DT 01-M
DT 01-M
DT 07-FI
DE CG311
GN ORFN

6.4e+02;

Pred. No.

83.3%;

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                            Berkeley Drosophila Genome Project;
Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.
Yu C., Rubin G.;
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                     "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Drosophila melanogaster release 4 sequence.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 305 AA; 32565 MW; 472F8AA40CFF9953 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
Thermoproteaceae; Thermoproteus.
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                                                                                                                                                                                                                                           systematic review.";
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002)
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GO; GO:0016491, F:oxidoreductase activity, IEA.
GO; GO:0006118, P:electron transport, IEA.
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InterPro; IPR009014; Transketo_C_like.
Pfam; PF01855; POR_N; 1.
Oxidoreductase; Pyruvate.
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Q70329;
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Matches 10; Conservative
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DB 2; Length 637;

84.0%; Score 42;

Query Match

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RY CLEACHINE SEQUENCE (LARGE SECALE GENOMIC DNA).

RY CLEACHINE SEQUENCE (LARGE SECALE GENOMIC DNA).

RY MADIANE-20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;

RA Adama M.D. (Pelniker S.E. I. iP DW. Hoskins R.A., Galle R.F.,

RA Adama M.D. (Pelniker S.E. I. iP DW. Hoskins R.A., Galle R.F.,

RA Banadides P.G., Scherer S.E. I. ip PW. Hoskins R.A., Galle R.F.,

RA Bardon R.C., Rogers Y.-H.C., Blazel R.G., Change M., Peleifers B.D.,

RA Bardon R.C., Rogers Y.-H.C., Blazel R.G., Change M., Peleifers B.D.,

RA BAILW R.M., Basu A., Barandal B.P., Bhandari D., Beasley E.M.,

RA BAILW R.M., Cawley S., Daller R., Carler A., Chandra I.,

RA BAILW R.M., Cawley S., Daller R., Carler A., Chandra I.,

RA BAILW R.M., Cawley S., Daller R., Carler A., Chandra I.,

RA BAILW R.M., Cawley S., Daller C., Davenport L.B., Davice P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rochs S., Dunkov B.C., Dunn P.,

Burtis R.C., Busam D.A., Heiman T.J., Herrandez J.R., Houck J.,

RA Goder C., Garrell J.H., Garg N.S., Gelbart W.M., Glasser K.,

RA Goder C., Garrell J.H., Garg N.S., Gelbart W.M., Glasser K.,

RA Harris N.L., Harvey D.A., Heiman T.J., Herrandez J.R., Houck J.,

RA Harris N.L., Harvey D.A., Heiman T.J., Herrandez J.R., Houck J.,

RA Harris N.L., Harvey D.A., Heiman T.J., Marchison J.A., Kechnison J.A.,

RA Harris N.L., Marvey D.A., Heiman T.J., Warny D.M., Nalson D.L.,

RA Mount S.M., Noy M., Wurphy B., Murphy L., Muzny D.M., Nalson D.L.,

RA Mount S.M., Noy M., Murphy B., Murphy L., Muzny D.M., Nalson D.L.,

RA Bailan R.M., May M., Murphy B., Murphy L., Marsh W. Saper M.G.,

RA Beiter K., Seadling A.C., Staplecon M., Stupes R., Santh T.,

RA Britans S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Britans S.M., Woodage T., Worley K.C., Wu D., Yang G., Zhao D., Zhao M., Wallson D.L.,

RA Britans S.M., Woodage T., Worley K.C., Wu D., Yang G., Zhao D., Zhao G., Zhao R., Saidh K., Zhao G., Zhao R., Zhao G., Zhao G., Zhao R., Zhao G., Z
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Canton-S;
MEDLINE=20296162; PubMed=10839352; DOI=10.1016/S0896-6273(00)81166-6;
Wan H.I., DiAntonio A., Fetter R.D., Bergstrom K., Strauss R.,
Goodman C.S.;
  Gaps
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                                                                                                                                                                                                                                                                                                                                            Name-hiw; ORFNames=CG32592;
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE [MRNA], FUNCTION, AND TISSUE SPECIFICITY
1; Indels
                                                                                                                                                                                                                                                                                                       Ubiquitin ligase protein highwire (EC 6.3.2.-) (Protein pam/highwire/rpm-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Highwire regulates synaptic growth in Drosophila.";
                                                                                                                                                                                                               Q9NB71; Q8M236; Q9VXZ5; 21-JUN-2005, integrated into UniProtKB/Swiss-Prot. 21-JUN-2005, sequence version 2. 07-MAR-2006, entry version 26.
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NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
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1; Mismatches
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10; Conservative
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COMFLICT
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                                                                                                                                                                                                                                                                                      NUCLECTIDE SEQUENCE [LARGE SCALE MRNA] OF 4083-5233.

NUCLECTIDE SEQUENCE [LARGE SCALE MRNA] OF 4083-5233.

STRAIN=Berkeley; TISSUE=Larva, and Pupae;
MEDLINE=22426066; PubMed=12537569;
A Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
Caralson J.W., Brokstein P., Yu C., Champe M.,
Cappeton M., Calliker S.E.;
A George R.A., Guarin H., Kromiller B., Pacleb J.M., Park S., Wan K.H.,
A Rubin G.M., Celniker S.E.;
Canome Biol. 3:RESEARCH0080.1-RESEARCH0080.8 (2002).

LISESEARCH0080.1-RESEARCH0080.8 (2002).

CI- FUNCTION: B3 ubiquitin ligase proteins mediate ubiquitination and subsequent proteasomal degradation of target proteins. Has a role during synaptogenesis negative regulator of synaptic growth.

CI- PATHWAY: Ubiquitin conjugation; third step.
CI- PATHWAY: Ubiquitin conjugation; third step.
CI- STRUELLUAR LOCATION: Nucleus (By similarity).
CI- STRUELLUAR LOCATION: Nucleus (By similarity).
CI- STRUELSE SPECIFICITY: Nervous system specific expression outside the caround which the synaptic neuropil forms. Expression outside the CNS starts at stage 16 in presynaptic terminals at the periactive exuberantly and are expanded in both the number of boutons and in the extent and length of branches.
CI- SIMILARITY: Contains 1 Rildanin repeat.
CI- SIMILARITY: Contains 1 Rildanin repeat.
CI- CAUTION: Ref.2 sequence differs from that shown due to erroneous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R GO; GO:0016023 C:Cytoplasmic membrane-bound vesicle; IDA.

GO; GO:0016023 C:Cytoplasmic membrane; IDA.

GO; GO:0005886; C:plasma membrane; IDA.

GO; GO:0004842; F:bicquitin-protein ligase activity; ISS.

GO; GO:0004842; F:ubiquitin-protein ligase activity; ISS.

GO; GO:0004842; F:ubiquitin-protein ligase activity; ISS.

R GO; GO:0004842; F:ubiquitin-protein ligase activity; ISS.

R GO; GO:0004842; F:ubiquitin-protein ligase activity; ISS.

R GO; GO:001509; P:BMP signaling pathway; IPI.

R GO; GO:0015014; P:negative regulation of BMP signaling pathway; IGI.

R GO; GO:0016567; P:protein ubiquitination; ISS.

InterPro; IPR011989; ARM-like.

R InterPro; IPR011989; PHR.

R InterPro; IPR0010408; Filamin.

R InterPro; IPR0011841; Znf_RING.

R Pfam; PF00415; RCC1; I.

R Pfam; PF00415; RCC1; I.

R Pfam; PF00415; RCC1; I.

R RINTS; RRO0633; RCCNDNSATION.

R RINTS; RRO0633; RCCNDNSATION.

R RART; RNOS1, RING; RING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
GENOME REANNOTATION.

GENOME REANNOTATION.

Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.B.,

Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.

Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,

Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                               "Annotation of the Drosophila melanogaster euchromatic genome:
                                                                                                                                                                                                                                      systematic review.";
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AF262977, AAF76150.1; -; mRNA.
EMBL, AE003497; AAF48411.2; ALT. SEQ, Genomic_DNA.
EMBL, AX113376; AAM29381.1; ALT. INIT; mRNA.
Ensembl; CG32592; Drosophila meTanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS50194; FILAMIN REPEAT; 1.
PS00625; RCC1 1; FALSE NEG.
PS00626; RCC1 2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FlyBase, FBgn0030600; hiw.
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                                                                                                                                                                                                Lewis S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN-RNC-1 / ATCC 700922 / JCM 11081;

MEDLINE=20504483; PubMed=11016950; DOI=10.1073/pnas.190337797;

NG W.V., Kennedy S.P., Mahairas G.G., Berguist B., Pan M.,

Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,

Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,

Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,

Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,

Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,

Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;

Manna M., Preitas G., Paniels C.J., Daniels C.J.,

Ecenome sequence of Halbbacterium species NRC-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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PROSITE; PS50012; RCC1 3; 1.
PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
PROSITE; PS50089; ZF_RING_2; 1.
Complete proteome; Ligase; Metal-binding; Nuclear protein; Repeat;
Synapse; Transcription; Transcription regulation;
Ubl conjugation pathway; Zinc; Zinc-finger.

Ubiquitin ligase protein highwire.

/FIId_PRO_000055971.
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RCC1 2.
RCC1 3.
RCC1 4.
RCC1 6.
Filamin.
Filamin.
RING-type, atypical.
N -> D (in Ref. 1).
C -> R (in Ref. 1).
C -> R (in Ref. 1).
G -> E (in Ref. 1).
G -> E (in Ref. 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 42; DB 1; Deng-
Pred. No. 3.6e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Halobacterium salinarium (Halobacterium halobium).
Archaea, Buryarchaeota, Halobacteria, Halobacteriales;
Halobacteriaceae, Halobacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181 (2000)
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100.0%; Pred. No. 1.7e+02;
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BioCyc; HSP64091:VNG1530H-MONOMER; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.0%;
90.9%;
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Best Local Similarity 90.9
Matches 10; Conservative
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4652
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SEQUENCE 85 AA;
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Science 309:1559-1563(2005)
1 AAMAAAAAAA 12
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NUCLEOTIDE SEQUENCE
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                    PubMed=16120803; DOI=10.1093/molbev/msi246;
Comeron J.M., Guthrie T.B.;
"Intragenic Hill-Robertson Interference Influences Selection Intensity
on Synonymous Mutations in Drosophila.";
Mol. Biol. Evol. 22:2519-2530(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP clade,
Pooideae, Triticeae, Triticum.
                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xu Z.S., Ma Y.Z., Cheng X.G., Li L.C., Chen M.;
"Isolation and functional identification of DRE binding protein in
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0
                                                                                                                          Drosophila erecta (Fruit fly).
Bukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                          82.0%; Score 41; DB 2; Length 174; 100.0%; Pred. No. 3e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82.0%; Score 41; DB 2; Length 243; 83.3%; Pred. No. 4e+02; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; DQ026517; AAY98505.1; -; mRNA.
SEQUENCE 243 AA; 25932 MW; C2F8705208B73E9B CRC64;
                                                                                                                                                                                                                                                                                                                                      174 AA; 17861 MW; 76E5A0CDB39E7C7E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-JAN-2006, sequence version 1.
07-FEB-2006, entry version 2.
Dehydration responsive element binding protein.
                                                                                20-DEC-2005, integrated into UniProtKB/TrEMBL. 20-DEC-2005, sequence version 1. CFEB-2006, entry version 3. CG13448 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-JAN-2006, integrated into UniProtKB/TrEMBL
                                                             174 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243 AA.
                                                                                                                                                                                                                                                                                                    EMBL; DQ138775; ABA86381.1; -; Genomic_DNA
                                                             PRT;
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                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Triticum aestivum (Wheat).
                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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        30 AAMAAAAAA 39
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                    NCBI_TaxID=7220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4565;
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Q2QK76;
                                                             QZXY87_DROER
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NON TER
SEQUENCE
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RYATINE-CS7BB/643; PubMed=12466851; DOI=10.1038/nature01266;

RA OKazaki Y., Puruno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

RA Blake J.A., Bradt D., Bult C., Hume D.A., Quackenbush J.,

RA Blake J.A., Bradt D., Bult C., Hume D.A., Quackenbush J.,

RA Gasterland T., Gariboldi M., Gibsi C., Godzik A., Gough J.,

RA Gasterland T., Gariboldi M., Gibsi C., Godzik A., Gough J.,

RA Gasterland T., Gariboldi M., Gibsi C., Godzik A., King B.L.,

RA Gasterland T., Gariboldi M., Gibsi C., Godzik A., King B.L.,

Ranai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

Ronagaya A., Kurochkin I.V., Lee Y., Lehhard B., Lyons P.A.,

Ronagaya A., Kurochkin I.V., Lee Y., Lehhard B.L., Miki H.,

RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RA Maglott D.R., Maltais U., Marchionni L., McKenzie L., Miki H.,

RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Kingwald M.,

Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

RA Verardo R., Wanner L., Wahlestett C., Setou M., Shimada K.,

Allming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang I.,

Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,

Hara A., Hashizawe T., Konno H., Nakamura M., Sakazume N., Sakazume A.,

Baniraki T., Wati K., Kawai J., Shibata K., Sakazume A.,

Baniraki T., Wati K., Sawai D., Shibata K., Shinagawa A.,

Baniyazaki A., Soshino M., Waterston R., Lander B.S., Rogers J.,

Baniraki Y., Yoshino W., Waterston R., Lander B.S., Rogers J.,

Baniraki Y., Tohilal-Length CDNAS.,;

Baniraki Y., Watunishi Y., Shinagawa A.,

Baniraki Y., Watunishi Y., Shinagawa A.,

Baniraki Y., Shinagawa Y.,

Baniraki Y., Shinagawa Y.,

Baniraki Y., Shinagawa Y.,

Baniraki Y., Shinagawa Y.,

Baniraki Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kawai D. Shubada 1217851; DOI=10.1038/3505500; Kawai D. Shinagawa A.; Shibata K.; Yoshino M.; Itoh M.; Ishii Y.; Kawai J.; Shinagawa A.; Shibata K.; Yoshino M.; Itoh M.; Ishii Y.; Arakawa T.; Hara A.; Pukunishi Y.; Komno H.; Adachi J.; Fukuda S.; Arakawa T.; Hara A.; Pukunishi Y.; Komno H.; Kaukwa T.; Yamanaka I.; Asito T.; Okazaki Y.; Golobori T.; Bono H.; Ksukwa T.; Saito R.; Ashburner M.; Batalov S.; Yamanaka I.; Radota K.; Matsuda H.A.; Ashburner M.; Batalov S.; Casavant T.; Ruhl P.; Lewis S.; Matsuo Y.; Nikaido I.; Pesole G.; Quackenbush J.; Kuhl P.; Lewis S.; Matsuo Y.; Nikaido I.; Pesole G.; Quackenbush J.; Sakai K.; Okido T.; Furuno M.; Aono H.; Baldarelli R.; Barsh G.; Blake J.; Bult C.; Fletcher C.; Fullita M.; Gariboldi M.; Blake J.; Bult C.; Fletcher C.; Fullita M.; Gariboldi M.; Bustincich S.; Hill D.; Hofmann M.; Hume D.A.; Kamiya M.; Lee N.H.; Nordone P.; Ring B.; Ringwald M.; Rodriguez I.; Sakamcho N.; Nordone P.; Ring B.; Ringwald M.; Rodriguez I.; Sakamcho N.; Sasaki H.; Sato K.; Schoenbach C.; Seya T.; Shibata Y.; Storch K.-F.; Whinawali H.; Toyo-oka K.; Wang K.H.; Weitz C.; Whittaker C.; Wilming L.; Wanshaw-Boris A.; Yoshida K.; Hasegawa Y.; Kawaji H.; Kohtsuki S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-CSTRICT TISSUE=Thymus;
MEDLINE-20499374; PubMed-11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
"repare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
STRAIN=C57BL/6J; TISSUE=Thymus; PubMed=16141073; DOI=10.1126/science.1112009; RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium; "Antisense Transcription in the Mammalian Transcriptome."; Science 309:1564-1566(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 409:685-690(2001).
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                                                                                                                                            NUCLEOTIDE SEQUENCE
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Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.;
MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600; MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibata K., Natawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara B., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; Rikik integrated sequence analysis (RISA) system-384-format Sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                           Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K., Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S., Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N., Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D., Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A., Muramatsu M., Hayashizaki Y.;
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21-FEB-2006, entry version 6.
Regulatory protein, LysR:LysR substrate binding domain precursor.
ORFNames=BproDRAFT_3748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hammon N., Israni S., Pitluck S., Richardson P.,
Sequencing of the draft genome and assembly of Polaromonas sp.
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Comamonadaceae, Polaromonas.
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GO; GO:0005737; C:cytoplasm; IDA.
GO; GO:0005737; C:cytoplasm; IDA.
GO; GO:0005737; P:nucleus; IDA.
GO; GO:0005737; P:nukla splice site selection; IMP.
InterPro; IPR000571; Znf CCCH.
InterPro; IPR00555; Zf-CCH; Z.
SMART; SM00356; Znf C3HL; Z.
SMART; SM00356; Znf C3HL; Z.
SEQUENCE 254 AA; Z6605 MW; 3030142F792FAAE3 CRC64;
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US DOE Joint Genome Institute (JGI-ORNL);
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Larimer F., Land M.;
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Q4B1F7;
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SIMILARITY: Contains 1 HMG box DNA-binding domain.
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HSSP; P48432; 1CTO.
SMR; Q80XF1; 67-145.
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                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50118; HMG BOX 2; 1.
DNA-binding; Nuclear protein; T
CHAIN 1 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37858 MW;
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83.3%;
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les 10; Conservative
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2223
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164
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                                                                                                                                                                                                                                                                                   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Purnellary, 9, 1841 D., Casey E.S., Harland R., Lovell-Badge R.;
"Expression of Sox3 throughout the developing central nervous system is dependent on the combined action of discrete, evolutionarily conserved, regulatory elements.; submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Nucleus.
-!- TISSUE SPECIFICITY: Mainly in the developing central nervous system. Expressed in developing urogenital ridge.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                      US DOE Joint Genome Institute (JGI-PGF);

Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T., Hammon N., Israni S., Pitluck S., Richardson P.;

Hammon N., Israni S., Pitluck S., Richardson P.;

Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.

-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                         EMBL; AAFQ02000004; EAM39845.1; -; Genomic DNA.
GO; GO:0003700; F:transcription factor actīvity; IEA.
GO; GO:000535; P:regulation of transcription, DNA-dependent; IEA.
GO; GO:000535; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IRR00847; FITH LYSR.
Pfam; PF00126; HTH 1; 1.
Pfam; PF00126; HTH 1; 1.
PRINTS; PR00039; HTHLVSR.
PROSITE; PS50931; HTH_LYSR; 1.
DNA-binding; Signal; Transcription; Transcription regulation.
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0
                                                                                                                                                                                                                                       preliminary data.
SIMILARITY: Contains 1 HTH lysR-type DNA-binding domain.
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"Annotation of the draft assembly of Polaromonas sp. JS6
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
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07-FEB-2006, entry version 35.
Transcription factor SOX-3.
Name=SoX3; Synonyms=Sox-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     331 AA; 36159 MW;
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ses 10; Conservative
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                                                               NUCLEOTIDE SEQUENCE
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                                                                                         STRAIN=JS666;
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P53784;
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MGI; MGI:88365; Sox3.

MGI:88365; Sox3.

MGI; MGI:88365; Sox3.

MGI; MGI:88365; Sox3.

MGI:
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Transcription factor SOX-3.
//FIIG_FRO_0000048721.
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tanaka S., Kamachi Y., Tanouchi A., Hamada H., Jing N., Kondoh H.; "Interplay of SOX and POU Factors in Regulation of the Nestin Gene in Neural Primordial Cells.";
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Pred. No. 5.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2A8477A10A517FEF CRC64;
                                                                                                                                                        01-JUN-2003, integrated into UniProtKB/TrEMBL
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Poly-Ala.
Poly-Pro.
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Poly-Ala.
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05-JUL-2005, sequence version 1.
07-FEB-2006, entry version 3.
Sox3 protein (Fragment).
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101 AAVAAAAAAFA 112
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Best Local Similarity 83.3
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                    NCBI_TaxID=39947;
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Q4VBD8_MOUSE
Q4VBD8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=Sox3;
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP clade,
Ehrhartoideae, Oryzeae, Oryza.
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                                                                                                                                                                                                                                                Gaps
                GO; GO:0006355; P:regulation of transcription, DNA-dependent; RCA. GO; GO:0048515; P:spermatid differentiation; IMP.
InterPro; IPR000910; HMG 12_box.
InterPro; IPR000505; HMG box; 1.
SMART; SM00398; HMG; 1.
PROSITE; PSS0118; HMG; 1.
SEQUENCE 375 AA; 37789 MW; 3E117E20D40BFE34 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82.0%; Score 41; DB 2; Length 403; 83.3%; Pred. No. 6e+02; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                  82.0%; Score 41; DB 2; Length 375; 83.3%; Pred. No. 5.7e+02;
                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hydrolase, Hypothetical protein.
SEQUENCE 403 AA; 42774 MW; 30722980A480A479 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0006725; P:aromatic compound metabolism; IEA.
InterPro; IPR003089; AB.hydrolase.
InterPro; IPR000073; AB.hydrolase_1.
InterPro; IPR000379; Ser_estrs.
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Q75KP7 ORYSA PRELIMINARY; PRT; 417 AA.
Q75KP7 OLYUL-2004, integrated into UniProtKB/TrEMBL.
05-JUL-2004, sequence version 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-NOV-2004, integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     403 AA.
    GO:0009887; P:organ morphogenesis; IMP.
                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AC137623; AAV25643.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-NOV-2004, sequence version 1.
07-FEB-2006, entry version 10.
Hypothetical protein P0426G01.8.
Name-P0426G01.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00561; Abhydrolase 1; 1. PRINTS; PR00111; ABHYDROLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                        284 AAAAAAAAAAAS 295
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                                                                                                                                                                                                                                                10; Conservative
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Best Local Similarity
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Best Local Similarity
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QEODW4;
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Q75KP7_ORY
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OGODMA ORY

OGODM

AC QGODM

AC QGODM

DT 23-NO

OC ENLAN

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Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
-!- DOMAIN: The RING-type zinc finger domain is essential for
ubiquitin ligase activity. It coordinates an additional third zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                            Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP clade,
Ehrhartoideae, Oryzeae, Oryza.
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                                                                                                                                                                                                                                                                                                                                         Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M., Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S., Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J., White O., Salzberg S.L., Frasscr C.M., "Oryza sativa chromosome 3 BAC OsJNBa0065F09 genomic sequence."; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
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MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 417;
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Go; GO:0005634; C:nucleus; IEA.

GO; GO:000151; C:ubiquitin ligase complex; IEA.

GO; GO:00046872; F:metal ion binding; IEA.

GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.

GO; GO:0016567; F:zinc ion binding; IEA.

GO; GO:0016567; P:protein ubiquitination; IEA.

InterPro; IRR001841; Znf RING.

PF00097; zf-C3HC4; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00184; RING; 1.
PROSITE; PS50089; ZF RING 2; 1.
Metal-binding; Woclear protein; Zinc; Zinc-finger.
SEQUENCE 417 AA; 42736 MW; 7CC9F220D3B7B83E CRC64;

    -!- SIMILARITY: Contains 1 RING-type zinc finger.

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83.3%; Pred. No. 6.2e+02;
iive 1; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AC099323; AAR87274.1; -; Genomic_DNA
Putative RING-H2 zinc finger protein.
Name=OSJNBa0065F09.2;
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Hum. Mol. Genet. 2:2013-2018(1993).
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COMPBIAS
COMPBIAS
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COMPBIAS
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SEQUENCE
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GO; GO:0005634; C:nucleus; RCA.

GO; GO:0005634; C:nucleus; RCA.

GO; GO:0005632; P:establishment and/or maintenance of chromat. . .; RCA.

GO; GO:0003090; P:forebrain development; IMP.

GO; GO:0009887; P:regulation of transcription, DNA-dependent; RCA.

GO; GO:00048515; P:spermatid differentiation; IMP.

GO; GO:00048515; P:spermatid differentiation; IMP.

FINTERPROPERS: IMG DOX; I.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82.0%; Score 41; DB 2; Length 436;
83.3%; Pred. No. 6.4e+02;
ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     436 AA; 43905 MW; C146DB68B042E6D1 CRC64;
                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOX3 HUMAN STANDARD; PRT; 446 AA. P412Z5; P35714; Q9NP49; 01-FEB-1995, integrated into UniProtKB/Swiss-Prot. 07-JUN-2004, sequence version 2. 07-JUN-2004, sequence version 38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; BC096018; AAH96018.1; -; mRNA.
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MEDLINE=94154672; PubMed=8111369;
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                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6; TISSUE=Brain;
NIH MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transcription factor SOX-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   345 AAAAAAAAMS 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 83.3
Les 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AAMAAAAAAMA 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SM00398; HMG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=SOX3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                     NUCLEOTIDE SEQUENCE OF 150-203.
MEDLINE=22310993; PubMed=1614875;
Denny P., Swift S., Brand N., Dabhade N., Barton P., Ashworth A.;
"A conserved family of genes related to the testis determining gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 41; DB 1; Length 446; Pred. No. 6.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HGNC; HGNC:11199; SOX3.

Mi; 313430; gene.

GO; GO:0003677; F:DNA binding; TAS.

GO; GO:0007417; P:Central nervous system development; TAS.

HGPSPC: TPRO0910; HMG 12_box.

Pfam; PF00505; HMG box; T.

SMART; SM00398; HMG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                  Gorry M.C., Hart P.S., Sashi V., Hart T.C.; "Clarification of the genomic sequence for human SOX3."; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L -> Q (in Ref. 3).
D -> E (in Ref. 3).
E -> D (in Ref. 3).
Missing (in Ref. 2).
F79E79C2D16BB929 CRC64;
                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: Nucleus.
-!- SIMILARITY: Contains 1 HMG box DNA-binding domain.
-!- CAUTION: Was originally (Ref.3) termed SOX-9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-MAY-2005, integrated into UniProtKB/TrEMBL 10-MAY-2005, sequence version 1. 07-FEB-2006, entry version 1. 07-FEB-2006, entry version 7. FEB-87X (Sex determining region Y)-box 3. Name-SOX3; ORFNames=RP11-51C14.3-001;
                                                                                                                                                                                                                                                                                                                                                                                                                      Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X71135; CAA50465.1; -; Genomic_DNA.
EMBL; AF264713; AAF73059.1; -; Genomic_DN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P48432; 1GT0.
SMR; P41225; 137-215.
TRANSFAC; T04916; ENSG0000134595; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Poly-Gly.
Poly-Ala.
Poly-Pro.
Poly-Ala.
Poly-Ala.
                                                                                                                                                                                                                    Nucleic Acids Res. 20:2887-2887(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HMG box.
                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X65665; CAA46616.1; -; mRNA.
PIR; 138239; 138239.
PIR; S22942; S22942.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSS0118; HMG_BOX_2; 1.
ng; Nuclear protein; Ti
1 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45210 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82.0%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OSJWI3 HUMAN PRELIMINARY;
OSJWI3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       355 AAAAAAAAAAAS 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AAMAAAAAAA 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        364
159
176
202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA-binding; Nuclear
NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         446 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1139
1129
2234
2234
3340
3353
1159
202
297
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sox3 protein
Name=Sox3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QSRKWO MOUSE
QSRKWO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loca
Matches
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Q5RKW0 MOU
1D Q5RKW
D7 21-DE
DT 21-DE
DT 21-DE
DT 80x3
DB 80x3
GN Names
OS MUS m
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                                                                                                                                               Klausner R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D., Rlausner R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scaelet T.B., Bonaldo M.F., Gasavant T.L., Scheet T.E., & Rephiston M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., & Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., & Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H., & Hochards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., & Pahey J., Helton E., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Ashar M.A., Schein J.E., Jones S.J.M., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
    Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0003677; F:DNA binding; IEÀ.
GO; GO:000355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR000910; HMG 12_box.
Pfam; PF00505; HMG_box; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                     MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 41; DB 2; Length 446;
Pred. No. 6.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                  Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00398; HMG; 1.
PROSITE; PS50118; HMG BOX 2; 1.
SEQUENCE 446 AA; 45210 MW; F79E79C2D16B8929 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL-2004, integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AL121875; CAB87584.1; -; Genomic_DNA.
EMBL; BC093865; AAH93865.1; -; mRNA.
EMBL; BC093863; AAH93863.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMR; Q5JW13; 137-215.
Ensembl; ENSG0000134595; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004, sequence version 1.
07-FEB-2006, entry version 13.
Sox3 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82.0%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            355 AAAAAAAAAAS 366
                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 82.0
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AAMAAAAAAMA 12
                                                       NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
                                                                                                              NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH MGC Project;
                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QEP564 MOUSE
QEP564;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=Sox3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 26
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1D Q66
AC Q66
DT 05
DT 07
DE S0
GN NA
OS MU
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MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Rausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratue P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nilalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffaxd G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimmood J.W., Schmutz J., Mysers R.M.,
Rodriguez A.C., Grimmood J.W., Schmutz J., Mysers R.M.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
Genneration and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0005634; C:nucleus; RCA.
GO; GO:0003704; F:transcription factor activity; RCA.
GO; GO:0003704; F:transcription and/or maintenance of chromat. . .; RCA.
GO; GO:00030900; P:forebrain development; IMP.
GO; GO:0009887; P:regulation of transcription, DNA-dependent; RCA.
GO; GO:00048515; P:regulation of transcription, IMP.
InterPro; IPR000910; HMG 12_box.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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Pred. No. 6.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             448 AA; 45157 MW; BC567C0808CA64C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-DEC-2004, integrated into UniProtKB/TrEMBL. 21-DEC-2004, sequence version 1. 07-FEB-2006, entry version 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              449 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, BC063061, AAH63061.1; -; mRNA.
SMR; Q6P564; 140-218.
Ensembl; ENSMUSG00000045179; Mus musculus.
MGI; MGI:99365; Sox3.
Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50118; HMG_BOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AAMAAAAAAMA 12
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                                                                                                     NUCLEOTIDE SEQUENCE
                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad.
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RESULT 29
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                                                                                  MEDLINE-22388257; PubMed-12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Alusener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina R., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C., Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C., Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M., Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Hahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Generation and initial analysis of more than 15,000 full-length human more and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0005634; C:nucleus; RCA.
GO; GO:0005634; C:nucleus; RCA.
GO; GO:0003700; F:transcription factor activity; RCA.
GO; GO:0006325; P:establishment and/or maintenance of chromat. . .; RCA.
GO; GO:0009897; P:organ morphogenesis; IMP.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; RCA.
GO; GO:0048515; P:spermatid differentiation; IMP.
InterPro; IPR00910; HMG_12_box.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Murinae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82.0%; Score 41; DB 2; Length 449; 83.3%; Pred. No. 6.6e+02; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
STRAIN=CS7BL/6; TISSUE=Brain;
Director MGC Project;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           449 AA; 45313 MW; B5386A3572C84DA7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QEBCZS DROLT PRELIMINARY, PRT, 515 AA. QEBCZS.
13-SEP-2004, integrated into UniProtKB/TrEMBL.
13-SEP-2006, sequence version 1.
07-FEB-2006, entry version 8.
CG4928 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMR; QSRKWO; 141-219.
Ensembl; ENSMUSG00000045179; Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; BC052024; AAH52024.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila Iutescens (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50118; HMG_BOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 83.3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       358 AAAAAAAAAA 369
                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGI; MGI:98365; Sox3.
                                                                          NUCLEOTIDE SEOUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SM00398; HMG
                                      NCBI_TaxID=10090;
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Q6BCZS I
1D Q6E
AC Q6E
DT 13-
DT 13-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                               Swanson W.J., Wong A., Wolfner M.F., Aquadro C.F.; "Evolutionary expressed sequence tag analysis of Drosophila female reproductive tracts identifies genes subjected to positive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-Berkeley; Stapleton D., Hong L., Agbayani A., Carlson J., Stapleton M., Broketein P., Hong L., Dresnek D., Farfan D., Frise E., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
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Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=51159;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 515;
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FlyBaae; FBgn0051122; CG31122.
SEQUENCE 524 AA; 57365 MW; A43288FD17FC3DC0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          515 AA; 56186 MW; 77FBDDA7864EF077 CRC64;
                                                                                                                                                                                     PubMed=15579698; DOI=10.1534/genetics.104.030478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 41; DB 2; L
Pred. No. 7.4e+02;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2002, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AY665388; AAT76555.1; -; mRNA.
InterPro; IPR010291; DUF895_euk.
Pfam; PF05978; DUF895; 1.
1
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                                                                                                                                                                                                                                                                                                                                           Genetics 168:1457-1465(2004).
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Best Local Similarity 83.3
Marches 10, Conservative
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Q8MQJS;
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Celniker S.;
                                                                                                                                                                                                                                                                                                                  selection.
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                                                                                              05-JUL-2004, sequence version 1.
05-JUL-2004, sequence version 1.
07-MAR-2006, entry version 16.
Hypothetical protein P0597G07.116.
Name=P0597G07.116,
Oryza sativa (japonica cultivar-group).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
Anophelinae; Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                         Sasaki T., Matsumoto T., Yamamoto K.; "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00271; DnāJ; 1.

PROSITE; PS50076; DNAJ 2; 1.

Chaperone; Hypothetical protein; Inner membrane; Membrane; Protein transport; Translocation; Transmembrane; Transport. SEQUENCE 603 AA, 64186 MW; 949D42CFD9143639 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 41; DB 2; Length 603;
Pred. No. 8.4e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                        Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70; GO: 0016021; C:integral to membrane; IEA.
70; GO: 0016020; C:membrane; IEA.
70; GO: 0019866; C:organelle inner membrane; IEA.
70; GO: 001986; F: binding; IEA.
70; GO: 0031072; F:heat shock protein binding; IEA.
70; GO: 001682; F:unfolded protein binding; IEA.
70; GO: 0006657; P:protein fargeting; IEA.
70; GO: 0006665; P:protein targeting; IEA.
70; GO: 0015031; P:protein transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-DEC-2003, integrated into UniProtKB/TrEMBL. 07-DEC-2004, sequence version 2. 07-REB-2006, entry version 8. 07-REB-2006, entry version 8. 08-SNACP0000016550 (Fragment). ORFNames=ENSANGG0000014161;
                                                                               05-JUL-2004, integrated into UniProtKB/TrEMBL
                                       603 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AP004316; BAC83507.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=PEST;
The Anopheles gambiae Sequence Committee;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001623; DnaJ N.
InterPro; IPR011990; TPR-Tike_helical.
InterPro; IPR013105; TPR_2.
Pfam; PF00226; DnaJ; 1.
Pfam; PF00226; DnaJ; 1.
                                     PRT;
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                                       PRELIMINARY;
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83.3%;
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Quest Local Similarity 83.35,
Best Local 10; Conservative
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                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                  NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                     clone: P0597G07
                                       Q7F010_ORYSA
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                     ORYSA
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RESULT 30
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RADILINE-20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., R.A. Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., R.A. Brandon R.C., Baxter E.G., Helf G., Nelson C.R., Miklos G.L.G., R.A. An H.-J., Andrews-Pfannkoch C., Baldwin D., R.A. Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Benos P.V., Berman B.P., Bhandari D., Botchan M.R., Bouck J., Brokstein P., Blothakov S., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., R. Achery J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., R. Achery J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Dunkov B.C., Dunn P., Docsher C., Gabrielian A.E., Garg N.S., Glabart W.M., Glasser K., Gabrielian A.E., Garg N.S., Glabart W.M., Glasser K., Glodek A., Gong F., Garrell J.H., Gu Z., Kennison J.A., Houston K.A., Howland T.J., Hernandez J.R., Houck J., R.A. Hostin D., Houston K.A., Howland T.J., Wei M.-H., J. Z., Liang Y., Lin X., Mattel B.E., Kodira C.D., Kraft C., Kernison D.A., Netherle B., Kalush F., Karpen G.H., Kra Z., Kennison D.A., Meinnel B.E., Kalush F., Karpen G.H., Kra Z., Kennison D., A., Merlush C., Musthia N.V., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Morlis J., Moshrefi A., R., Mount S.M., Moy M., Murphy B., Murphy L., Morlis D.R., Pacleb D.R., Nelson D.R., Pacleb D.R., Nixon K., Nusekern D.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                            The Anopheles gambiae Sequence Committee;
Submitted (ARF-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 635;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 41; DB 2; Length 635
Pred. No. 8.7e+02;
1; Mismatches 1; Indels
"Anopheles gambiae re-annotation.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         635 AA; 71145 MW; 860CC8CFEC3D541C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AAAB01008986; EAA00301.3; -; Genomic_DNA.
InterPro; IPR004343; Plus-3.
Pfam; PF03126; Plus-3; 1.
SMART; SM00719; Plus3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000, integrated into UniProtKB/TrEMBL
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                  preliminary data.
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                                                                                                                                               SEQUENCE
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STRAIN=PEST;
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Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun B., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wasasarman D.A., Weinstock G.M., Weissenbach J., Walliams S.M., Woodege T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Zheng E.M., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster.";
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WICLECTIDE SEQUENCE.

WEDLINES-22486070; Pubmed=12537573;

Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.;

"The transposable elements of the Drosophila melanogaster euchromatin: a genomics perspective.";

Genomics perspective.";

Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MCLEOTIDE SEQUENCE.
MEDLINE=22436065; Pubbled=12537568;
MEDLINE=22436065; Pubbled=12537568;
Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe W., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Path S., Peiffer B.D., Richards S., Sodergren B.J., Kichards S., Sodergren B.J., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; Finlangaster euchromatic genome sequence."; Gibbs R.A., Rubin G.M.; Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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MEDLINE=22426069; PubMed=12537572;
Mista S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9VJU5:BG:DS00180.10; NbExp=1; IntAct=EBI-94009, EBI-163876;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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FlyBase, FBgn0051122, CG31122.
GO; GO:005515; F:protein binding; IPI.
SEQUENCE 642 AA; 70834 MW; 7F54E6806E05C487 CRC64;
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Berkeley Drosophila Genome Project;
Celniker S., Carlson J., Wan K., Pfeiffer B., Frise
Hoskins R., Stapleton M., Pacleb J., Park S., Syirsk
Yu C., Rubin G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'Drosophila melanogaster release 4 sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE003722; AAF55560.3; -; Genomic_DNA
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                                                                                                                                                                                                                                                                                                                                                MEDLINE=20231739; PubMed=10767535; DOI=10.1016/S0378-1119(00)00064-0; Davis T. Kurihara J., Yamanoto D.; "Genomic organization and charaterization of the neural sexdenomic organization and fruitless (fru) in the Hawaiian species Drosophila
                            Gaps
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                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Ĥexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                  Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=32382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.0%; Score 41; DB 2; Length 698; 100.0%; Pred. No. 9.4e+02; ive 0; Mismatches 0; Indels
 Length 642;
                           1; Indels
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EMBL; AF051662; AAF61178.2; JOINED; Genomic_DNA.
FlyBase; FB900029402; Dhet\fru.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0046872; F:metal ion binding; IEA.
GO; GO:0003576; F:nucleic acid binding; IEA.
GO; GO:0008515; F:protein binding; IEA.
InterPro; IPR0010010; BTB.
InterPro; IPR013069; BTB.
InterPro; IPR013069; BTB_POZ.
InterPro; IPR013069; BTB_POZ.
InterPro; IPR0070817; Znf_C2H2.
Score 41; DB 2; I
Pred. No. 8.8e+02;
                                                                                                                                                                            01-OCT-2000, integrated into UniProtKB/TrEMBL.
01-OCT-2000, sequence version 1.
21-FEB-2006, entry version 30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUL-2004, integrated into UniProtKB/TrEMBL. 05-JUL-2004, sequence version 1. 21-FEB-2006, entry version 25.
                                                                                                                                                   698 AA.
                         1; Mismatches
                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                 Drosophila heteroneura (Fruit fly)
                                                                                                                                                  Q9NJZ3_DROHE PRELIMINARY;
Q9NJZ3;
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                                                                                163 AAQAAAAAAA 174
                            10; Conservative
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Matches 10; Conservative
                                                     1 AAMAAAAAAMA 12
                                                                                                                                                                                                                                                                                                                                                                                                                    Gene 246:143-149(2000).
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Query Match
Best Local Similarity
Matches 10; Conserv
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Q7KSD2;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P., Bettemcourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                 Frise E., George R.,
Svirskas R., Smith E.
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                                                                                                                      "Annotation of the Drosophila melanogaster euchromatic genome:
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                                                                                                                                                                                                                Berkeley Drosophila Genome Project;
Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E.,
Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R
                                                                                                                                                                                                                                                                                         "Drosophila melanogaster release 4 sequence.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JAN-2006) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00651; BTB; 1.
Pfam; PF00065; zf-C2H2; 1.
SMART; SM00225; BTB; 1.
SMART; SM00255; ZHC ZH2; 1.
PROSITE; PS50097; BTB; 1.
PROSITE; PS50028; ZINC FINGER C2H2 1; 1.
PROSITE; PS50157; ZINC FINGER C2H2 2; 1.
Metal-binding; Nuclear protein; Zinc; Zinc-finger.
SEQUENCE 705 AA; 76675 MW; F2D99E279741D9EE CRC64;
                                                                                                                                           systematic review.";
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002)
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Pred. No. 9.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AE003722, AAS65172.1; -; Genomic_DNA. FlyBase; FBgn0004652; fru. GO; GO:0005634; C:nucleus; IEA. GO; GO:0005634; C:nucleus; IEA. GO; GO:0003676; F:metal ion binding; IEA. GO; GO:0008276; F:nucleic acid binding; IEA. GO; GO:0008276; F:protein binding; IEA. InterPro; IPR00101; BTB. InterPro; IPR013069; BTB_POZ. InterPro; IPR013069; BTB_POZ.
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NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
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                                                                                                                                                                                                                                                                            Yu C., Rubin G.;
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ID PHLPP HUMAN
                                                                                                                                           systematic
                                                                                                        Lewis S.E.
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MEDLINE-22386257; PubMed-12477932; DOI-10.1073/pnas.242603899;
A Straubberg R.L., Feahgold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B. E.S., Wagner L., Schamen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.R., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
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Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Brownstein M.J., WcKernan N.J., Malek J.A., Gunarathe P.H.,
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Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
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Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Placenta;

XY Pubmed-14702039; DOI-10.1038/ng1285;

Bubmed-14702039; DOI-10.1038/ng1285;

Ota T. Suzuki Y. Nishikawa T., Otsuki T., Sugiyama T., Irie R., Makamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H., Askamatsu A., Hayashi K., Sato H., Nishi T., Shibahara T., Tanaka T., Ishii S., Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K., Murakami K., Yasuda T., Ikawai Y., Isono Y., Nagahari K., Murakami K., Yasuda T., Ishibashi T., Xaku Y., Kodaira H., Kohasha M., Sato H., Tanikawa M., Yamazaki M., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K., Anai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishibashi Fujii A., Hara H., Tanase T.-O., Nomura Y., Takayachi S., Watanabe M., Hara H., Tanase T.-O., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Houta T., Kusano J., Togiya S., Komai F., Horshima A., Sasaki N., Aotsuka S., Nomikawa Y., Wukit H., Othihara T., Shiohata N., Sano S.,
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Taylor T.D., Whittaker C.A., Chang J.L., Cuomo C.A., Dewar K.,

FitzGerald M.G., Yang X., Abouellell M., Allen N.R., Anderson S.,

Bloom T., Bugalter B., Butler J., Cook A., DeCaprio D., Engels R.,

Garber M., Ghirke A., Hafez N., Hall J.L., Norman C.H., Itoh T.,

Jaffe D.B., Kuroki Y., Lehoczky J., Lui A., Macdonald P., Mauceli E.,

Mikkelsen T.S., Naylor J.W., Nicol R., Nguyen C., Noguchi H.,

O'Leary S.B., Piqani B., Smith C.L., Talamas J.A., Topham K.,

Totoki Y., Toyoda A., Wain H.M., Young S.K., Zeng Q., Zimmer A.R.,

Fujiyama A., Hattori M., Birren B.W., Sakaki Y., Lander E.S.;

"DNA sequence and analysis of human chromosome 18.";
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                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 349-1717.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O., Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H., Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B., Yamazaki M., Watanabe T., Sugiyama A., Ttakura S., Fukuzumi Y., A. Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T., Rawabata A., Hikiji T., Robatake N., Inagaki H., Ikema Y., Okamoto S., Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M., Angashi T., Oyama M., Hata H., Matanabe M., Komatsu T., Anizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K., Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Vamashita R., Nakamura Y., Ohara O., Isogai T., Sugano S., T., Complete sequencing and characterization of 21,243 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            apoptosis, and suppresses tumor growth.";
Mol. Cell 18:13-24(2005)
-!- FUNCTION: Protein phosphatase that specifically mediates
dephosphorylation of Ser-473 of AKT1, a protein that regulate the
balance between cell survival and apoptosis through a cascade that
primarily alters the function of transcription factors that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             act as a negative regulator of K-Ras signaling in the membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     regulate pro- and antiapoptotic genes. Dephosphorylation of Ser-473 of AKT1 triggers apoptosis and suppression of tumor growth.
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PubMed=15808505; DOI-0.10.6/j.molcel.2005.03.008;
Gao T., Furnari F., Newton A.C.;
"PHLPP: a phosphatase that directly dephosphorylates Akt, promotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: A phosphoprotein + H(2)0 = a protein +
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EMBL; AC022046; -; NOT ANNOTATED CDS; Genomic DNA.
EMBL; AC027553; -; NOT ANNOTATED CDS; Genomic DNA.
EMBL; AB011178; BAA25532.2; -; mRNA.
EMBL; BC014927; AAH10706.1; -; mRNA.
EMBL; BC047653; AAH4727.2; -; mRNA.
EMBL; BC06519; AAH63219.1; -; mRNA.
EMBL; BC082244; AAH63219.1; -; mRNA.
EMBL; AK001924; BAA91980.1; ALT TERM; mRNA.
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InterPro; IPR001591; LRR typ.
InterPro; IPR001849; PH.
InterPro; IPR001932; PP2C-like.
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Liu F., Lu J., Hu W., Wang S.-Y., Cui S.-J., Chi M., Yan Q.,

Liu F., Lu J., Hu W., Wang S.-Y., Cui S.-J., Chang X.-L., Wang Z.-Q.,

Wang X.-R., Song H.-D., Xu X.-N., Wang J.-J., Zhang X.-L., Wang Z.-Q.,

Xue C.-L., Brindley P.J., McManus D.P., Yang P.-Y., Feng Z., Chen Z.,

Han Z.-G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa (Rice).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                      Schistosoma japonicum (Blood fluke).
Sukaryotas, Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
Schistosomatoidea; Schistosomatidae; Schistosoma.
                                                                                                                                                                                                                                                                                                                                                                                                  "The full-length cDNA sequences of Schistosoma japonicum genes."; Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "New Perspectives on Host-parasite Interplay by Comparative
Transcriptomic and Proteomic Analyses of the Human Blood Fluke,
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Pred. No. 2.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Nipponbare;
McCombie W.R.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schistosoma japonicum.";
Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 109 AA; 10655 MW; ZEA7EF32B06A6CEF CRC64;
DAD82B0F05ED1B8F CRC64;
                            Score 40; DB 2; I
Pred. No. 2.5e+02;
0; Mismatches 1;
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                                                                                                                                                                                                                             29-MAR-2005, integrated into UniProtKB/TrEMBL. 29-MAR-2005, sequence version 1. 07-FRB-2006, entry version 4. SCHGCO7588 protein. (Blood fluke).
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 94 AA; 8628 MW;
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Matches 10, Conservative
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
Ehrhartoideae; Oryzeae; Oryza.
                 Pfam; PF00169; PH; 2.
Pfam; PF00481; PP2C; 2.
PRINTS; PR00019; LEWICHRPT.
SMART; SM00312; PP2Cc; 1.
PROSITE; PS50003; PH DOWAIN; 1.
PROSITE; PS50003; PH Lowaln; 1.
Rapatcosis; Hydrolase; Leucine-rich repeat; Manganese; Membrane;
Metal-binding; Protein phosphatase; Repeat.
CHAIN 1717 PH domain leucine-rich repeat-containing
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STRAIN=1RA4; TISSUE-Anther;
Lee J.-Y.K., Hodges T.K.;
Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                            protein phosphatase.
/FTId=PRO_0000057781
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 2e+03;
1; Mismatches
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PIR; T03285; T03285
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PDZ-binding.
Poly-Ala.
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      PF00560;
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            Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; BK002040; DAA02885.1; -; Genomic DNA.
SEQUENCE 156 AA; 16458 MW; 2EASCBB33330E61C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "An integrated gene annotation and transcriptional profiling approach towards the full gene content of the Drosophila genome."; Genome Biol. 5:RESEARCH0003.1-RESEARCH0003.17(2003).
-!- MISCELLANBOUS: The sequence shown here is derived from an EMBL/GenBank/DDBJ third party annotation (TPA) entry.
                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glomeris marginata.
Eukaryota, Metazoa, Arthropoda, Myriapoda, Diplopoda, Pentazonia,
Glomerida, Glomeridae, Glomeris.
NCBI_TaxID=62006;
                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.

NUMBAG=14709175, DOI=10.1186/gb-2003-5-1-r3;
Hild M., Beckmann B., Haas S.A., Koch B., Solovyev V., Busold C.,
Fellenberg K., Boutros M., Vingron M., Sauer F., Hoheisel J.D.,
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                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).

Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophila.
                                                                                                                    80.0%; Score 40; DB 2; Length 149; 75.0%; Pred. No. 3.6e+02; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80.0%; Score 40; DB 2; Length 156; 83.3%; Pred. No. 3.8e+02; ive 1; Mismatches 1; Indels
                                                            Gramene; Q94102; -.
Hypothetical protein.
SEQUENCE 149 AA; 14809 MW; E9125D3203F934A2 CRC64;
                                                                                                                                                                                                                                                                                              05-JUL-2004, integrated into UniProtKB/TrEMBL.
05-JUL-2004, sequence version 1.
07-FEB-2006, entry version 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2003, integrated into UniProtKB/TrEMBL. 01-OCT-2003, sequence version 1. 07-FEB-2006, entry version 11. Distal-less protein (Fragment). Name=dll;
                                                                                                                                                                                                                                                                    QĞILHG DROME PRELIMINARY; PRT; 156 AA.
QGILHG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               163 AA.
                                                   EMBL; AC022352; AAK51587.1; -; Genomic_DNA
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Q7YTA3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 83.39,
Best Local 10; Conservative
                                                                                                                                               9; Conservative
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60 AALAAAAAVALA 71
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                                                                                                                                   Best Local Similarity
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                                                                                                                     Query Match
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MEDLINE=22767335, PubMed=12885558; DOI=10.1016/S0012-1606(03)00217-3; Prpic N.M., Tautz D.; Prpic N.M., Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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GO; GO:0005634; C:nucleus; IEA.

GO; GO:0003100; F:transcription factor activity; IEA.

GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR001356; Homeobox.

InterPro; IPR012287; Homeodomain-rel.
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                                                                                                                                                                                                                                                                                                                                                           head appendages.";
Dev. Biol. 260:97-112(2003).
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA-binding; Homeobox; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR012287; Homeodomai
Pfam; PF00046; Homeobox; 1.
ProDom; PD000010; Homeobox; 1.
PROSITE; PS50071; HOMEOBOX 2; 1
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Best Local Similarity 90.9'
....hes 10; Conservative
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	GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.	
OM protein - prot	OM protein - protein search, using sw model	
Run on:	September 9, 2006, 22:37:17; Search time 97.4177 Seconds (without alignments) 61.014 Million cell updates/sec	
Title: Perfect score: Sequence:	US-10-617-568-3 53 1 AAMAAAAAAAAA 13	
Scoring table: E	BLOSUM62 Gapop 10.0 , Gapext 0.5	
Searched:	2589679 seqs, 457216429 residues	
Total number of }	Total number of hits satisfying chosen parameters: 2589679	
Minimum DB seg length: 0 Maximum DB seg length: 200000000	ngth: 0 ngth: 2000000000	
Post-processing: Minimum Match 0% Maximum Match 10 Listing first 10	Minimum Match 0% Maximum Match 100% Listing first 100 summaries	
Database : 1 2 2 3 3 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	A_Geneseq_8:* 1:geneseqp1980s:* 2:geneseqp1980s:* 3:geneseqp2000s:* 4:geneseqp2001s:* 5:geneseqp2003as:* 6:geneseqp2003as:* 8:geneseqp20048:* 9:geneseqp2006s:*	

Pred. No. is the number of regults predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	1	17 Lung spec	Plan	46 Plant ful	67 Human gen	01 Novel hum	93 Zorocrate		04 Drosophil	17 Novel hum	77 Drosophil	78 Human SEC	35 Transcrip			74 Human SEC		50 Drosophil		99 Drosophil	40 Drosophil	77 Drosophil	78 Murine ub
scri	Adi 29007	Adr98917	Ady09213	Adx78446	Abo58367	Abg15501	Aao16493	Aae36894	Abb65204	Abg18917	Abb69577	Aae35778	Ado61835	Abp65077	Aam25623	Aae35774	Adb64824	Abb59750	Aab92956	Abb70499	Abp54340	Abb71577	Abu64278
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SUMMARIES	ADI29007	8917	ADY09213	ADX78446	ABO58367	5501	AA016493	AAE36894	ABB65204	ABG18917	9577	AAE35778	ADO61835	5077	AAM25623	AAE35774	ADB64824	ABB59750	AAB92956	ABB70499	ABP54340	ABB71577	ABU64278
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ADH7356 ADR8969 ADS3424 ADT7790 ADU7730 ADU6899 ADU6899 ADZ6642 AEA1063 AEC3473 AEC3473 ABGC9609 ABBC609	ABG1566 ABB5898 AAB5898 AAD12677 AD12677 AD12677 AD12670 AD12900 AD12674 ADV7864 ADV7864 ABC5221 ABC53336 ABC53336 ABC53336 ABC53336 ABC53336	ABK3836 ABK3836 ADK3810 ADV7864 AAW3222 ADV7864 AAW3222 ADV7864 AAW3222 ADV7868939	9 ADV78587 4 AAB69489 7 ADH47641 7 ADH47641 8 ADH58955 8 ADH58955 9 ADV78588 4 AAB69490 7 ADJ81342 7 ADJ81342 9 ADV78590 9 ADV78590 9 ADV78591 7 ADJ81343 7 ADJ81343 7 ADJ81344 7 ADJ81344 9 AEB23105 9 AEB23105
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The present invention describes an isolated WHC class II compound (I) comprising: (a) an MHC class II component comprising at least a portion of an MHC class II alpha chain and at least a portion of an MHC class II beta of an MHC class II alpha chain and MHC class II beta chain, such that the MHC class II alpha chain and MHC class II beta chain form a peptide binding groove; (b) a spaceholder molecule; and (c) an effector component, MHS described; (l) a pharmaceutical composition comprising the MHC class II molecule and a carrier; (2) a method of producing an MHC class II compound; (3) a method of directly identifying an antigen-specific T cell; (4) a method of tregulating an immune disorder in a subject; (i) a method of regulating an immune disorder in a subject; (i) a method of treating an immune disorder ex vivo in a subject; and (7) a method of treating an immune disorder ex vivo in a subject; and (7) a method of treating an immune disorder ex vivo in a subject; and continuation in gene therapy. The MHC class II compound (I) can be used for preparing a composition for treating immune continuence represents a spaceholder molecule peptide, which can be used in the present invention.

Sequence represents a spaceholder molecule peptide, which can be used in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MHC class II compound; MHC class II component; MHC class II alpha chain; MHC class II beta chain; peptide binding groove; spaceholder molecule; effector component; immune response; immune disorder; virucide; antibacterial; antiparastitic; cytostatic; immunosuppressive; gene therapy; viral infections; bacterial infection; parastitic infection;
Cell adhe
Wound dre
Auxiliary
Auxilliar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New MHC class II compound, useful for preparing a composition for treating immune disorders e.g. viral infections, bacterial infections, parasitic infections, neoplastic disease, autoimmunity or toxicity.
Aeb23103 (
Aed01242 I
Aee05648 }
                                                                                                     Aee01614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human MHC class II compound spaceholder molecule SEQ ID NO:3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neoplastic disease; autoimmunity; toxicity; human.
                                                                                                                                                                                                      ALIGNMENTS
                                     AED01242
AEE05648
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          AEB23103
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                                                                                                                                                                                                                                                                                                                                                                        ADI29007 standard; peptide; 13 AA
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22-JUL-2002; 2002US-0397893P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-122876/12.
      88.7
88.7
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                                                                                                                                                                                                                                                                                                                                       ADI29007
XX XX ADI3
XX
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          98 80
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The invention relates to a new isolated lung specific nucleic acid

C molecule (I) comprising any of 113 fully defined nucleotide sequences

c given in the specification, their encoded protein sequences, sequences

c selectively hybridizing to the nucleotide sequences or a sequence having

at least 60% identity to the nucleotide sequences. The methods and

c compositions of the present invention are useful for identifying,

c diagnosing, monitoring, staging, imaging and treating lung cancer and non-

c annex monitoring and identifying and/or designing entagonists of the

c polypeptide of the invention, gene therapy, production of transgenic

c polypeptide of the invention, gene therapy, production of transgenic

c polypeptide of the invention of engineered lung tissue for treatment and

c research. Lung specific genes (LSGS) were identified by a systematic

c research. Lung specific genes (LSGS) were identified by a systematic

c analysis of gene expression data in the LIFESEQ Gold database using the

data mining software package candidate lead automatic search program

(CLASP). Genes were grouped into gene bins where each bin is a cluster of

sequences grouped together where they share a common contig.

C percentage level in the targeted tissue versus all the other tissues. The

c percentage level in the targeted tissue versus all the other tissues. The

c tumour tissues from cancer patients were compared with the expression

c percentage level in the invention of the invention

c levels in tissue libraries associated with tumour or disease. This
            - °
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated human lung specific nucleic acid molecule, useful for identifying, diagnosing, monitoring, staging, imaging and treating lung cancer and non-cancerous diseases of the lung.
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                       cytostatic; gene therapy; vaccine; lung; diagnosis; cancer; non-cancerous lung disease; lung tissue; antagonist; gene therapy; transgenic animal; splice variant.
                                      ö
Score 53; DB 8; Length 13;
Pred. No. 0.24;
                                      0; Indels
                                                                                                                                                                                                                                                                                                                                        Lung specific gene splice variant encoded protein #89.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence represents a protein of the invention.
                                        Mismatches
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                                                                                                                                                                                                                      ADR98917 standard; protein; 278 AA.
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  100.0%;
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06-DEC-2002; 2002US-0431510P.
06-DEC-2002; 2002US-0431516P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-DEC-2003; 2003WO-US038896.
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                                                                               1 AAMAAAAAAAAA 13
                                                                                                                    AAMAAAAAAAA 13
                                          13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (DIAD-) DIADEXUS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-635553/61.
                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ADR98780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2004074430-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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  Query Match
Best Local S:
Matches 13
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                                                                                                                                                                                   RESULT 2
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Sequence 278 AA;

Sequence 13 AA;

the

polypeptide that can be used in the recombinant DNA construct of

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The invention describes a recombinant DNA construct comprising a polymucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at available in electronic form from the US patent office at the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, hear, drought, herbicides, extreme commotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, ingnin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake curess condition or for modifying seed oil or protein yield and/or content. This is the amino acid sequence of a plant full length insert
                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for
                                                                                                                                                                                                                                                                                                                          plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomanna production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield;
                                                  Gaps
                                                  ö
                  8; Length 278;
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                                                                                                                                                                                                                                                                                             Plant full length insert polypeptide seqid 65028.
               Score 53; DB 8
Pred. No. 4.2;
                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 65028; 15pp; English.
                                                                                                                                                                                             ADY09213 standard; protein; 646 AA
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0
                100.0%;
100.0%;
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                                                                                                                                                                                                                                                             (first entry)
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                                                                               1 AAMAAAAAAAA 13
                                                  Conservative
Query Match
Best Local Similarity
Local 13; Conserve
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KOVALIC D K.
SCREEN S E.
TABASKA J E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-180133/17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               improving yield.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein content
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(CAOY/) CAO Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified
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                                                                                                                                                                                                                                                             21-APR-2005
                                                                                                                                                                                                                             ADY09213;
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(SCRE/)
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                                                                                                                                                                                                                                                                                                                                                                                recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield; protein content.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 recombinant DNA construct, useful for improving plant tolerance to 1, heat, drought, herbicides, extreme osmotic conditions, pathogens s, for conferring increased resistance to plant disease, or for
                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                       plant protectant; plant growth regulant; gene therapy; plant;
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                                                                       Length 646;
                                                                                                   0; Indels
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                                                                                                                                                                                                                                                                                                                                       Plant full length insert polypeptide seqid 47812.
                                                                      8;
                                                                    100.0%; Score 53; DB 8
100.0%; Pred. No. 9.3;
                                                                                                    Mismatches
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                                                                                                                                                                                                                                    ADX78446 standard; protein; 333 AA.
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05-NOV-2001; 2001US-00985678.
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hes 13; Conservative
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                                          Sequence 646 AA;
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improving yield.
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ZHOU Y.
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21-APR-2005
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                invention.
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(CAOY/)
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(SCRE/)
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ADX78446
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SSXS
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lignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This is the amino acid sequence of a plant full length insert polypeptide that can be used in the recombinant DNA construct of the
                                                                                                                                                                                               invention.
          88888888888888
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Revised record issued on 23-MAR-2006 : Corrected organism line

Seguence 333 AA;

Length 333; 0; Indels Score 50; DB 8; Pred. No. 13; 1; Mismatches ä 94.3%; 157 SAMAAAAAAAA 169 1 AAMAAAAAAAAA 13 Local Similarity 92.3 les 12; Conservative Query Match Matches 요 8

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Gaps

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RESULT

ABO58367 standard; protein; 109 AA ABO58367;

Human genome derived single exon protein #4601. (first entry) 29-JUL-2004

Human, gene expression, single exon probe, microarray, alternative splicing event, genomic alteration.

Homo sapiens.

US2003194704-A1.

16-OCT-2003.

03-APR-2002; 2002US-00029386

03-APR-2002; 2002US-00029386

(PENN/) PENN S G. (RANK/) RANK D R. (HANZ/) HANZEL D K.

Penn SG, Rank DR, Hanzel DK

WPI; 2004-119264/12.

New human genome-derived single exon nucleic acid probes useful for hume gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for surveying tissues.

Claim 45; SEQ ID NO 32001; 80pp; English.

The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-addressable set of single exon nucleic acid probes for measuring human gene expression (comprising a plurality of single exon nucleic acid probes cited above, where each of the plurality of probes is separately and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a method of measuring human gene expression, a method of 

probe cited above, an ORF-encoded peptide comprising at least 8
contiguous amino acids of any of the above- mentioned amino acid
sequences (optionally with conservative amino acid substitutions), an
isolated antibody that binds specifically to a peptide cited above.

C methods of selling and/or licensing single exon probes or microarrays to
a customer desiring to measure gene expression, a method of providing
the many gene expression data by subscription, and a computer-readable
c storage medium which contains a database having a plurality of records
c teach record including data on the expression of a single exon probe
c cited above. The probe, methods and apparatus are useful in gene
c expression analysis. The probes may be used as tools for surveying
c tissues to detect the presence of expressed messages that contain their
c specific exon, or in constructing genome-derived single exon microarrays.

C naddition, the probes are used in identifying and characterising
c alternative splicing events, in detecting and characterising
c alternative splicing events, in detecting and characterising
c alternative splicing events, in priming the synthesis of nucleic a human
c smaller genomic alterations, in priming the synthesis of nucleic a human
c single exon probe protein of the invention. Note: The sequence data for
this patent did not form part of the printed specification, but was
c possible and proper processed the printed specification, but was ö Gaps .. 0 Score 49; DB 8; Length 109; Pred. No. 6.3; 1; Mismatches 0; Indels segdata.uspto.gov/sequence.html?DocID=20030194704 92.5%; 92.3%; Conservative Local Similarity nes 12; Conserv Sequence 109 AA; Query Match **datches** 

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ABG15501

ABG15501 standard; protein; 112 AA. (first entry) 18-FEB-2002 ABG15501;

Novel human diagnostic protein #15492. 

Human, chromosome mapping, gene mapping, gene therapy, forensic; food supplement, medical imaging, diagnostic, genetic disorder.

Homo sapiens.

WO200175067-A2.

11-OCT-2001.

30-MAR-2001; 2001WO-US008631.

31-MAR-2000; 2000US-00540217. 23-AUG-2000; 2000US-00649167.

(HYSE-) HYSEQ INC.

Tang YT; Drmanac RT, Liu C,

WPI; 2001-639362/73 N-PSDB; AAS79688 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity

Claim 20; SEQ ID NO 45860; 103pp; English.

The invention relates to isolated polynuclectide (I) and polypeptide (II)

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in diagnostics as expressed sequence tags for identifying expressed genes. (1) is useful in gene therapy techniques to restore normal cativity of (II) or to tread disease states involving (II). (II) is useful in gene therapy techniques to restore normal suctivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forenise, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from MIPO at
sequences. (I) is useful as hybridisation probes, polymerase causer reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 112 AA;
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1; 91 AAVAAAAAAAA 103 1 AAMAAAAAAAA 13 12; 셤 8

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Gaps

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Mismatches

Score 49; Pred. No. 6

92.5%; 92.3%;

Query Match Best Local Similarity

Conservative

DB 4; Length 112; 0; Indels

> AAO16493 standard; protein; 252 AA 01-MAY-2003 AA016493; RESULT 7 AA016493

silk protein, fabric, suture, medical covering, rope, reinforced plastic. Zorocrates fibronin 1 protein. (first entry) Spider silk; spider high-tech clothing;

Zorocrates sp.

MO200299082-A2. 12-DEC-2002.

06-JUN-2001; 2001US-0296184P. 06-JUN-2002; 2002WO-US018256

(UYWY-) UNIV WYOMING.

Roth DA, Lewis RV;

WPI; 2003-140616/13. N-PSDB; AAL51692 Expressing spider silk protein in a higher plant, by contacting a plant cell with silk protein encoding a gene linked to a gene that confers resistance to selection agent, and selecting cells that survive when incubated with the agent.

Claim 52; Fig 11; 114pp; English.

The invention comprises a method for expressing spider silk in a higher plant (e.g. arabidopsis, tobacco, tubers, sunflower, canola, alfalfa, soybean, maize, sorghum, wheat, cotton, small grains and rice). The method is useful for expressing spider silk in a higher plant. The silk

ö produced is useful in the production of fabrics, sutures, medical coverings, high-tech clothing, rope, reinforced plastics, and other applications in which various combinations of strength and elasticity are required. The present amino acid sequence represents a spider silk-related protein The invention relates to novel spider silk proteins e.g. major ampullate spidroin 1-like (MaSp1) spider silk protein, major ampullate spidroin 2-like (MaSp2) spider silk protein; (Flagelliform (Flag)-like spider silk proteins comprising atypical repetitive motifs. proteins and spider silk proteins comprising atypical repetitive motifs. Sequences of the invention are useful for producing fabrics, sutures, medical coverings, high-tech clothing, rope and reinforced plastics. They are used to make high-tech clothing, rope, salls, parachutes, wings on aerial devices (e.g. hand gliders), flexible tie downs for electrical components, sutures and as biomaterials for implantation (e.g. artificial ligaments or acrtic banding). Blomedical applications of the spider silk fibers in Spider silk protein; flagelliform-like spider silk protein; FLAG; MaSp; major ampullate spidroin; fabric; medical covering; clothing; parachute; rope; reinforced plastic; suture; aerial device wing; sail; hand glider; implantation biomaterial; resin product; fiber-reinforced plastic; thermal injected plastic; fibroin 1. sutures used in surgical procedures, including eye surgery, vascular closure, bowel surgery, cosmetic surgery, reconstructive surgery (e.g. nerve or tympanic membrane reconstruction) and central nervous system surgery. Natural and synthetic spider silk fibers are also used in the generation of antibiotic impregnated sutures and implant material and matrix material for reconstruction of bone and connective tissue. Spider Gaps Novel spider silk protein e.g. major ampullate spidroin 2-like, flagelliform (Plag)-like spider silk proteins, useful for producing fabric, sutures, medical coverings, high-tech clothing, rope. ö Length 252; 0; Indels 9 Motriuk D; DB 14; 1; Mismatches Score 49; Pred. No. Zorocrates species fibroin 1 protein. AAE36894 standard; protein; 252 AA. Gatesy JE, Claim 58; Page 98; 99pp; English. 28-MAR-2002; 2002WO-US009663. 29-AUG-2001; 2001US-0315529P 92.5%; 92.3%; (first entry) 13 83 AAVAAAAAAAA 95 12; Conservative 1 AAMAAAAAAAAA Lewis RV, Hayashi CY, UYWY-) UNIV WYOMING WPI; 2003-290190/28. Query Match Best Local Similarity N-PSDB; AAD55739. Sequence 252 AA; WO2003020916-A2 Zorocrates sp. 13-MAR-2003. 07-AUG-2003 AAE36894; Matches AAE36894 RESULT 88888888 ઠ 셤 CCCCCCCCCCCCCCCX8X1H1X8BX1XBXHXHXAXRXRXXBXBXBXBXBXAXA

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fibroin and different spider silk proteins. Synthetic spider silk fibers may be mixed with various plastics and/or resins to prepare a fiber reinforced plastic and/or resin product. They are useful as structural reinforcement material in thermal injected plastics. The present sequence is Zorocrates species fibroin 1 protein. This sequence is used in the exemplification of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidaring cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                                                                                                             6; Length 252;
                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster polypeptide SEQ ID NO 22404.
                                                                                                                                                                             Score 49; DB
Pred. No. 14;
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92.3%;
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11-JUL-2000; 2000US-00614150.
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                                                                                                                                             Sequence 252 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pharmaceutical
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed control of the control of the control of the control of cacivity of (II) is useful in gene therapy techniques to restore normal consectul for generating antibodies against it, detecting or quantitating a useful for generating antibodies against it, detecting or quantitating a colypeptide in tissue, as molecular weight markers and as a food of sites expressing (II). (I) and (II) and its binding partners are useful in medical imaging of supplement. (II) and its binding partners are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences of the invention. Note: The sequence data for this camino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in celectronic format directly from WIPO at
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                                                                                                                                                                                                                                                                                               Human, chromosome mapping, gene mapping, gene therapy, forensic; food supplement, medical imaging, diagnostic, genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 20; SEQ ID NO 49276; 103pp; English.
                                                                                                                                                                                                                                                         Novel human diagnostic protein #18908.
                                                                                                                                     ABG18917 standard; protein; 316 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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                                 189 AAIAAAAAAAA 201
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Gaps

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Indels

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1; Mismatches

Query Match 92.5 Best Local Similarity 92.3 Matches 12; Conservative

92.5%; Score 49; DB 4; Length 285; 92.3%; Pred. No. 16;

18 AAVAAAAAAAA 30

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIGITS-ABLIGITS), and the encoded proteins (ABBS7737-ABB72072). The sequence data for this patent did not form part of the
                                                                                                                                                                                                                                                                                                                                                                                                                               detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, secreted protein, SECP, cell proliferative disorder, cirrhosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in electronic format directly
                                                                                                                Drosophila, developmental biology, cell signalling; insecticide, pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 35523; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92.5%; Score 49; DB 4; Length 337; 92.3%; Pred. No. 18; cive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         printed specification, but was obtained in electronic from WIPO at ftp.wipo.int/pub/published pct sequences
                                                                                      Drosophila melanogaster polypeptide SEQ ID NO 35523.
                                                                                                                                                                                                                                                                                                                                                          Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE35778 standard; protein; 373 AA.
ABB69577 standard; protein; 337 AA
                                                                                                                                                                                                                                                                                                                                                          Li PWD,
                                                                                                                                                                                                                                                    23-MAR-2001; 2001WO-US009231.
                                                                                                                                                                                                                                                                                23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid genes from Drosophila and interactions.
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                                                         (first entry)
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                                                                                                                                                              Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                         Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-656860/75.
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nes 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB, ABL13680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 337 AA;
                                                                                                                                                                                         WO200171042-A2
                                                         26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-JUN-2003
                                                                                                                                                                                                                        27-SEP-2001
                            ABB69577;
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Gaps

Huntington's disease; stroke; dementia; Parkinson's disease; anxiety; amyotrophic lateral sclerosis, schizophrenic disorder; mental disorder; roucette's disorder; muscular dystrophy; autoimmune disorder; mood; ALDS; inflammatory disorder; acquired immunodeficiency syndrome; allergy; ARDS; adult respiratory disirses syndrome; diabetes mellitus; cronn's disease; asthma; autoimmune thyroiditis; glomerulonephritis; rheumatoid arthritis; atopic dermatitis; ulcerative collins; trauma; cardiovascular disorder; infection; congestive heart failure; heart disease; angina pectoris; myocardial infarction; myocardiis; transgenic animal; gene therapy; transgenic; vaccine; virucide; antibacterial; fungicide; antiparasitic; Novel human secreted proteins and genes encoding the proteins, useful for treating, diagnosing and preventing cell proliferative, autoimmune/inflammatory, cardiovascular, developmental or neurological The present invention relates to novel human secreted proteins (SECP) and polymucleotides encoding such proteins. SECP sequences are useful for diagnosing, treating and preventing cell proliferative disorders including cancer (e.g. arteriosclerosis, cirrhosis, hepatitis, psoriasis and atherosclerosis), developmental disorders (e.g. seizure disorders, renal tubular acidosis, anaemia, cataract and sensorimeural hearing loss), neurological disorders (e.g. epilepsy, ischaemic cerebrovascular disease, Alzheimer's disease, Pick's disease, Huntington's disease, stroke, dementia, Parkinson's disease, amyotrophic lateral sclerosis, schizophrenic disorders, mental disorders including mood and anxiety, Tourette's disorder and muscular dystrophy), autoimmune/infammatory disorders (e.g. acquired immunodeficiency syndrome (AIDS), allergy, adult respiratory distress syndrome (ARDS), asthma, autoimmune thyroiditis, cancer; arteriosclerosis; hepatitis; psoriasis; developmental disorder; atherosclerosis; setzure disorder; renal tubultar acidosis; anaemia; cataract; sensorineural hearing loss; neurological disorder; epilepsy; ischemic cerebrovascular disease; Alzheimer's disease; Pick's disease; Yue H, Lee EA, Becha SD, Baughn MR, Yao MG, Tang YT;
Au-Young JK, Lal PG, Warren BA, Duggan BM, Tran UK, Xu Y;
Thangavelu K, Richardson TW, Bandman O, Jones KA, Yang J;
Emerling BM, Swarnakar A, Luo W, Walia NK, Azimzai Y, Khan FA;
Liu DAM, Griffin JA, Lee SY, Burford N, Blliott VS, Honchell CD;
He A, Mason PM, Li JX, Hafalia AJA, Gururajan R; l. .48 /label= Signal\_peptide\_#1 Claim 85; Page 168-169; 192pp; English. .ocation/Qualifiers 25-MAY-2001; 2001US-0293728P. 08-JUN-2001; 2001US-0297019P. 19-JUN-2001; 2001US-0299297P. 2001US-0301936P. 2002US-0362439P. 2002US-0363649P. 21-MAY-2002; 2002WO-US016234 2001US-0300537P 2002US-0366041P. (INCY-) INCYTE GENOMICS INC. WPI; 2003-129519/12. N-PSDB; AAD54316 WO200297035-A2 protozoacide. Homo sapiens 22-JUN-2001; 29-JUN-2001; 06-MAR-2002; 19-MAR-2002; 05-DEC-2002 disorders Peptide Peptide Protein 

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diabetes mellitus, Crohn's disease, glomerulonephritis, rheumatoid arthritis, atopic dermatitis, ulcerative colitis, trauma and viral, bacterial, fungal, parasitic, protozoal and helminthic infections) and cardiovascular disorders (e.g. congestive heart failure, ischaemic heart disease, angina pectoris, myocardial infarction, hypertensive heart disease, congenital heart disease and myocarditis). They are useful for creating knocking humanised animals or transgenic animals to model human diseases. Sequences of the invention are useful in somatic or germline gene therapy and in diagnostic purposes. They are also used as vaccines. The present sequence is human SECP-30 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plant; transcription factor; transgenic plant; abiotic stress tolerance; osmotic stress tolerance; cold tolerance; heat tolerance; low nitrogen tolerance; low phosphate tolerance; fungal disease; glyphosate resistance; flowering; fertility; seed development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to novel plant transcription factor proteins (I) and nucleotide sequences (II) (ADO61534-ADO63778). The sequences can be used to produce transgenic plants, which overexpress (II), where the transgenic plant has an altered trait as compared to a non-transgenic plant or wild type plant. The transgenic plant comprises increased tolerance to osmotic stress, increased tolerance to objotic stress, increased tolerance to cold, increased tolerance to cold, increased tolerance to heat, increased germination in cold, increased tolerance to heat, increased germination in heat, increased tolerance to freezing conditions, increased tolerance to low nitrogen conditions, increased tolerance to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New recombinant polynucleotide encoding transcription factor polypeptides, useful for producing transgenic plants with advantageous properties compared to a reference plant.
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Sherman BK;
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Pred. No. 20;
1; Mismatches
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V, Dubell AN,
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17-DEC-2002; 2002US-0434166P.
24-APR-2003; 2003US-0465809P.
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                                                                                                                                                                                                                                                    92.5%;
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                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana
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Best Local Similarity
Matches 12; Conserv
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                                                                                                                                                                                                              Sequence 373 AA;
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100.0%; Fic
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08-FEB-2001; 2001GB-0003156.
25-OCT-2001; 2001GB-00025666.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 377 AA;
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AAE35774;
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AAE35774
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;
antiinflamcterial; endocrine; cardiant; central nervous system; virucide;
anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;
antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema;
antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema;
dermatological; antialergic; antiasthmatic; antidiabetic; cytostatic;
neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
munostimulant; gene therapy; antisense therapy; vaccine; inflammation;
antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
thrombocytopaenia; osteoporosis; severe combined immunodeficiency;
allergic rhinitis; diabetes; multiple sclerosis; depression;
Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                              The present invention relates to methods for identifying genes and proteins that are implicated in a specific disease or physiological condition. The method comparing the transcriptome/proteome of a specialised cell type implicated in a disease or condition with that of second specialised cell type, under two experimental conditions, and identifying a gene that is differentially regulated in the two specialised cell types under experimental conditions, and specialised cell types under experimental conditions ABN77873-ABN7816 and ABP65061-ABP65257 were identified using the methods of the invention. The coding sequences and proteins are useful for treating a disease in a patient, for manufacture of a medicament for treating hypoxia-regulated conditions, and for regulating tumourigenesis, anglogenesis, apoptosis, biological response to hypoxia conditions, or hypoxic-associated
                                                                                                                                                                                                                                                                                                                  pathology in a patient. The coding sequences and proteins are also useful for monitoring the therapeutic treatment of a disease or physiological condition, such as cancer, ischaemic conditions, repertuasion injury, retinopathy, neonatal stress, preeclapmesia, atherosclerosis, inflammatory conditions, wound healing, inflammation, erythropoiesis or hair loss
                            Identifying a gene involved in disease for treating hypoxia-regulated conditions, comprises comparing the transcriptome/protecome of two cell types under different conditions and identifying a differentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                       Claim 13; Page 281; 538pp; English.
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les 12; Conservative
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WPI; 2002-627238/67.
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 378 AA;
                                                                           regulated gene
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AAM25963. The proteins can have activities based on the tissues and cells they are expressed in, such as: antiinflammatory; antirheumatic; cantiarthric; immunosuppressive; antibacterial; endocrine; cardiant; cardiant; cardiant; cardiant; cardiant; antiamaemic; antibacterial; endocrine; cardiant; cardiavascular; antiamaemic; antiagragant; haemostatic; vulnerary; cardiavascular; antiamaemic; antiagragant; haemostatic; uninerary; antidabetic; cytostatic; neuroprotective; antidaperssant; nootropic; antidabetic; cytostatic; neuroprotective; antidaperssant; nootropic; antidabetic; cytostatic; neuroprotective; antidaperssant; nootropic; cantidabetic; cytostatic; neuroprotective; antidaperssant; nootropic; cantidabetic; cytostatics; neuroprotective; antidaperspand vaccine conting them can be used in gene therapy, antisense therapy and vaccine concing them can be used in gene therapy, antisense therapy and vaccine concing them can be used in gene therapy, antisense therapy and vaccine configuration of disorders associated with the activity of a protein e.g. inflammation, rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, curdent anticimunity, genetic diseases, haematopoietic disorders, caneemia, placelet disorders, thrombocytopaenia, wounds, burns, ulcers, osteoporosis, severe combined immunodeficiency, eczema, allergic rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression, challed and disorders multiple sclerosis, depression, cardiac disease, neurological disorders and energy and dispenses and cancer, multiple sclerosis, depression, cardiac disease, neurological disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer; arreriosclerosis; hepatitis; psoriasis; developmental disorder; atherosclerosis; seizure disorder; renal tubular acidosis; anaemia; atherosclerosis; seizure disorder; renal tubular acidosis; anaemia; catact; sensorineural hearing loss; neurological disorder; epilepsy; schaemic cerebrovascular disease; Alzheimer's disease; Pick's disease; Huntington's disease; stroke; dementia, Parkinson's disease; anxiety; amyotrophic lateral sclerosis; schizophrenic disorder; mental disorder; wrourette's disorder; muscular dystrophy; autoimmune disorder; modol AIDS; inflammatory disorder; acquired immunodeficiency syndrome; allergy; ARDS; adult respiratory distress syndrome; diabetes mellitus; Crohn's disease; asthma; autoimmune thyroiditis; glomerulonephritis; rheumaroid arthritis; atthma; autoimmune thyroiditis; glomerulonephritis; rheumaroid arthritis; infection; congestive heart failure; heart disease; angina pectoris; infection; congestive heart failure; heart disease; angina pectoris; myocardial infarction; wyocarditis; transgenic animal; gene therapy; transgenic; vaccine; virucide; antibacterial; fungicide; antiparasitic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated human polynucleotides encoding polypeptides, useful for the treatment and diagnosis of e.g. cancer, ulcers and HIV infection.
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1; Mismatches
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21-JAN-2000; 2000US-00488725
25-APR-2000; 2000US-00552317
                                                                                                                                                                                                                                                         Tang YT, Liu C, Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92.3%;
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                                                                                                                                                                                                                                                                                                                                                                      2001-457603/49.
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                                                                                                                                                        (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAH99564.
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Location/Qualifiers

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protozoacide
  Homo sapiens
                                                 disorders
     Peptide
        Peptide
            Protein
          Domain
8X8XETTTTTTTTTTTTTXX8XX
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The present invention relates to novel human secreted proteins (SECP) and polynucleotides encoding such proteins. SECP sequences are useful for diagnosing, treating and preventing cell proliferative disorders including cancer (e.g. arteriosclerosis, cirrhosis, hepatitis, psoriasis and atherosclerosis), developmental disorders (e.g. seizure disorders, cand tubular acidosis, anaemia, cataract and sensorineural hearing consist, neurological disorders (e.g. epilepsy, ischaemic cerebrovascular disease, Alzheimer's disorders, pick's disease, Huntington's disease, Strizophrenic disorders, mental disorders including mood and anxiety, crowette's disorders mential disorders including mood and anxiety, disorders (e.g. acquired immunodeficiency syndrome (AIDS), allergy, adult crespiratory distress syndrome (ARDS), autoimmune thyroiditis, disorders mellitus, Crohn's disease, glomerulonephritis, rheumatoid arthritis, atopic dermatitis, ulcerative collits, trauma and viral, bacterial, fungal, parasitic, protozoal and helminthic infections) and cardisease, angina pectoris, myocardial infarction, hypertensive heart cisease, congenital heart disease and myocarditis). They are useful for creating knocking humanised animals or transgenic animals to model human cliseases. Sequences of the invention are useful in somatic or germiline gene therapy and in diagnostic purposes. They are also used as vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human secreted proteins and genes encoding the proteins, useful for treating, diagnosing and preventing cell proliferative, autoimmune/inflammatory, cardiovascular, developmental or neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yue H, Lee EA, Becha SD, Baughn MR, Yao MG, Tang YT;
Au-Young JK, Lal PG, Warren BA, Duggan BM, Tran UK, Xu Y;
Thangavelu K, Richardson TW, Bandman O, Jones KA, Yang J;
Emerling BM, Swarnakar A, Luo W, Walia NK, Azimzai Y, Khan FA;
Lu DAM, Griffin JA, Lee SY, Burford N, Elliott VS, Honchell CD;
He A, Mason PM, Li JX, Hafalia AJA, Gururajan R;
                                                                                                                                                                                                                                                                                     /note= "Mature SECP-26 protein"
                                                                                                                                                               27. .47
/note= "Transmembrane domain"
49. .394
1. .48
/label= Signal_peptide_#1
                                                                                                                     /label= Signal_peptide_#2
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08-JUN-2001; 2001US-0297019P.
19-JUN-2001; 2001US-029937P.
22-JUN-2001; 2001US-0300537P.
29-JUN-2001; 2001US-0304936P.
06-MAR-2002; 2002US-03636439P.
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Emerling BM, Swarman...
Lu DAM, Griffin JA, Lee
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N-PSDB; AAD54312.
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Sequence 394 AA;

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The invention discloses a polymuclectide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel comparities to the polymetides. Also claimed is a polymetide encoded by the polymetide or it partial peptide, an antibody binding to the polymetide or peptide or the polymetide of the polymetide of the polymetide or peptide or peptide or peptide of the polymetide or peptide or proteins are useful as pharmaceutical agents and many disease-related proteins are useful as pharmaceutical agents and many disease-related proteins of their expression and activity or as targets of generation. Membrane proteins, disease-related proteins, disease-related proteins and genes or proteins to medicine for each as indicators for diseases (e.g. osteoproreis, encoding them can be used as indicators for diseases (e.g. osteoproreis, concert, the activity or expression of the encoded protein to treat diseases. The sequence presented is a protein of the invention. Note: Some of the
                                                                                                                                                                                                                                                                                                                                                                                   Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration; cell regeneration; membrane protein; signal transduction-related protein; transcription-related protein; osteoporosis; neurological disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Otsuki T, Wakamatsu A, Sato H, Ishii S;
Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polynuclectides and polypeptides, useful for developing a diagnostic ear or medicines for regulation of their expression and activity, or
                                               Gaps
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0
          Length 394;
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            9
                                                                                                                                                                                                                                                                                                                                                Human protein encoded by clone OCBBF20120950.
        ore 49; DB (red. No. 21; Mismatches
            Score 49;
Pred. No.
                                                                                                                                                                                                                                 ADB64824 standard; protein; 512 AA.
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(REAS-) RES ASSOC BIOTECHNOLOGY.
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25-JAN-2002; 2002US-00350978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        as targets of gene therapy
                                                                                                                                                                                                                                                                                                               04-DEC-2003 (first entry)
Query Match
Best Local Similarity 92.3
                                                                                                                1 AAMAAAAAAA 13
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famamoto J, Isono Y, I
seki N, Yoshikawa T, (
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N-PSDB; ADB62854.
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Primer sets for synthesizing polynucleotides, particularly the 5602 full-
length cDNAs defined in the specification, and for the detection and/or
diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                Human; primer; detection; diagnosis; antisense therapy; gene therapy.
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                                                                                                                                                                                                       Human protein sequence SEQ ID NO:11642.
                                                                       AAB92956 standard; protein; 708 AA.
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Sugiyama T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-AUG-1999; 99JP-00300253.
11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
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                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                       EP1074617-A2.
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                                                                                                                                                         26-JUN-2001
                                                                                                                  AAB92956;
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                           RESULT 19
                                                    4AB92956
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABBS7737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                  Gaps
sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             developmental biology; cell signalling; insecticide;
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                                                                                                                                  Score 49; DB 7; Length 512;
Pred. No. 27;
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                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster polypeptide SEQ ID NO 6042.
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                                                                                                                                    92.5%;
                                                                                                                                                                                                                                                                   136 AAVAAAAAAAA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                           Query Match
Best Local Similarity 92.5.
To 12; Conservative
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                                                                                           Sequence 512 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila; de
pharmaceutical
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Saito K, Yamamoto J; , Otsuki T;

Hayashi K, S A, Nagai K,

Wakamatsu

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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence complementary to a polynucleotide comprises at least 15 nucleotides and the combination of
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01-FEB-2002; 2002WO-CH000063
                                                                                                                                                                             23-MAR-2001; 2001US-0277976P
                 Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                         WPI; 2003-018884/01.
                                                                                                                                                                                                                                                                                                                               N-PSDB; ABQ83200
                                                       WO200277023-A2.
                                                                                                03-OCT-2002
                                                                                                                                                                                                                                                                     Kramps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB97737). ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster daughter of legless (Doll) protein SEQ ID NO:6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
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                                                                                                                                                                                                                                                  Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                         Drosophila melanogaster polypeptide SEQ ID NO 38289.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABP54340 standard; protein; 815 AA.
                                                                                 ABB70499 standard; protein; 815 AA.
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11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-656860/75
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Best Local Similarity
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                                                                                                                            ABB70499;
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                                             RESULT 20
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The present invention describes a nucleic acid sequence and its encoded colypeptide, which are part of at least one signalling pathway in insects and vertebrates. The nucleic acid sequence is the daughter of legless cand vertebrates. The nucleic acid sequence is the daughter of legless (doll) gene, as well as its homologues, fragments, derivatives, or functional or structural analogues. The polypeptide is the daughter of edrivatives, or functional or structural analogues. Doll sequences have cycostatic activity, and can be used in gene therapy. The doll nucleic cycostatic activity, and can be used in gene therapy. The doll nucleic acid, Doll protein, or their homologues, derivatives or fragments can be used for developing a therapeutic and diagnostic compound (e.g. antibodies or its fragments, doll antisense DNA or RNA, doll double stranded RNA, or chemical or naturally occurring compounds interfering with doll function) for the treatment or diagnosis of disorders of call face, differentiation or proliferation. Fragments of the doll DNA sequences is useful as a hybridisation probe. The disorders which can be treated using doll sequences includes human tumours, (pre-) neophastic, condition-) malignant or cancerous conditions. The present sequence represents
Nucleic acid sequences of the Drosophila melanogaster Daughter of Legless gene and its encoded polypeptide, useful for developing therapeutic or diagnostic compound for treating or diagnosing e.g. tumors or cancerous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                           Claim 15; Fig 1; 68pp; English.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 815 AA;
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                                                                                                                                  conditions.
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a POSH (plenty
                                                                                      The present invention relates to a method of identifying an antiproliferative agent, comprising providing a POSH (plenty of SH3 domains) polypeptide and a test agent, and identifying the test agent that interacts with the POSH polypeptide. The POSH protein is a ubiquitin ligase enzyme. The method is useful for identifying agents for treating a neoplastic condition, preferably cancer selected from thyroid carcinoma, liver cancer (hepatocellular cancer), lung cancer, cervical cancer, ovarian cancer, renal cell carcinoma, lymphoma, osteosacoma, liposarcoma, leukaemia, breast carcinoma and breast adenocarcinoma. The present sequence is a protein sequence shown in the exemplification of the
 neoplasia,
identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid encoding a POSH (plen of SH3 domains) polypeptide. The polypeptide sequence additionally comprises a RING domain. The nucleic acid mitigates a POSH loss of function phenotype in a cell. The POSH loss of function phenotype in a cell. The POSH loss of function phenotype is a decrease in HIV virus like particle production. The method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Virucide, ligase inhibitor, gene therapy; POSH; plenty of SH3 domains; RING domain, envelop virus; retroid virus; RNA virus; retrovirus; rhabdovirus; lentivirus; filovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New POSH nucleic acids and polypeptides useful for treating viral disorders, particularly disorders caused by envelop viruses, retroid viruses and RNA viruses, including retroviruses, rhabdoviruses,
                                                                                                                                                                                                                                                                                                                                                  ö
Identifying an anti-proliferative agent, useful for treating comprises providing a POSH polypeptide and a test agent, and the test agent that interacts with the POSH polypeptide.
                                                                                                                                                                                                                                                                                                                 DB 7; Length 892;
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                                                                                                                                                                                                                                                                                                                 Score 49;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse POSH protein sequence, SEQ ID 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADH73564 standard; protein; 892 AA.
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                                                               2; Fig 15; 151pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lentiviruses and filoviruses.
                                                                                                                                                                                                                                                                                                                92.5%;
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15-MAR-2002; 2002US-0364530P.
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419 AAVAAAAAAAA 431
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                                                                                                                                                                                                                                                                                                                                                12; Conservative
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                                                                                                                                                                                                                                                                                    Sequence 892 AA;
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                                                                                                                                                                                                                                                     invention
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                                                               Claim
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cell proliferation, enzyme; cytostatic, cancer.
                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                    New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murine ubiquitin ligase POSH protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABU64278 standard; protein; 892 AA
                                                                                                                          PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92.5%;
92.3%;
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26-JUN-2002; 2002US-0391629P.
27-NOV-2002; 2002US-0429916P.
              23-MAR-2001; 2001WO-US009231.
                                           23-MAR-2000; 2000US-0191637P.
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108 AAVAAAAAAAAA 120
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                                                                                                                          Venter JC, Adams M,
                                                                                                                                                       2001-656860/75
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                                                                                           (PEKE ) PE CORP NY
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Best Local Similarity
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N-PSDB; ABL15680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 855 AA;
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                                                                                                                                                                                                                                       interactions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABU64278;
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Gaps

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invention involves producing a recombinant POSH polypeptide. Also disclosed is a method for identifying an antiviral or antiapoptotic agent, comprising providing a POSH polypeptide and a test agent, and identifying a test agent that interacts with the POSH polypeptide. The POSH polypeptide comprises an SH3 or RING domain, where the test agent binds. The test agent is a polypeptide, an antibody, a small molecule or a peptidomimetic. The test agent that interacts with POSH decreases the maturation of a virus containing the PTAP or PPEY motif. The interaction with POSH and day polypeptide. Alternatively, identifying an antiviral agent comprises providing a POSH nucleic acid and a test agent, and identifying a test agent that binds to the POSH nucleic acid. The test agent, and identifying a test agent that binds to the POSH nucleic acid. The test agent is a contained a test agent is a contained acid, an antisense oligomuclectide, a RNAi construct, a DNA enzyme or a ribozyme. The nucleic acids, polypeptides, compositions and methods of the invention are useful for treating viral disorders, and and a test agent is a contained with a construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disorders caused by envelop viruses, retroid viruses and RNA luding retroviruses, rhabdoviruses, lentiviruses and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    filoviruses. The current sequence represents the mouse POSH protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            viruses, including retroviruses,
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Sequence 892 AA;

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Gaps
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0
92.5%; Score 49; DB 7; Length 892; 92.3%; Pred. No. 45; ive 1; Mismatches 0; Indels
                                                                                    419 AAVAAAAAAAAA 431
                                                                 1 AAMAAAAAAAA 13
                   Best Local Similarity 92.3
Matches 12; Conservative
      Query Match
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ADR89697 standard; protein; 892 AA. (first entry) 18-NOV-2004 ADR89697; RESULT

Mouse; POSH; plenty of SH3 domains; virucide; anti-HIV; cytostatic; Murine POSH (Plenty of SH3 domains) coding sequence. vaccine.

Mus sp.

WO2004073609-A2

02-SEP-2004.

05-FEB-2004; 2004WO-US003600.

05-FEB-2003; 2003US-0445534P. 03-MAR-2003; 2003US-0451437P. 21-APR-2003; 2003US-0464285P. 16-SEP-2003; 2003US-0503931P.

(PROT-) PROTEOLOGICS INC.

Tuvia S; Taglicht DN, Reiss Y, Yaar L, Alroy I,

WPI; 2004-635468/61. N-PSDB; ADR89696.

New complex comprising a Plenty Of SH3 (POSH) polypeptide and a POSH-associated kinase (POSH-AK) or its subunit, useful in preparing a composition for treating or preventing a POSH associated cancer.

03-MAR-2003; 2003US-0451437P. 05-MAR-2003; 2003US-0455284P. 19-MAR-2003; 2003US-045576PP. 20-MAR-2003; 2003US-0456640P.

03-APR-2003; 2003US-0460526P. 04-APR-2003; 2003US-0460792P. 21-APR-2003; 2003US-0464285P.

2003US-0469462P 2003US-0471378P

21-APR-2003; 2 09-MAY-2003; 2 15-MAY-2003; 2

Disclosure; SEQ ID NO 9; 163pp; English

The present sequence is the protein sequence of murine Plenty Of SH3 domains (POSH). The invention provides novel complexes of POSH

polypeptides and POSH associated kinases (POSH-AKB). An isolated, countied or recombinant complex comprising a POSH polypeptide and a POSH-AK but it is claimed. The complex is used in methods for identifying agents that modulate an activity of POSH or POSH-AK by disrupting a complex of POSH and POSH-AK. These modulator agents can be used as antivital agents, especially where the virus is an envelope virus, HIV or West Nile virus, or as anti-apoptotic or anti-cancer agents in which a modulator agent will decrease the proliferation or survival of a POSH-associated cancer cell. The modulator agents may also inhibit crafficking of a protein through the seretory pathway. An inhibitor of POSH, e.g. an agent that inhibits a POSH-AP, or an agent that inhibits or posh expression, can be used to inhibit the Jun kinase (JNK) pathway in a human cell and hence to treat a JNK pathway-associated disease. A POSH inhibitor may also be used to treat a protein kinase (JNK) pathway in a cell and hence to treat a protein kinase (JNK) pathway in a second protein in a cell comprises contacting the cell with an agent that inhibits phosphorylated POSH polypeptide is claimed, which is phosphorylated POSH polypeptide is claimed, which is phosphorylated POSH polypeptide is claimed, which is a sportion of a POSH polypeptide including a consensus PKA phosphorylation site, at a site of sequence K/R-R-X-S/T-hydrophobic or R-X-X-S/T-hydrophobic. Also claimed is a postion mammalian POSH polypeptide including a consensus PKA phosphorylation of POSH. ô cytostatic; nootropic; neuroprotective; antiparkinsonian; anticonvulsant; antiviral; neuroleptic; central nervous system; POSH polypeptide; POSH-associated protein; POSH-AP; HERPUDI; Ubiquitin ligase; antiviral agent; anti-apoptotic agent; anti-cancer agent; neurological disorder propression disorder; Alzheimer's disease; Parkinson's disease; Huntington's disease; schizophrenia; Gaps .; 0 Score 49; DB 8; Length 892; Pred. No. 45; 1; Mismatches 0; Indels ADS34245 standard; protein; 892 AA. POSH protein associated protein #4. 92.5%; 92.3%; 02-MAR-2004; 2004WO-US006308 ||:||||||||| 419 AAVAAAAAAAAA 431 02-DEC-2004 (first entry) 1 AAMAAAAAAAA 13 Local Similarity 92.3 nes 12; Conservative Niemann-Pick's disease WO2004078130-A2. Sequence 892 AA; Homo sapiens. 16-SEP-2004. ADS34245; Query Match Matches RESULT 26 ADS34245 ò 셤

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05-MAR-2003; 2003US-0452284P.
20-MAR-2003; 2003US-0456640P.
09-MAY-2003; 2003US-0469462P.
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                                                                                                                                                                                                                      WPI; 2004-748573/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                         N-PSDB; ADT77903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 892 AA;
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   21-OCT-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated, purified or recombinant complex (I) comprising a PoSH polypeptide and a PoSH-associated protein (POSH-AP) (a) or HERPUDI and a Ubiquitin ligase (b). Methods using (I), (a) or (b) are useful for identifying an agent that modulates an activity of a POSH polypeptide or POSH-AP, for identifying an antiviral agent, an anti-apoptotic agent, an anti-cancer agent, an agent that inhibits trafficking of a protein through the secretory pathway, an agent that inhibits the progression of a neurological disorder, an agent that modulates a POSH function, an agent that modulates a HERPUDI function. The methods can be used for treating a viral infection, for inhibiting an activity of a POSH-associated disease is viral infection, POSH-associated cancer or POSH-associated disease is viral infection, POSH-associated cancer or POSH-associated neurological disorder. The methods are useful for treating or preventing POSH-associated neurological disorder. The methods are useful for treating or preventing POSH-associated neurological disorder in a subject e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease, schizophrenia, Niemann-Pick's disease. This sequence corresponds to a protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                 Isolated, purified or recombinant complex, useful for identifying an antiviral, anti-apoptotic or anti-cancer, comprising POSH polypeptide and POSH-associated protein (POSH-AP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse; POSH; plenty of SH3 domains; ubiquitin ligase; enzyme; neuroprotective; nootropic; antiparkinsonian; anticonvulsant; cerebroprotective; CNS-gen.; antidepressant; neuroleptic; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Pred. No. 45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                           Yaar L,
                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 9; 374pp; English.
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                                                                                                                                                                                                                                                                         Taglicht DN, Alroy I, Reiss Y,
                                                                                       19-JUN-2003; 2003US-0480376P.

08-AUG-2003; 2003US-0493860P.

28-AUG-2003; 2003US-0498534P.

16-SEP-2003; 2003US-0503931P.

10-NOV-2003; 2003WG-US035712.

05-EEB-2004; 2004WG-US003600.

02-MAR-2004; 2004US-054986F9.
   2003US-0472327P.
                                       2003US-0475825P.
                                                      2003US-0479317P.
2003US-0480215P.
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92.3%;
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Best Local Similarity
----- 12; Conserva
                                                                                                                                                                                                                                                                                                                               WPI; 2004-662346/64.
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20-MAY-2003; 30-MAY-2003; 30-MAY-2003; 303-JUN-2003; 3
                                                      17-JUN-2003;
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                                                                                                                                                                                                                                                                                            Greener T;
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The present sequence is the protein sequence of murine POSH (plenty of SH3 domains), a ubiquitin ligase. The invention relates to POSH and to the discoverty of novel interactions between POSH and POSH and to the discoverty of novel interactions between POSH and POSH associated proteins, especially HERPUDI. Methods are provided for modulating a process in which POSH participates by targeting HERPUDI or the participates by targeting HERPUDI or the participates by targeting a process in which HERPUDI participates by targeting POSH. A claimed method of treating a neurological disorder comprises administering an agent that inhibits a ubiquitination. The neurological disorder is selected from: Alzheimer's disease, Parkinson's disease, Huntington's disease, Pick's disease, Niemann-Pick's disease, Huntington's disease, depression and schizophrenia. The modulator agent is a short interfering RNA (siRNA) construct, a small molecule, an antibody or an antisense construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New complex of POSH polypeptides and POSH-associated protein (POSH-AP) useful for identifying an agent for treating neurological disorder e.g. Alzheimer's disease, Parkinson's disease.
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                                                                                                                                                                                                                                                                                                                                                                       Taglicht DN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 9; 145pp; English.
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                                                                                03-APR-2003; 2003US-0460526P.
03-JUN-2003; 2003US-0475825P.
02-MAR-2004; 2004WO-US006308.
05-APR-2004; 2004WO-US010582
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                                                                                                                                                                                                                                                                                                                                                                  Yaar L, Alroy I, Reiss Y,
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The present sequence is the protein sequence of mouse POSH. The invention relates to novel associations between Cbl-b and POSH. Cbl-b and POSH are involved in viral maturation, including the production, post-translational processing, assembly and/or release of proteins in a viral particle. Viral infections may be ameliorated by inhibiting an activity (e.g. ubiquitin ligase activity or target protein interaction) of POSH or Cbl-b. The virus is a retroid virus, an RNA virus or an envelope virus, capecially a human immunodeficiency virus. A claimed method of identifying an antiviral agent comprises identifying a test agent that disrupts a complex of a Cbl-b polypeptide and a POSH polypeptide. A claimed method of treating a viral infection comprises administering an agent that inhibits the expression or activity of Cbl-b. The agent is preferably an siRNA construct ADU73816 that inhibits expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of human Cb1-b, an antisense construct, and the cora and antised or a small molecule. Also claimed are: methods of identifying and evaluating agents that modulate a Cb1-b or POSH function by measuring the effect of the agent on Cb1-b-mediated or POSH-mediated builduination or on budding, release, infectivity or reverse transcriptase activity of a virus or virus-like particle; methods of identifying an anti-apoptotic agent, an anti-cancer agent or an agent that inhibits progression of a neurological disorder, where the agent disrupts a complex comprising Cb1-b and POSH (or a CB1-b-associated protein such as POSH-associated neurological disorder or POSH-associated viral disorder using an agent that inhibits the expression or an activity of a CB1-b-bolypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein secretion; protein localization; golgi apparatus; plenty of SH3 domains protein; POSH; neuroprotective; nootropic; antidiabetic; antiinflammatory, virucide; antibacterial; antiparasitic; immunosuppressive; antiparatinsonian; anticonvulsant; neuroleptic; cytostatic; CNS-Gen.; cardiovascular disease, viral infection; bacterial infection; bacterial infection; microbial protein; neurological disease; immune disorder; Alzheimers disease; parkinsons disease;
                                                                                                                                                                                                                                                                   polypeptide, a POSH polypeptide, useful for treating Cbl-associated diseases, e.g. cancer, viral infection, disorders of the immune system,
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                                                                                                                                                                                                                                               isolated, purified or recombinant complex comprises a Cbl-b
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Pred. No. 45;
1; Mismatches 0; Indels
                                                                                                                                     Barr HM;
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                                                                                                                                     Tuvia S,
                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 9; 190pp; English.
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15-MAY-2003; 2003US-0471378P.
19-JUN-2003; 2003US-0480215P.
19-JUN-2003; 2003US-0480376P.
                                                                                                                                                                                                                                                                                          diseases, e.g. cancer, vir. or neurological disorders.
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Best Local Similarity 92.5.
Local 2; Conservative
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                                                                                         (PROT-) PROTEOLOGICS INC
                                                                                                                                     Reiss Y, Taglicht DN,
                                                                                                                                                                                 WPI; 2004-805123/79.
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Gaps

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The invention relates to a novel method for modulating the activity or localization of a trans-Golgi network (TGN) -associated protein. The method involves modulating the activity of one or more TGN-associated or proteins chosen from plenty of SH3 domains protein (POSH), a POSH-pathway CC proteins chosen from plenty of SH3 domains protein (POSH), a POSH-pathway cp polypeptide, a POSH-pathway polypeptide, a posH-associated polypeptide or a POSH binding protein. The method of the invention demonstrates neuroprotective, nootrople; cm antidabetic, antiinflammatory, virucide, antibacterial, antiparsitic, immunosuppressive, antiparkinsonian, anticonvulsant, neuroleptic, cytostatic and CNS-Gen applications. The method of the invention may be cytostatic and CNS-Gen applications. The method of the invention may be cytostatic for modulating the activity or localization of a TGN-associated protein, in particular, the method may be useful in inhibiting processing of a protein associated with a neurological disorder, cardiovascular disease or immunological disorder, in the subject, where the subject exhibits a neurological disorder chosen from Alzheimer's cardiovascular disease and prion-associated disease, preferably continumuno pick's disease and prion-associated disease, preferably continumuno disorder chosen from an inflammatory disease or an inflammatory disease or an inflammatory disease.
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SH3
niemann pick disease; prion infection; inflammation; autoimmune disease; diabetes mellitus; glycosylation; liver tumor; hepatocellular carcinoma; lung tumor; cervical dysplasia; colorectal tumor; ovary tumor; renal carcinoma; lymphoma; osteosarcoma; prostate tumor; leukemia; breast tumor; thyroid tumor; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modulating activity or localization of trans-Golgi network (TGN)-associated protein useful, eg, for inhibiting Beta amyloid production reducing virus infectivity comprises modulating activity of plenty of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tuvia S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 22; SEQ ID NO 9; 248pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alroy I, Reiss Y, Taglicht DN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JAN-2003; 2003US-0443495P.
                                                                                                                                                                                                                                                                                                                                                                                                                                        10-NOV-2003; 2003WO-US035712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-2003; 2003US-0491891P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PROT-) PROTEOLOGICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       domains protein (POSH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-833580/82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ADU68996
                                                                                                                                                                                                                                                                                                   WO2004098492-A2
                                                                                                                                                                                                                                  Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-NOV-2002;
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Gaps

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92.5%; Score 49; DB 92.3%; Pred. No. 45; ive 1; Mismatches

Best Local Similarity

Query Match Matches

Sequence 892 AA;

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1 AAMAAAAAAAA 13 12; Conservative

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8; Length 892; Indels

carcinoma and breast adeno-carcinoma, preferably breast cancer or colorectal cancer. The current sequence is that of a POSH protein of the

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419 AAVAAAAAAAA 431

RESULT 30

ADW87412 standard; protein; 892 AA

ADW87412;

(first entry) 07-APR-2005

Mouse POSH protein SEQ ID NO 9.

POSH inhibitor; ubiquitin ligase inhibitor; APP; cell proliferation; amyloid precursor protein; viral infection; neurological disease; Huntingtons chorea; Alzheimers disease; parkinsons disease; cytostatic; virucide; anti-HIV; neuroprotective; nootropic; anticonvulsant; antidepressant; pick's disease; major depressive disorder; schizophrenia; cancer; neuroleptic

Mus sp.

WO2005007141-A2.

27-JAN-2005

09-JUL-2004; 2004WO-US021900

11-JUL-2003; 2003US-0486730P.
24-JUL-2003; 2003US-0489795F.
10-NOV-2003; 2003US-05998712.
02-MAR-2004; 2004US-US065198.
05-MAR-2004; 2004WO-US066519.
05-APR-2004; 2004WO-US0106619.

28-MAY-2004; 2004WO-US016865

(PROT-) PROTEOLOGICS INC

N-PSDB; ADW87411

Levi-Hacham O; Alroy I, Tuvia S, Reiss Y, WPI; 2005-132260/14.

Claim 45; SEQ ID NO 9; 171pp; English.

cancers

New small molecule inhibitor of a POSH polypeptide useful e.g. to inhibit ubiquitin ligase activity of polypeptide, to treat viral infections, neurological disorder e.g. Alzheimer's disease, and to treat or prevent

This invention describes a novel small molecule inhibitor of a POSH polypeptide chosen from human Cbl-b polypeptide, a human PEM-3-like polypeptide, a SIAH1 polypeptide or a TTC3 polypeptide, comprising a RING domain. The POSH polypeptide is ARIH2, ASFIB, ATP5A1, BANF1, BAT3, BCAR1, BCL9, BIAA, BRA9, CLK2, COLIA1, DAP, DDX31, DKFZp434B1211, DKFZp761A052, DLG5, DNM2, DRP2, ERFHA1, EGLN2, EIFFERPPL, EWSR1, FAF1, EG1-27, CIC, CL25084, CLM25084, CLM2, SPF1A1, EGLN3, EIFFERPPL, EWSR1, FAF1, FE3557, FLJ1321, FLJ13479, FUJ7147, FST11, GC20, GLUL, HEBP2, CLJ13155, Hs.380933, HSPAIB, HSPC016, HSPC142, ITGB, J03930, KHDRBS1, CRAA1011, KIAAA111, KIAAA199, FUJ7147, FST11, GC20, GLUL, HEBP2, CLM31315, HSPAIB, HSPC016, HSPC142, ITGB, J03930, KHDRBS1, CRAA1111, KIAAA199, FUJ7147, FST11, GC20, GLUL, HEBP2, CCNT2, PGD, PIASY, POLQ, POLR212, RPMX5, PROL4, RAPB0, RBAF600, RNH, RPL, CCNT2, PGD, PIASY, POLQ, POLR212, SRPX5, RST41, SRPX1, SRT51, FRYS1, SRY3, ST711, TPC2, UBB21, HSPS1, SRY3, ST711, TPC2, UBB21, HSPS1, SPR11, SNX1, SN 

ö transport of amyloid precursor protein (APP) in a cell or cell proliferation or amyloid polypeptide production in a cell and also for the treatment of a viral infection (an envelope, a retroviral or a human immunodeficiency viral infections) or neurological disorder (Alzheimer's disease, Parkinson's disease, Huntington's disease, pick's disease, depression or schizophrenia). The inhibitor is also useful in the treatment and prevention of cancer, in a method of inhibiting ubiquitin ligase activity of a polypeptide, for maturation of a virus in a cell, for transport of APP and is capable of targeting one or more proteins. The products of the invention have cytostatic, virucide, anti-HIV, cerebroprotective, nootropic, anticonvulsant, antiparkinsonian, cerebroprotective, antidepressant and neuroleptic activity. This sequence represents a mouse POSH protein. Gaps ö 9; Length 892; 0; Indels Score 49; DB 9 Pred. No. 45; 1; Mismatches ADZ66429 standard; protein; 892 AA. 92.5%; ||:|||||||| 419 AAVAAAAAAAA 431 (first entry) 1 AAMAAAAAAAA 13 12; Conservative Query Match Best Local Similarity Sequence 892 AA; 14-JUL-2005 ADZ66429; Matches RESULT 31 ADZ66429 g ò

Virucide, human; ubiquitin ligase, Ub; plenty of SH3 domains; POSH, POSH-associated protein; POSH-AP; SH3 domain; viral maturation; ubiquitinylation; vesicular trafficking; viral infection; enzyme. 18-OCT-2004; 2004WO-US034498. 17-OCT-2003; 2003US-0512046P. WO2005038007-A2 28-APR-2005. Мив вр.

Mouse POSH

(PROT-) PROTEOLOGICS INC. Reiss Y;

WPI; 2005-322863/33. N-PSDB; ADZ66428

Isolated, purified or recombinant complex useful for identifying antiviral agent and anti-apoptotic agent, comprises plenty of SH3 domains POSH polypeptide and POSH-associated proteins POSH-AP.

Disclosure; SEQ ID NO 9; 171pp; English

This sequence represents a mouse ubiquitin (Ub) ligase, plenty of SH3 domains (POSH). The composition of the invention comprises a human POSH polypeptide and a POSH-associated protein (POSH-AP), or a polypeptide comprising a domain that is 90% identical to a POSH SH3 domain and a POSH -AP comprising an E2. Interactions between POSH and POSH-AP may be involved in many cellular processes, including viral maturation, regulating Nac or JNK signaling pathway, etc. An antibody which is immunoreactive with the epitope of human POSH amino acid sequence, where the antibody disrupts the interaction between a POSH polypeptide and a POSH-AP may be used for inhibiting viral infection. The POSH-AP comprises

Gaps

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Indels

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Mismatches

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Matches

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The invention relates to a novel method for identifying a protein substrate for an E3 protein comprising expression of an E3 protein, a coubstrate for an E3 protein and a prey fusion protein in a cell, where the E3 protein mediates covalent attachment of the bait protein to a prey protein that is a protein substrate of the E3 protein. The physical protein; the proteins induces an output signal which is detected. The ubiquitin-mediated proteolysis system is the major pathway for the selective, controlled degradation of intracellular proteins in eukaryotic calls. The process of degradation is catalyzed by a ubiquitin-activating enzyme (E1) and a ubiquitin-conjugating enzyme (E2), but may also require auxiliary substrate recognition proteins (E3s). The method of the invention may be useful for identifying a protein substrate for an E3 protein, which is subsequently useful for mediating ligation of ubiquitin or ubiquitin-like proteins. The current sequence is that of the murine post (plenty of SH3 domains) protein of the invention.
                                                                                                                                                                                           ö
BE2, which is chosen from UBC13, UBC5a, UBC5c and UBC6. The UBC13 is in a heterodimeric complex with a Ub conjugating enzyme variant (UBV) protein eg. UBV1a. The composition of the invention is useful for identifying an anti-viral agent and an anti-apoptotic agent, which involves identifying a test agent that disrupts the compound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying a protein substrate for an E3 protein, useful to allow modulation of ubiquitination, comprises expression of an E3 protein, a bait fusion protein, and a prey protein in a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein degradation; protein interaction; POSH; plenty of SH3 domains.
                                                                                                                                                                                           Gaps
                                                                                                                                                                                           ö
                                                                                                                                                       DB 9; Length 892
                                                                                                                                                                                           0; Indels
                                                                                                                                                     Score 49; DB 9
Pred. No. 45;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murine POSH (plenty of SH3 domains) protein.
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                                                                                                                                                                                                                                                                                                                                                              AEA10631 standard; protein; 892 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-OCT-2003; 2003US-0516152P.
                                                                                                                                                       92.5%;
92.3%;
                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                            Query Match
Best Local Similarity 92.3'
                                                                                                                                                                                                                               1 AAMAAAAAAAA 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tuvia S, Taglicht DN;
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REFSEQ; NP 067481.1.
                                                                                                                   Sequence 892 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
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AEA10631
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DB 9; Length 892; 45;

Score 49; Pred. No.

92.5**%**; 92.3**%**;

Best Local Similarity

Query Match

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The invention relates to a method for identifying an agent that modulates an activity of a HERPUDI polypeptide. The method comprises identifying an agent that modulates a complex comprising a HERPUDI polypeptide and a Nef polypeptide and a Nef polypeptide is an agent that modulates an activity of the HERPUDI polypeptide. Also described: (1) a method of inhibiting a MERPUDI polypeptide and a Cell infected with HIV; (2) a method of inhibiting a confinite in a subject infected with HIV; (3) an isolated, purified, or recombinant complex comprising a HERPUDI polypeptide and a Nef polypeptide; (4) a method of inhibiting an entity of a method of inhibiting a viral infection in a subject; (7) a HERPUDI colypeptide; and (8) a Nef polypeptide. The methods are useful for inhibiting a nagent that modulates an activity of a HERPUDI polypeptide, and (8) a Nef polypeptide. The methods are useful for inhibiting a Nef-mediated process in a cell infected with HIV, and inhibiting the progression of AIDS in a subject infected with HIV. The present sequence represents mouse POSH, which is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying agent that modulates activity of HERPUDI polypeptide, by identifying agent that modulates a complex comprising HERPUDI and Nef polypeptide, where agent that modulates the complex modulates activity of HERPUDI polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                    viral maturation inhibition; viral replication; viral infection; antiviral; anti-HIV; POSH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 49; DB 9; Length 892;
Pred. No. 45;
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1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 9; 141pp; English
                                                                                                                                                    AEC94736 standard; protein; 892 AA.
                                                                                                                                                                                                                                                        Mouse POSH protein SEQ ID NO:9.
                                                                                                                                                                                                                                                                                                                                                                                                                                              02-MAR-2005; 2005US-00070332.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-MAR-2004; 2004US-0549568P.
19-JUL-2004; 2004US-0589261P.
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92.3%;
                                                    Ouery Match
Best Local Similarity 92...
Best Local 12; Conservative
                                                                                                                                                                                                                       01-DEC-2005 (first entry)
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12; Conservative
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N-PSDB; AEC94735.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reiss Y, Alroy I;
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                                                                                                                                                                                                                                                                                                                                                                                                             29-SEP-2005
                                                                                                                                                                                       AEC94736;
                                                                                                                                                                                                                                                                                                                                              Mus sp.
                                                                                                                   RESULT 33
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developmental biology; cell signalling; insecticide;

Drosophila melanogaster.

Drosophila; de pharmaceutical

WO200171042-A2.

27-SEP-2001.

Drosophila melanogaster polypeptide SEQ ID NO 24801.

(first entry)

26-MAR-2002

ABB66003;

ABB66003 standard; protein; 1184 AA.

RESULT 35

ABB66003

419 AAVAAAAAAAAA 431

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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving oxpressed cativity of (II) or to treat disease states involving or quantitating a polypeptide in tissue, as molecular weight markers and as a food polypeptide in tissue, as molecular weight markers and as a food involving aberrant protein expression or biological activity. The involving aberrant protein expression or biological activity. The colypeptide and polymucleotide sequences have applications in a diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                 Human; chromosome mapping; gene mapping; gene therapy, forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 992;
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Pred. No. 50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                            Novel human diagnostic protein #5900.
ABG05909 standard; protein; 992 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tang YT;
                                                                                                                                                                                                                                                                                                                      30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                             31-MAR-2000; 2000US-00540217, 23-AUG-2000; 2000US-00649167,
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                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-639362/73
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Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAS70096
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                                                                                                                                                                                                                                          WO200175067-A2.
                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           biodiversity.
                                                                         13-FEB-2002
                                                                                                                                                                                                                                                                                 11-OCT-2001
                                    ABG05909;
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New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell

Myers EW;

PWD,

댜

Adams M,

Venter JC,

(PEKE ) PE CORP NY.

WPI; 2001-656860/75.

N-PSDB; ABL10106

interactions.

23-MAR-2001; 2001WO-US009231 23-MAR-2000; 2000US-0191637P 11-JUL-2000; 2000US-00614150

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                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 24801; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster polypeptide SEQ ID NO 2271.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB58493 standard; protein; 1235 AA.
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| 101 AAVAAAAAAAAA 713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1184 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB58493;
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ABB58493
ID ABB5
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Gaps

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Indels

0;

1; Mismatches

4 AAVAAAAAAAAA 16 1 AAMAAAAAAAA 13 12; Conservative

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed continuate protuction of (II). The polynucleotides are also used continuate to treat disease states involving aspressed activity of (II) or to treat disease states involving or quantitating a useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in celectronic format directly from WIPO at
                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila; developmental biology; cell signalling; insecticide;
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Pred. No. 71;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster polypeptide SEQ ID NO 3747.
                                                                                                                                                                                   Claim 20; SEQ ID NO 46026; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB58985 standard; protein; 1937 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           782 AAIAAAAAAAA 794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adams M,
               WPI; 2001-639362/73.
N-PSDB; AAS79854.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1444 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200171042-A2.
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                                                                                                                                            biodiversity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB58985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 38
ABB58985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABBS7737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, chromosome mapping, gene mapping, gene therapy, forensic; food supplement, medical imaging, diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 2271; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 61;
1; Mismatches
                                                                                                                                                                                                                                                                            Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human diagnostic protein #15658.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG15667 standard; protein; 1444 AA.
                                                                                                                                                                                                                                                                              PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92.5%;
                                                                                                                           23-MAR-2001; 2001WO-US009231.
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11-JUL-2000; 2000US-00614150.
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  Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liu C,
                                                                                                                                                                                                                                                                                                                     WPI; 2001-656860/75.
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Best Local Similarity
                                                                                                                                                                                                                                  (PEKE ) PE CORP NY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1235 AA;
                                                                                                                                                                                                                                                                                                                                          N-PSDB; ABL02596
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                                             WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                          interactions.
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                                                                                    27-SEP-2001
                                                                                                                                                                                                                                                                              Venter JC,
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ADI26773;
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                                                                                                                                                                                                                                                                                                                                                                                          Human, p53 pathway, therapeutic, angiogenic disorder, apoptotic disorder, chromodomain helicase DNA binding protein, CHD, cancer, gene therapy, cell proliferative disorder, chromatin organisation modifier domain,
                                                                        The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eutaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the princed specification, but was obtained in electronic format directly
                  isolated nucleic acid detection reagent for detecting 1000 or more as from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Funke RP;
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                                                      Disclosure; SEQ ID NO 3747; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                      DB 4; Length 1937;
                                                                                                                                                                                                                                                                                                                                                                       Human chromodomain helicase DNA binding protein (CHD) #5.
                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ij
                                                                                                                                                              from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Conserved C-terminal domain"
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                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                               93;
                                                                                                                                                                                                     92.5%; Score 49; 92.3%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Chromodomain"
739. .1035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "SNF2N domain"
1100. .1174
                                                                                                                                                                                                                                                                                                              AAE36107 standard; protein; 1944 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; 2001US-0328605P.
; 2001US-0338733P.
; 2002US-0357253P.
; 2002US-0357600P.
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                                                                                                                                                                                                                                                             330 AAVAAAAAAAA 342
                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                           1 AAMAAAAAAA 13
                                                                                                                                                                                                              Local Similarity 92.3
nes 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (EXEL-) EXELIXIS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-156840/15.
                                                                                                                                                                                  Sequence 1937 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200298899-A2
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22-OCT-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-FEB-2002;
                                      interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-DEC-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                       cytostatic.
                                                                                                                                                                                                                                                                                                                                 AAE36107;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Domain
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                            genes
                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                          RESULT 39
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The present invention relates to a method for identifying candidate p53 pathway modulating agents. The method involves contacting an assay system comprising purified chromatin organisation modifier (chromo) domain helicase DNA binding proteins (CHD), nucleic acids, their functionally active fragments or derivatives, with a test agent under conditions where, but for the presence of the test agent, the system provides a reference activity. The methods are useful for identifying modulators of the p53 pathway as therapeutic targets for disorders associated with defective p53 function, such as angiogenic disorders, apoptotic disorders or call proliferative disorders, e.g. cancer. The modulators are useful as research reagents, diagnostics and therapeutics. The invention is also useful in gene therapy. The present sequence is human chromodomain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antiinflammatory, Antiarteriosclerotic, Antipsoriatic; Gynaecological; Vasotropic; Vulnerary; Hypotensive; Antianginal; Cardiant; Osteopathic; gene therapy; antiangiogenic; tumour vascularisation; retinopathy; rheumatoid arthritis; Crohn disease; atherosclerosis; ovarian hyperstimulation; psoriasis; endometriosis; neovascularization; restenosis; cardiovascular disease; hypertension; Raynaud disease; muscular degeneration; osteoporosis; human; CHD3.
Identifying a candidate p53 pathway-modulating agent as therapeutic targets for disorders related to defective p53 function e.g. cancer by contacting an assay system having purified CHD polypeptide or nucleic acid, with a test agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antiangiogenic composition, useful for treating e.g. tumors, comprises new angiogenesis-related nucleic acids or related polypeptides, antibodies or antisense sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 49; DB
Pred. No. 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                Claim 13; Page 207-215; 278pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92.5%;
92.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human CHD3, SEQ ID 30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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Claim 5; SEQ ID NO 34; 110pp; French.

The present invention relates to antiangiogenic pharmaceutical compositions. The compositions comprise, as active ingredient, one or compositions. The compositions comprise, as active ingredient, one or more of: nucleac acid (1; ADIS6740-ADIS6730 encoded by (15. or instance) an endothelial cell gene the expression of which is induced by an antiopact, or its complement or fragment; polypeptide (11; ADIS6730 encoded by (1), or its fragment; can antisense nucleic acid (111; ADIS6750-ADIS6753) able to inhibit an antisense nucleic acid (111; ADIS6750-ADIS6753) able to inhibit care used for treating a wide range of angiogenic diseases: tumour vascularisation; retinopathy; rheumatoid arthritis; Crohn disease; carborosis; ovarian hyperstimulation; psoriasis; endometriosis atherosclerosis; ovarian hyperstimulation; psoriasis; endometriosis associated with neovascularization; restenosis (arterial or after balloon cargoplasty); overgrowth of cells in wound healing; peripheral vascular disease; hypertension; vascular inflammation; Raynaud disease; aneurysm; chrombophlebitis; lymphedema; ischaemia; angina; myocardial infarct; chrombophlebitis; lymphedema; ischaemia; angina; myocardial infarct; chrombophlebitis; lymphedema; ischaemia; angina; myocardial infarct; chrombophlebitis (composition) and osteoporosis. This sequence is chromodomain 

Sequence 1944 AA;

Query Match

92.5%; Score 49; DB 7; Length 1944;
Best Local Similarity 92.3%; Pred. No. 94;
Matches 12; Conservative 1; Mismatches 0; Indels

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Gaps

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||:||||||||| 207 AAVAAAAAAAA 219 1 AAMAAAAAAAA 13

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Search completed: September 9, 2006, 22:48:07 Job time : 101.418 secs

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probable glutamate acyl CoA dehydroge probable acyl coen probable acyl coen probable potassium pro-neural achaete hypothetical prote hypothetical prote hypothetical prote conserved hypothet probable membrane probable phosphoes probable 2,3-bisph fumarate hydratase hypothetical prote ATP-dependent prot DNA helicase II (E ribonucleoside-dip prote prote hypothetical prote hypothetical prote hypothetical prote genome polyprotein polyprotein - deng hypothetical prote hypothetical prote cobyric acid synth cobyric acid synth negative modulator negative modulator seqA protein - Esc ribosomal protein NADH-ubiquinone ox carbon-monoxide de hypothetical prote hypothetical prote genome polyprotein polyprotein hypothetical prote sugar ABC transpor probable ABC trans probable two compo sensor protein Cpx nypothetical prote protein-tyrosine-p vitellogenin vit-2 vitellogenin vit-1 CT365 hypothetical conserved hypothet hypothetical prote conserved hypothet phosphoribosylglyc hypothetical prote r-cell surface pro aryl sulfotransfer T24D18.18 protein prote DNA repair protein hypothetical prote hypothetical prote conserved hypothet genome polyprotein proteinase (EC 3.4 proteinase (EC 3.4 protein vit-2 [imp nypothetical prote hypothetical prote nonstructural prot protein protein C34G6.6 hypothetical hypothetical hypothetical DNA repair pr genome C86115 AB0024 B25817 E96674 GNWVDP GNWV16 GNWV16 GNWV26 JS0219 S37848 A56548 E72688 AB0446 T20198 D96798 S76260 S76260 T72143 T72143 R5MUL9 D82822 A56279 S46805 I71128 C91274 T29076 H64702 G71817 G96986 E95406 PRLJSA PRLJMP H95966 S76229 T20850 T26238 C82194 T13593 C87789 T13592 F83085 T20851 C70868 AI0467 D70309 AG2921 H97695 D70614 A49724 A43081 F89528 T16600 E83233 S74394 A34866 JC5000 F86295 AD0994 T24660 B90186 D71544 D72466 414 463 463 470 470 505 505 510 720 801 1011 1130 1131 1181 181 181 

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Gaps

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class II histocompatibility antigen-associated gamma chain Ii, 41K splice form - mouse NyAlternate names: Ia-associated invariant chain Ii41; invariant chain proteoglycan core NyAlternate names: Ia-associated invariant chain Ii41; invariant chain proteoglycan core C; Species: Gamma chain Ii, 31K splice for C; Species: Mus musculus (house mouse) C; Date: 17-Mar-1987 #sequence revision 12-Apr-1996 #text change 09-Jul-2004 C; Accession: B27866; A27866; A02244; A43530; S03099; S09284; A28956 R; Koch, N; Lauer, W; Habicht, J; Dobberstein, B. BMBO J. 6, 1677-1683, 1987 A; Title: Primary structure of the gene for the murine Ia antigen-associated invariant of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Note: the authors translated the codon AAC for residue 70 as Asp
R;Singer, P.A.; Lauer, W.; Dembic, Z.; Mayer, W.E.; Lipp, J.; Koch, N.; Hammerling, G.;
EMBO J. 3, 873-877, 1984
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A;Reaidues: 47-191,256-279 <SIN>
A;Cross-references: UNIPARC:UPI000016CEFA; GB:X00496; NID:g53102; PIDN:CAA25191.1; PID::
R;Eades, A.M.; Litfin, M.; Rahmsdorf, H.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-25 - READ-
A; Cross-references: UNIPARC: UPI0000089341; GB: M35872; NID: g194129; PIDN: AAA37897.1; PID
A; Cross-references: UNIPARC: UPI0000089341; GB: M35872; NID: g194129; PIDN: AAA37897.1; PID
B; Stone, J.; Perry, R.; Todd, J.A.; McDevitt, H.O.
B; Stone, J.; Perry, R.; Todd, J.A.; March 1988
A; Reference number: S03099
A; Accession: S03099
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Nucleic Acids Res. 17, 447-448, 1989
A;Title: Complete sequence of the murine invariant chain (Ii) gene.
A;Reference number: S09284; MUID:89098406; PMID:2492095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Structure of the murine Ia-associated invariant (Ii) chain as deduced from A;Reference number: A02244; MUID:84207946; PMID:6327293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Immunol. 144, 4399-4409, 1990
A;Title: The IFN-gamma response of the murine invariant chain gene is mediated by A;Reference number: A43530; MUD:90257363; PMID:2111346
A;Accession: A43530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-279 <KOC>
A;Cross-references: UNIPROT:P04441; UNIPROT:019452; UNIPARC:UPI000017382A
                                                                                                                                                                                                                                                                                                                                                                        #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 216;
A;Cross-references: GDB:119846; OMIM:142790
A;Map position: 5q31-5q33
A;Introns: 26/2; 84/1; 110/3; 131/3; 163/3; 193/1; 214/1
C;Superfamily: thyroglobulin type I repeat homology
C;Keywords: glycoprotein; transmembrane protein
F;130/Domain: intracellular #status predicted (INT>F;31-56/Domain: rransmembrane #status predicted <TMM>F;71-216/Domain: extracellular #status predicted <TMM>F;71-216/Domain: extracellular #status predicted <EXT>F;71-216/Domain: extracellular #status predicted <EXT>F;114,120/Binding site: carbobydrate (Asn) (covalent) #st
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100.0%; Pred. No. 2.7e-06;
iive 0; Mismatches 0;
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A;Cross-references: UNIPARC:UPI000003E32
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A; Residues: 1-58 <STO:
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A,Fitle: Structure of the human Ia-associated invariant (gamma)-chain gene: identificating A,Reference number: A94103; WUID:86233451; PMID:3459184
A,Reference number: A94103
A,Rolecule type: DNA
A,Residues: 1-216 <0SU>A,Residues: 1-216 <0SU>A,Reference number: S28903; WUID:93078879; PMID:1448172
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C;Comment: Both cell-free translation experiments and the consensus sequence for the initian additional sixteen residues upstream of the initiator, but this region is not
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A;Cross-references: UNIPARC:UP10000173828
A;Cross-references: UNIPARC:UP10000173828
A;Nudo, J.; Chao, L.Y.; Narni, F.; Saunders, G.F.
Nucleic Acids Res. 13, 8827-8841, 1985
A;Title: Structure of the human gene encoding the invariant gamma-chain of class II hist
A;Reference number: A93602; MUID:86093681; PMID:3001652
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 'MHRRESGREDQKDV',1-216 <STR>
A; Cross-references: UNIPARC:UP1000002AB09; EMBL:X00497; NID:g32130; PIDN:CAA25192.1; PID
A; Accession: A33234
A; Molecule type: DNA
A; Residues: 'MHRRESGREDQKDV',1-4 <STR2>
A; Residues: 'MHRRESGREDQKDV',1-4 <STR2>
A; Cross-references: UNIPARC:UP100000895C2
A; Katunuma, N.; Kakegawa, H.; Matsunaga, Y.; Saibara, T.
R; Katunuma, N.; Kakegawa, H.; Matsunaga, Y.; Saibara, T.
A; Title: Immunological significances of invariant chain from the aspect of its structura
A; Reference number: S46255; MUID:94326933; PMID:8050579
A; Contents: annotation in this reference are based on the assumption; with no experime
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                                                                                                                                                                                                                                                class II histocompatibility antigen-associated gamma chain - human
N,Alternate names: CD74 antigen; HLA-DR antigen-associated invariant chain; MHC class II
                                                                                                                                                                                                                                                                                                                                            C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 0.4-Dec-1906 #sequence_revision 26-Jan-1996 #text_change 31-Dec-2004
C;Accession: A93981; B93981; A93602; A94103; S28903; S07182; A33234; A02243; A27551; A30
R;Claesson, L.; Larhammar, D.; Rask, L.; Peterson, P.A.
R;Claesson, L.; Larhammar, D.; Rask, L.; Peterson, P.A.
A;Title: CDNA clone for the human invariant gamma chain of class II histocompatibility a A;Reference number: A93981; MUID:84170234; PMID:6324166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-216 <CL1>
A;Cross.references: UNIPROT:P04233; UNIPROT:O19685; UNIPARC:UPI000016AA48; GB:K01144; NI
A;Accession: B93981
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A;Residues: 81-104 <RIB>
A;Cross-references: UNIPARC:UPI000002F1B4
R;Strubin, M.; Mach, B.; Long, E.O.
EMBO J. 3, 869-872, 1984
A;Title: The complete sequence of the mRNA for the HLA-DR--associated invariant chain A;Reference number: S07182; MUID:84207945; PMID:6586420
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A;Molecule type: DNA
A;Residues: 'MHRRRSRSCREDOKPV',1-150,'T',152-216 <KUD>
                                ALIGNMENTS
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A; Status: preliminary
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N;Contains: class II histocompatibility antigen-associated gamma chain, short splice for C;Species: Rattus norvegicus (Norway rat)
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
C;Accession: S04362; S02182
R;McKnight, A.J.; Mason, D.W.; Barclay, A.N.
R;McKnight, A.J.; Mason, D.W.; Barclay, A.N.
A;Title: Sequence of a rat MHC class II-associated invariant chain cDNA clone containing A;Reference number: S04362; MUID:89282409; PMID:2499873
                                                                                                                                                                                                                                                                                                                                                   A,Molecule type: mRNA
A,Residues: 1-280 <MCK>
A,Residues: 1-280 <MCK>
A,Residues: 1-280 <MCK>
A,Cross-references: UNIPROT:P10247, UNIPARC:UPI000012C6BC, EMBL:X14254; NID:956652; PIDI
R;Henkes, W.; Syha, J.; Reske, K.
Nucleic Acids Res. 16, 11822, 1988
A,Title: Nucleotide sequence of rat invariant gamma chain cDNA clone pLR-gamma-34.3.
A,Reference number: S02182; MUID:89098337; PMID:3264906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-327 <STO>
A;Cross-references: UNIPARC:UPI0000502CC; GB:AE002093; NID:g6598626; PIDN:AAF18659.1;
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Afitle: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: 684420
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C;Detc: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T44583
R;Summer, E.J.; McCaffery, M.W.; Cline, K.
submitted to the EMBL Data Library, April 1999
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C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 24-Aug-2001
C;Accession: G84420
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A;Residues: 1-192,257-280 <HEN>
A;Cross-references: UNIPARC:UP1000002AB0A; EMBL:X13044; NID:956497;
A;Cross-references: UNIPARC:UP1000002AB0A; EMBL:X13044; NID:956497;
A;Note: the authors translated the codon ATC for residue 16 as Asn, of C;Noperfamily: class II histocompatibility antigen-associated gamma of;Keywords: alternative splicing; transmembrane protein
C;Neywords: alternative splicing; transmembrane protein
F;197-255/Domain: thyroglobulin type I repeat homology <THYI>
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Pred. No. 3.4;
3; Mismatches 1; Indels
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C;Superfamily: conserved hypothetical protein HI0188
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66.7%;
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Best Local Similarity 66.7.,
Best Local Similarity 67.7.
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Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                A;Accession: S04362
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                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Cross-references: UNIPARC:UPI000017382C
A;Mote: proof by site-directed mutagenesis that the sole chondroitin sulfate glycosaminc
C;Genetics: 26/2; 83/1; 109/3; 130/3; 161/3; 192/1; 256/1; 277/1
A;Mirtons: 26/2; 83/1; 109/3; 130/3; 161/3; 192/1; 256/1; 277/1
C;Moperdemily: class II histocompatibility antigen-associated gamma chain; thyroglobulin
C;Moperdemily: class II histocompatibility antigen-associated gamma chain Ii, 41K spli
F;1-29/Ponduc: class II histocompatibility antigen-associated gamma chain Ii,
F;1-29/Ponduin: intracellular #status predicted <CYT>
F;30-55/Domain: extracellular #status predicted <TWN>
F;56-279/Domain: thyroglobulin type I repeat homology <THY1>
F;30-55/Domain: thyroglobulin type I repeat homology <THY1>
F;30-53/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;13,119,239,253/Binding site: carbohydrate (Ser) (covalent) #status experimental
A;Molecule type: DNA
A;Residues: 1-9, M',11-112, Q',114-228,'STG',232-279 <ZHU>
A;Residues: 1-9, M',11-112,'Q',114-228,'STG',232-279 <ZHU>
A;Cross-references: UNIPARC:UP100001738
B;Miller, J.; Hatch, J.A:; Simonis, S.; Cullen, S.E.
Proc. Natl. Acad. Sci. U.S.A. 85, 1359-1363, 1988
A;Title: Identification of the glycosaminoglycan-attachment site of mouse invariant-chain A;Reference number: A28956; MUID:88144436; PMID:3422739
A;Accession: A28956
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C;Keywords: glycoprotein; transmembrane protein
F;1-30/Domain: intracellular (fragment) #status predicted <INT>
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F;31-5/Domain: transmembrane #status predicted <TMM>-
F;37-204/Domain: extracellular #status predicted <EXT>-
F;81-104/Region: class II associated invariant chain CLIP motif
F;112,118/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Pred. No. 0.00069;
2; Mismatches 0; Indels
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A,Molacule type: mRNA
A,Residues: 1-204 <NII>A,Cross-references: UNIPROT:Q29630,
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PMSOMRMATPMLMRA 101
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Best Local Similarity 85.7
Matches 12; Conservative
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PIDN:CAA31450.1; PII CTG for residue 17 a

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class II histocompatibility antigen-associated gamma chain, long splice form - rat

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enterica serovar Typhi (strain C

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C;Accession: AG0918
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, Lth, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Reference number: AB0502; MUID:21534947; PMID:11677608
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C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
                                                                                                                                                C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology C;Reywords: heme; iron; metalloprotein P;341-500/Domain: cytochrome P450 homology <P45> F;478/Binding site: heme iron (Cys) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                               Length 543
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14;
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2; Mismatches
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Pred. No.
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72.7%;
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Best Local Similarity 70.0
Matches 7; Conservative
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                T20D16.18; At2g23190
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C;Superfamily: helicase II
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Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-720 <PAR>
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hes 8; Conser
                                                            A; Map position: 2
A; Introns: 211/3; 339/3
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A; Status: preliminary
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Matches
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A;Residues: 1-543 CNUJA
A;Cross-references: UNIPROT:022188; UNIPARC:UPI00000A8D78; EMBL:AC002391; NID:g2642427;
A;Experimental source: cultivar Columbia
A;Experimental source: cultivar Columbia
R:Lin, X; Kaul, S:; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. auss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. A;Reterence number: A84420; MulD:20083487; PMID:10617197
A;Accession: F84621
A;Acc
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A; Description: An Arabidopsis homolog of TatC/YCF43.
A; Reference number: 222800
A; Reference number: 222800
A; Accession: T44583
A; Accession: T44583
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residuas: 1-340 < SUM>A; Residuas: 1-340 < SUM > A; Cross-references: UNIPROT: O9SJVS; UNIPARC: UP10180
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Pred. No. 3.5;
3; Mismatches 1; Indels
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Pred. No. 2.2;
2; Mismatches
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A,Molecule type: DNA
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57.1%;
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Best Local Similarity 66.7%;
Matches 8; Conservative
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314 PVTQMLLATPLL 325
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Best Local Similarity
8; Conserva
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C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43466
R;Blum, H.; Bauersachs, S.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, December 1999
A;Reference number: 222517
                                                    Gaps
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A; Cross-references: UNIPROT: Q9UNNS; UNIPARC: UPI000016AC9D; EMBL: AL133631
A; Experimental source: adult testis; clone DKFZp434P1723
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Length 720;
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A,Cross-references: UNIPARC:UP10000172EBA; GB:M38257
C;Comment: The gene that codes for this protein is induced during the SOS response; the
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C; Superfamily: helicase II
C; Keywords: ATP; DNA binding; DNA repair; DNA replication; hydrolase; nucleotide binding
F; 29-36/Region: nucleotide-binding motif A (P-loop)
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A.Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen. A.Reference number: A99629; MUID:21156231; PMID:11258796
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A;Residues: 1-720 <HAY>
A;Cross-references: UNIPROT:Q8X8P5; UNIPARC:UPI0000D08F3; GB:BA000007; PIDN:BAB38166.1.
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
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A;Note: expression is induced by DNA-damaging agents, e.g. nalidixic acid or mitomycin
A;Title: Analysis of the Escherichia coli genome: DNA sequence of the region from 84.5 A;Aeference number: $30660; MUID:9238234; PMID:1379743 A;Accession: $30703 A;Accession: $30703 A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                       A; Molecule type: DNA
A; Residues: 1-47, XY, 49-91, XY, 93-97, XXY, 100-720 «DAN»
A; Residues: 1-47, XY, 49-91, XY, 93-97, XXY, 100-720 «DAN»
A; Cross-treferences: UNIPARC: UPI0000172EB9; EMBL: M87049
A; Note: the mucleotide sequence was submitted to the EMBL Data Library, November 1992
B; Colloms, S.D.; Sykora, P.; Szatmari, G.; Sherratt, D.J.
J; Bacteriol. 172, 6973-6980, 1990
A; Title: Recombination at ColEl cer requires the Escherichia coli xerC gene product, a A; Reference number: A37841; MUID: 91072248; PMID: 2254268
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B86068
DNA-dependent ATPase I and helicase II [imported] - Escherichia coli (strain O157:H7,
C;Species: Escherichia coli
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C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
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Pred. No. 29;
2; Mismatches
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Mismatches
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Pred. No.
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58.3%;
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58.3%;
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Best Local Similarity
T, Conserve
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Best Local Similarity
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A;Experimental source: strain K-12, substrain MG1655
R;Yamamoto, Y.; Ogawa, T.; Shinagawa, H.; Nakayama, T.; Matsuo, H.; Ogawa, H.
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A;Residues: 1-437, R, 439-720 <YAM>
A;Cross-references: UNIPARC:UPI000016F607; GB:D00069; GB:N00069; NID:g216672; PIDN:BAA00
A;Cross-residues: 1-24 week confirmed by protein sequencing
A;Finch, P. W.; Emmerson, P. T.
Nucleic Acids Res. 12, 5789-5799, 1984
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R;Daniels, D.L.; Plunkett III, G.; Burland, V.; Blattner, F.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PI
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A;Residues: 1-223,'N',225-290,'N',292,'R',294-329,'T',331-539,'V',541-720 <FIN>
A;Cross-references: UNIPARC:UPI000016F606; GB:X00738; GB:K01148; GB:X00225; NID:g43296;
R;Easton, A.M.; Kushner, S.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the
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BNA helicase II (EC 3.6.1.-) [validated] - Escherichia coli (strain K-12)

N;Contains: adenosinetriphosphatase (EC 3.6.1.3)

C;Species: Escherichia coli

C;Date: 17-Mar-1987 #sequence revision 10-Oct-1997 #text change 09-Jul-2004

C;Accession: F65185; JS0014; A93528; A93498; S30703; E37841; A03549

R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; (A.; Rose, D.J.; Mau, B.; Shao, Y.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-650 <RYU>
A;Cross-references: UNIPROT:Q9UNNS; UNIPARC:UP100001698CA; GB:AF106798; NID:g5805207;
A;Experimental source: HeLa cell
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                                                                                                                                                                                                                                                                                                                                              associated factor 1, hFAF1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                C;Species: Homo sapiens (man)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: JC7093
R;Ryu, S.W.; Chae, S.K.; Lee, K.J.; Kim, E.
Biochem. Biochem. Rss. Commun. 262, 388-394, 1999
A;Title: Identification and characterization of human Fas associated factor A;Reference number: JC7093; MUID:99393315; PMID:10462485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID:97426617; PMID:9278503
A; Accession: F65185
A; Stauus: nucleic acid sequence not shown; translation not shown A; Molecule type: DNA
A; Residues: 1-720 <BLAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Length 650,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 39; DB
Pred. No. 26;
2; Mismatches
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A;Title: Transcription of the uvrD gene of
A;Reference number: A93498; MUID:84169504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53.4%;
                                                                                                                                                       Fas associated factor 1 - human
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Best Local Similarity 70.0
Matches 7; Conservative
476 PVSKLRIRTP 485
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PVSKLRIRTP 581
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                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: JC7093
A; Molecule type: mRNA
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셤 8

16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004

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R;Buchrieser, C.; Rusniok, C.; Couve, E.; Frangeul, L.; Billault, A.; Kunst, F.; Carniel submitted to the EMBL Data Library, October 1998
A;Description: DNA sequence of the 102 kbases unstable region of Yersinia pestis.
A;Reference number: Z24348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: T47054
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-168 <BUC>
A;Cross-references: UNIPROT: Q9R7V2; UNIPARC:UPI00000B59CF; EMBL:AL031866; PIDN:CAA21397.
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R;Fetherston, J.D.; Bertolino, V.J.; Perry, R.D.
Mol. Microbiol. 32, 289-299, 1999
A;Title: Ybtp and YbtQ; two ABC transporters required for iron uptake in Yersinia pestis A;Accession: T17446
A;Accession: T17446
A;Status: preliminary; translated from GB/EMBL/DDBJ
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R. M. Parkhill, J.; Wren, B. W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Mature 413, 523-527, 2001

A. Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A. Reference number: AB0001; MUID:21470413; PMID:11586360
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C;Species: Yersinia pestis
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                   C,Species: Yersinia pestis
C,Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 09-Jul-2004
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C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
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Pred. No. 11;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 52.1%; Score 38; DB 2; Length 168; Best Local Similarity 63.6%; Pred. No. 9.8; Matches 7; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: strain 6/69
C; Superfamily: Yersinia pestis hypothetical 21.1K protein
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                                                                                                                                   hypothetical protein [imported] - Yersinia pestis
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Local Similarity 63.6%;
Loc 7; Conservative
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A; Residues: 1-184 <FET>
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T17446
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                                                   RESULT 16
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A;Molecule type: genomic RNA
A;Molecule type: genomic RNA
A;Residues: 1-3390 cOSA-
A;Residues: 1-3390 cOSA-
A;Cross-references: UNIPROT: P27915; UNIPARC: UPI0000131DFE; GB:M93130; NID:g323468; PIDN:
C;Superfamily: hepatitis C virus genome polyprotein
C;Reywords: ATP; capsid protein; envelope protein; glycoprotein; nonstructural protein;
C;Reywords: ATP; capsid protein #status predicted cAPP-
F;1-14/Product: membrane protein precursor #status predicted cMEP-
F;15-265/Domain: transmembrane protein #status predicted cMEM-
F;26-280/Product: membrane protein #status predicted cMEM-
F;26-280/Domain: transmembrane #status predicted cMEM-
F;26-280/Domain: transmembrane #status predicted cMM-
F;73-771/Domain: transmembrane #status predicted cMM-
F;115-1134/Product: nonstructural protein NS2 #status predicted cM2A-
F;118-1134/Product: nonstructural protein NS2 #status predicted cM2A-
F;116-1175/Domain: unicleotide-binding motif A (P-loop)
F;75-176-176/A/Region: nucleotide-binding motif B
F;75-176/Domain: protein NS2 #status predicted cMS3-
F;1667-1674/Region: nucleotide-binding motif B
F;77-176/Domain: protein NS2 #status predicted cMS3-
F;77-176/Domain: protein NS2 #status predicted cMS3-
F;1667-1674/Region: nucleotide-binding motif B
F;77-176/Product: nonstructural protein NS3 #status predicted cMS3-
F;77-176/Product: nonstructural protein NS3 #status predicted cMS3-
F;1667-1674/Region: nucleotide-binding motif B
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N;Contains: capsid protein; envelope protein; membrane protein; nonstructural protein NS
a; nonstructural protein NS4b; nonstructural protein NS5
c;Species: dengue virus type 3
C;Species: dengue virus type 3
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 31-Dec-2004
C;Accession: A34774
R;Osatomi, X; Sumiyoshi H.
N;Osatomi, X; Sumiyoshi H.
N;Title: Complete nucleotide sequence of dengue type 3 virus genome RNA.
Cincesion: B6068
Riperna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, B.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: B86068
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-720 <<770>
A;Residues: 1-720 <<770
A;Residues: 1-720 <<770
A;Residues: 1-720 </70>
A;Residues: 1-720 </ri>
A;Residue
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F;2379-2490/Product: nonstructural protein NS4b #status predicted <N4B>
F;2491-3390/Product: nonstructural protein NS5 #status predicted <NS5>
F;183,347,433,750,903,980,1132,1188,1661,2300,2304,2386,2456,2702,2712/Binding site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 39; DB 2; Length 720;
Pred. No. 29;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.4%;
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653 PVSHORMGTPMV 664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Les 7; Conservative
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Best Local Similarity
7, Conserva
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GNWVD3
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A, Reference number: 219554
A, Accession: T22367
A, Accession: T22367
A, Molecule type: DNA
A, Molecule type: DNA
A, Residuae: 1-828 c MILL-
A, Residuaes: 1-828 c MILL-
A, Eschences: UNIPROT: Q20550, UNIPARC: UPI0000080941; EMBL: 274035; PIDN: CAA98485.1.
A, Experimental source: clone F4769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Molecule type: DNA
A,Residues: 69-222,'R',224-283,'T',285,'PP',288-337,'KCKNAVRSHYAGVPGDVSVLAEYASNADPHHCGTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Cross-references: UNIPARC:UP10000178D3F; EMBL:X57948; NID:g510827; PIDN:CAA41017.1; P1
                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: UNIPARC: UPI0000080941; EMBL: Z74041; PIDN: CAA98523.1; GSPDB: GN00023;
                      C,Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acriflavin resistance protein acrF - Escherichia coli (strain K-12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Introns: 62/1; 181/1; 375/2; 420/1; 452/1; 585/2; 662/2; 740/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 828;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
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                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 38; DB 2
Pred. No. 52;
3; Mismatches
                                                                                                                                                                                                                                                                 R,Mortimore, B. submitted to the EMBL Data Library, June 1996 A,Reference number: 219887 AACcession: T24409
                                                                                        submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: strain K-12
                                                                                                                                                                                                                                                                                                                                                                                                                                              Experimental source: clone T03F7
    Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.1%;
53.8%;
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312 ISRRRMALPMLAQ 324
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Matches 7; Conservative
                                           C; Accession: T22367; T24409
R; White, S.
                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-828 <WI2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene: CESP:F47G9.3
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R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew Iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A; Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A; Reference number: A85480; MUID:21074935; PMID:11206551
A;Cross-references: UNIPROT:Q9ZFZ9; UNIPARC:UP100000CAC1; EMBL:AF091251; NID:g3818595; C;Superfamily: Yersinia pestis hypothetical 21.1K protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:Q8X9A3; UNIPARC:UPI00000D0849; GB:BA000007; PIDN:BAB37561.1;
A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:Q8X9A3; UNIPARC:UPI0000D0849; GB:AE005174; NID:g12517896; A;Experimental source: strain 0157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable integral transmembrane protein acrF_l [similarity] - Escherichia coli (strain
                                                                                                                                                                                                                                                                                                            probable integral transmembrane protein [imported] - Escherichia coli (strain 0157:H7, C,Species: Escherichia coli
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C.Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
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                                                               Score 38; DB 2; Length 184; Pred. No. 11; Mismatches 3; Indels
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Pred. No. 39;
4; Mismatches
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39;
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Pred. No.
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                                                                    52.1%;
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58.3%;
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58.3%;
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109 NKLQLATPLLPQ 120
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109 NKLQLATPLLPQ 120
                                                                                      Best Local Similarity 63.6
Matches 7; Conservative
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112 PISPSRMTTPL 122
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                                                                                                                                                        1 PVSKMRMATPL 11
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Best Local Similarity
7; Conserva
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Best Local Similarity
Matches 7; Conserv
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-628 <STO>
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                                                                 Query Match
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Length 1046; Indels

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A;Residues: 1-1046 <STO>
A;Cross-references: UNIPROT:P52002; UNIPARC:UP1000012F022; GB:AE004479; GB:AE004091; NID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genome polyprotein - dengue virus type 1 (strain Singapore S275/90)
N;Contains: capsid protein; envelope protein; membrane protein; nonstructural protein NS
A; nonstructural protein NS4b; nonstructural protein NS5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AttA2-like ABC transporter, permease protein SMa0952 [imported] - Sinorhizobium meliloti C; Species: Sinorhizobium meliloti C; Species: Sinorhizobium meliloti C; Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004 C; Accession: C9536 R; Barnett, M.J.; Pisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowe ; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: ATP; capsid protein; envelope protein; glycoprotein; nonstructural protein;
F;1-114/Product: capsid protein #status predicted <CAP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Fu, J.; Tan, B.H.; Yap, B.H.; Chan, Y.C.; Tan, Y.H.
Virology 188, 953-958, 1992
A;Title: Full-length cDNA sequence of dengue type 1 virus (Singapore strain S275/90).
A;Reference number: A42551; MUID:92263809; PMID:1585663
A;Accession: A42551
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F;2244-2492/Product: nonstructural protein NS4b #status predicted <N4B>
F;2493-3396/Product: nonstructural protein NS5 #status predicted <NS5>
F;183,347,433/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: dengue virus type 1
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Dec-2004
C;Accession: A42551
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F.115-204/Domain: nonterminal signal sequence #status predicted <SIG>
F.115-204/Domain: nonterminal signal sequence #status predicted <SIG>
F.1505-281/Product: membrane protein #status predicted <MEM>
F.267-279/Domain: transmembrane #status predicted <MIN>
F.282-774/Product: envelope protein #status predicted <ENV>
F.753-769/Domain: transmembrane #status predicted <MIN>
F.751-769/Domain: transmembrane #status predicted <MN>
F.751-1127/Product: nonstructural protein NS2a #status predicted <NS3>
F.1184-11474/Product: nonstructural protein NS2b #status predicted <NS3>
F.1688-1675/Region: nucleotide-binding motif B (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: UNIPROT: P33478; UNIPARC: UPI000002F845; GB: M87512
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Pred. No. 2.3e+02;
2; Mismatches 3; Indels
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67;
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                                                                                                                                                                                                                                                                       A,Gene: mexB, PA0426
C,Superfamily: acriflavin resistance protein
                                                                                                                                                                                                                                                                                                                                                                                    Score 38;
Pred. No.
                                                                                                                                                                                      A; Experimental source: strain PAO1
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58.3%;
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58.3%;
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A; Residues: 1-3396 <FUJ>
                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                    A, Status: preliminary
A, Molecule type: DNA
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    Accession:
                                                                                                                                                                                                                                       C;Genetics:
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C95326
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C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: E8359.
C;Accession: E8359.
A;Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Jory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathol A;Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 23
839630
multidrug-efflux transport protein B - Pseudomonas aeruginosa
MyAlternate names: multidrug resistance protein B
C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Species: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession. 839630
R;Poole, K.; Heinrichs, D.E.; Neshat, S.
Mol. Microbiol. 10, 529-544, 1993
A;Title: Cloning and sequence analysis of an EnvCD homologue in Pseudomonas aeruginosa: A;Reference number: 839639; MUID:95058196; PMID:7968531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-1046 <POO>
A;Cross-references: UNIPROT:P52002; UNIPARC:UPI000016FC9A; GB:L11616; NID:g438852; PIDN:
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V.Function
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                                                                                                                                                                                                                                                                                                                                                    1; Indels
F;472-488/Domain: transmembrane #status predicted <TM6>
F;540-556/Domain: transmembrane #status predicted <TM7>
F;874-890/Domain: transmembrane #status predicted <TM8>
F;898-914/Domain: transmembrane #status predicted <TM9>
F;974-990/Domain: transmembrane #status predicted <TM0>
F;1012-1028/Domain: transmembrane #status predicted <TM10>
                                                                                                                                                                                                                                                                       Score 38; DB 2
Pred. No. 66;
4; Mismatches
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Best Local Similarity 58.39
7; Conservative
                                                                                                                                                                                                                                       Query Match
Best Local Similarity 58.3
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NKLQLATPLLPQ 120
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A;Gene: mexB
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A;Accession: A04028
A;Molecule type: genomic RNA
A;Residues: 1-514 <RCZ>
A;Cross-references: UNIPARC:UPI0000174A76; GB:M10242; NID:g323245
A;Note: the codons given for residues 54-Lys (AAU) and 55-Ile (GUC) are inconsistent wi
C;Superfamily: paramyxovirus nucleocapsid protein
C;Keywords: nucleocapsid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable acyl Co-A dehydrogenase [imported] - Salmonella enterica subsp. enterica serovo probable acyl Co-A dehydrogenase [imported] - Salmonella enterica subsp. enterica serovar Typhi shote: this species has also been called Salmonella typhi c;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: Al1050

R;Parkhill, J: Dougan, G:; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher R;Parkhill, J:; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Parrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K., A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica seron A;Reference number: AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-540 < PRR>
A;Cross-references: UNIPARC:UPI0000CDBCE; GB:AL513382; PIDN:CAD06854.1; PID:g16505502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable exported protein YPO3664 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 31-Dec-2004
C;Accession: AB0446,
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: UNIPROT: Q8ZAW7; UNIPARC: UPI00000DCE73; GB: ALS90842; PIDN: CAC93134.1
                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 49;
3; Mismatches
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Pred. No. 52;
2; Mismatches
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A;Gene: YPO3664
C;Superfamily: MSHA biogenesis protein MshH
                                                                                                                                                                                                                                                                                              50.7%;
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8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           484 IAKMRMLTKMLSQ 496
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Best Local Similarity 53.8
Matches 7; Conservative
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Best Local Similarity
Matches 8; Conserv
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A;Molecule type: DNA
A;Residues: 1-638 <KUR>
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C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AE350
C;Accession: AE350
C;Accession: AE350
C;Accession: AE3520
C;Accession: AE3520
C;Accession: AE3520
C;Accession: Brucella melitensis
C;Berve Charles Brucella melitens
C;Berve C; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Accession: AE3520
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilod A;Reference number: A95262, MUD:21396509; PMID:11481432
A;Accession: C95326
                                                                                                                                                                 A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Kossidues: 1-296 cKUR>
A;Coss = references: UNIPROT:Q92ZH0; UNIPARC:UPI00000CB0FC; GB:AE006469; PIDN:AAK65173.1;
A;Experimental source: strain 1021, megaplasmid pSymA
R;Galibert, F.; Finan, T.M.; Long, S.R.; Publer, A.; Abola, P.; Ampe, F.; Barloy-Hubler, Dela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, Hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
C;Gonetics: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-303 <KUR>
A;Cross-references: UNIPROT:Q8YDT8; UNIPROT:Q8FXQ8; UNIPARC:UPI0000058346; GB:AE008918;
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C;Species: canine distemper virus
C;Species: canine distemper virus
C;Dacession: A04028
R;Rozension: A04028
R;Rozenblatt, S.; Eizenberg, O.; Ben-Levy, R.; Lavie, V.; Bellini, W.J.
J. Virol. 53, 684-690, 1985
A;Fitle: Sequence homber: A93006; MUID:85108164; PMID:3838193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: spermidine/putrescine transport system permease protein potH
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Pred. No. 28;
3; Mismatches 1; Indels
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Pred. No. 27;
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C;Superfamily: probable ribose ABC transporter rbsC-2
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50.0%;
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Best Local Similarity 63.6°
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PIASMALVTPLL 36
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18 LRVATPLLLAA 28
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: SMa0952
A;Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: BMEII0087
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C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: 876260
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; Kaneko, T.; Sato, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda A; Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;cross_references: UNIPROT:Q55605; UNIPARC:UP100000C0F10; EMBL:D64000; GB:AB001339; NID
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Defrococcus radiodurans
C;Dacession: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: G75435
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ms.; Saith, H.O.; Venter, J.C.; Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-163 «WHI>
A;Cross-references: UNIPROT:Q9RVB7; UNIPARC:UPI00000C1897; GB:AE001961; GB:AE000513; NII
A;Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans A;Reference number: A75250; MUID:20036896; PMID:10567266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22143
F;Kershaw, J.
Submitted to the EMBL Data Library, September 1996
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                                                                                                                                                                                          hypothetical protein slr0770 - Synechocystis sp. (strain PCC 6803)
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A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Reference number: S74322; MUID:97061201; PMID:8905231
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Pred. No. 14;
3; Mismatches
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Pred. No. 2
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782 IGDMRRATPKLAQA 795
12
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Best Local Similarity 53.8
7, Conservative
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EMRSSTPSLMEA 96
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Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: G75435
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                                                                                                                                                                         C;Species: Caemorhabditis elegans
C;Species: Caemorhabditis elegans
C;Date: 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20198; T23659
R;Lightning, J.
R;Lecssion: T20198
A;Reference number: Z19236
A;Recession: T20198
A;Reference number: J1920
A;Reference number: J1920
A;Reference number: J1920
A;Residues: J1980
A;Residues: J1980
A;Residues: J1980
A;Residues: J1980
A;Residues: J1980
A;Residues: J1980
A;Reserimental source: Clone C54C6
B;Sims, M.
B;Sims, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Map position: 3
A;Introns: 26/3; 71/1; 234/3; 375/2; 506/3; 539/1; 580/2; 639/2; 687/3; 927/1; 958/2
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Pred. No. 1.1e+02;
1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.7%; Score 37; DB 2; Length 980; 50.0%; Pred. No. 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, October 1994
A;Reference number: 219778
A;Accession: T23659
A;Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local Similarity 57.1%;
Matches 8; Conservative
        14
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57 PINKKREWLPLMMQ 70
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PVTKTRYSTPMM 104
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Matches 6; Conservative
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        PVSKMRMATPLLMQ
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A;Residues: 1-1108 <STO>
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A;Gene: F22K20.5
A;Map position: 1
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C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: D82822
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide SequerNature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-222 <SIM>
A;Cross-references: UNIPROT:Q9PGI6; UNIPARC:UPI00000C2382; GB:AE003884; GB:AE003849; NII
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rismpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, Bas-Neco, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohn D.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigi chado, M.A.; Madeira, A.M.B.N.; Madeira, H.F.; Marrino, C.L.; Marques, M.V.; Martins, A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; palmieri, D.M. Rodrigues, V.; Rosa, A.J. de M.; da Silva, V.E.; da Silva, A.M.; Silva Jr., W.A.; da Silvai, M.A.; da Silva, A.M.; Silva Jr., W.A.; da Silvai, Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.;
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C;Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004
C;Accession: A56279; PL0141; A46361
R;Schuebel, U; Kraut, M.; Moersdorf, G.; Meyer, O.
J. Bacteriol. 177, 2197-2203, 1995
A;Title: Molecular characterization of the gene cluster coxMSL encoding the molybdenum-04;Reference number: A56279; MUID:95238294; PMID:7721710
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A;Cross-references: UNIPROT: P19920; UNIPARC: UPI000011274D; GB: X82447; NID: 9809563; PIDN
A;Cross-references: UNIPROT: P19920; UNIPARC: UPI000011274D; GB: X82447; NID: 9809563; PIDN
A;Note: the source is designated as Oligotropha carboxidovorans
R;Kraut, M.; Hugendieck, I.; Herwig, S.; Meyer, O.
Arch. Microbiol. 152, 335-341, 1989
A;Title: Homology and distribution of CO dehydrogenase structural genes in carboxydotrol
A;Reference number: PL0138; MUID: 90055678; PMID: 2818128
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Arch. Microbiol. 157, 301-304, 1992
A;Title: The structural genes encoding CO dehydrogenase subunits (cox L, M and S) in Pse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               carbon-monoxide dehydrogenase (EC 1.2.99.2) medium chain - Pseudomonas carboxydovorans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Experimental source: strain OM5
A;Note: although the chemical evidence is good for an amino-terminal Met-Met sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: protein
A;Residues: 1,'PSAR',6-10,'IPGKS',16-29 <HUG>
A;Cross-references: UNIPARC:UP10000178C94; PIDN:AAB22965.1; PID:9253868
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A;Reference number: A48361; MUID:92378472; PMID:1510563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
32;
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Pred. No.
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A;Residues: 'M',1-14 <KRA>
A;Cross-references: UNIPARC:UP10000178C93
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Best Local Similarity
7, Conserve
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A;Reference number: 219523
A;Accession: T22143
A;Accession: T22143
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rotecule type: DNA
A;Residues: 1-179 <WIL>
A;Cross-references: UNIPROT:Q93715; UNIPARC:UPI00000825A1; EMBL:Z79755; PIDN:CAB02105.1;
A;Csnerics: A;Gsnerics: A;Gsnerics: A;Gsnerics: A;Gsnerics: 1
A;Map position: 1
A;Map position: 1
A;Introns: 30/3; 80/1; 111/1; 148/1
C;Superfamily: Caenorhabditis elegans hypothetical protein F43G9.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ribosomal protein L9 precursor, chloroplast [similarity] - Arabidopsis thaliana N,Alternate names: protein F28D10_80 (Species Arabidopsis thaliana (mouse-ear cress) (C,Species: Arabidopsis thaliana (mouse-ear cress) (Species: 31-Mar-1992 #sequence Tar180; 31-8043; S22121 (S,Accession: S20943; S22960; T51786; S18025; S22121 (S,Thompson, M.D.; Jacks, C.M.; Lenvik, T.R.; Gantt, J.S. (Plant Mol. Biol. 18, 931-944, 1992 (A)Title: Characterization of rps17, rp19 and rp115: three nucleus-encoded plastid ribosc A;Reference number: S20942; MUID:92256814; PMID:1581570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPARC:UF10000001AF8; EMBL:Z11129; NID:g16498; PIDN:CAA77480.1; PID Ryblason, M.; Berger, C.; Cooke, R.; Grellet, F.; Laudie, M.; Mewes, H.W.; Rudd, S.; Le submitted to the Protein Sequence Database, August 2000 A;Reference number: Z25454
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C;Species: Xylella fastidiosa
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A;Accession: S22960
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A;Introns: 51/3; 94/2; 109/3; 142/2; 158/2
A;Note: F28D10_80
C;Superfamily: Escherichia coli ribosomal protein L9
C;Keywords: chloroplast; protein biosynthesis; ribosome
F;1-37/Domain: transit peptide (chloroplast) #status predicted <TNP>
F;38-197/Product: ribosomal protein L9 #status predicted <MAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49.3%; Score 36; DB 2; Length 179; 87.5%; Pred. No. 25; ive 1; Mismatches 0; Indels
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42.9%; Pred. No. 28;
ive 4; Mismatches 4; Indels
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A;Experimental source: cultivar Columbia; BAC clone F28D10
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PTGKAQLMTPLLLK 94
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PVSRMRMA 62
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A; Residues: 1-197 < TH2>
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A; Residues: 1-197 <THO>
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A; Status: preliminary
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Search completed: September 9, 2006, 23:01:55 Job time: 20.0886 secs
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Cispecies: Treponema pallidum subsp. pallidum (syphilis spirochete)
Cispecies: Treponema pallidum subsp. pallidum (syphilis spirochete)
Cispecies: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Oct-2004
CiAccession: D71288 #sequence_revision 24-Jul-1998 #text_change 05-Oct-2004
CiAccession: D71288 #sinth, H.O.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDd rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDd rson, J.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71250; MUID:98332770; PMID:9665876
A;Accession: D71288
A;Accession: D71288
A;Accession: D71288
A;Accession: D7028
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A;Cross-references: UNIPROT: ONIPARC: UPI00000D3295; GB:AE001245; GB:AE000520; NID
A;Experimental source: strain Nichols
C;Genetics:
A;Gene: TP0735
C;Superfamily: glutamate synthase. small subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 39
846805

hypotherical protein YHR085w - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
C;Accession: 846805
R;Favello, T
Submitted to the EMBL Data Library, June 1994
A;Bescription: The sequence of S. cerevisiae cosmid 9205.
A;Reference number: 846795
A;Recession type: DNA
A;Residues: 1-334 <FAV>
A;Cross_references: UNIPROT:P38803; UNIPARC:UPI0000053233; EMBL:U10556; NID:g500825; PIE
A; Experimental source: strain OMS, plasmid pHCG3
A; Note: sequence extracted from NCBI backbone (NCBIP:111732); sequence misidentified as C;Genetics coxM; codH
A; Start codon: GTG
C;Complex: heterotrimer of large (see PIR:C56279), medium, and small (see PIR:B56279) ch
C;Superfamily: carbon monoxide dehydrogenase medium chain
C;Keywords: heterotrimer; oxidoreductase
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49.3%; Score 36; DB 2; Length 518;
Best Local Similarity 50.0%; Pred. No. 77;
Matches 9; Conservative 2; Mismatches 3; Indels
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                                                                                                                                                                                                                                                  Score 36; DB 2; Length 288;
Pred. No. 41;
2; Mismatches 2; Indels
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60.0%;
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A,Cross-references: SGD:S0001127
A,Map position: 8R
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84 IIKSRLMTPLLTQS 97
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Best Local Similarity 60.0
Matches 6; Conservative
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39 PIMKTRLATP 48
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058F34 PONPY
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MEDINE-21388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDINE-21388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MALSCHOLS R.D., Collins F.S., Wagner L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhar N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhar N.K.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A promstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Scheetz T.E.,

Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.J.,

Braha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S.W., Worlby K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

N. Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mitching M., Madan J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
                                                                                                                                                                                                                                                                                                    Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                           MEDLINE-92375199; PubMed=1380674; DOI=10.1038/358764a0;
Chicz R.M., Urban R.G., Lane W.S., Gorga J.C., Stern L.J.,
Vignall D.A., Strominger J.L.;
"Predominant naturally processed peptides bound to HLA-DR1 are derived
from MHC-related molecules and are heterogeneous in size.";
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                          01-MAY-2000, sequence version 1.
07-FEB-2006, entry version 10.
HLA class II-associated invariant chain II (Fragment).
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25 AA; 2793 MW; 2F80100276A802F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-UNN-2002, integrated into UniProtKB/TrEMBL. 01-UUN-2002, sequence version 1. 07-FEB-2006, entry version 15. CD74 antigen, isoform c.
                                                                 01-MAY-2000, integrated into UniProtKB/TrEMBL
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QBSNAO;
                                        25 AA.
                                                                                                                                                                                                                                                                                                                                     Ensembl; ENSG0000019582; Homo sapiens.
                                      PRT;
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                                                                                                                                                                                                                                                                             Nature 358:764-768(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 PVSKMRMATPLLMQA
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nes 15; Conservative
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                                                                                                                                                                                                                                                                                                        Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-MAY-2005, integrated into UniProtKB/TrEWBL.
10-MAY-2005, sequence version 1.
07-FEB-2006, entry version 3.
CD74 antigen (Invariant polypeptide of major histocompatibility complex, class II antigen-associated).
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                                                                                                                                                                                                                                                       Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases
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GO; GO:0006955; P:immune response; IEA.
InterPro; IPR011988; MHCLI invariant.
SEQUENCE 232 AA; 26399 MW; 5144439D0FD27C99 CRC64;
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Ensembl; ENSG00000019582; Homo sapiens.
SEQUENCE 160 AA; 18328 MW; 95CB3D7226497DE8 CRC64;
                                                                                      and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 73; DB 2; I
100.0%; Pred. No. 1.5e-05;
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Ensembl; ENSG0000019582; Homo sapiens.
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Matches 15; Conserv
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                                                                                                                                                                                                             Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-84207945; PubMed-6586420;
Strubin M., Mach B., Long B.O.;
"The complete sequence of the mRNA for the HLA-DR-associated invariant
                                                                       Pongo pygmaeus (Orangutan).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                TISSUE=Kidney;
The German cDNA Consortium;
Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
Han M., Wiemann S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 HG2A HUMAN STANDARD; PRT; 296 AA. P04233; Q14597; Q29832; Q8WLP6; 20-WAR-1987, integrated into UniProtKB/Swiss-Prot. 16-APR-2002, sequence version 3. 07-WAR-2006, entry version 74. HLA class II histocompatibility antigen, gamma chain (HLA-DR antigensassociated invariant chain) (Ia antigen-associated invariant chain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chain reveals a polypeptide with an unusual transmembrane polarity.";
EMBO J. 3:869-872(1984).
                                                                                                                                                                                                                                                                                                                                                        Gaps
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MEDLINE=6609361; PubMed=3001652;
Kudo J., Chao L.-Y., Narni F., Saunders G.F.;
"Structure of the Yman gine moroding the invariant gamma-chain of class II histocompatibility antigens.";
Nucleic Acids Res. 13:8827-8841(1985).
                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                                  Length 232;
                                                                                                                                                                                                                                                                                                                                Score 73; DB 2; Length 23
Pred. No. 2.3e-05;
Mismatches 0; Indels
                                                                                                                                                                                          Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                  .l protein.
232 AA; 26411 MW; DE5D7AC72AF7439F CRC64;
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                    21-DEC-2004, integrated into UniProtKB/TrEMBL.
 232 AA.
                                                                                                                                                                                                                                                      SMR; QSRFJ4; 134-208.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR011988; MHCII_invariant.
                                                                                                                                                                                                                                            EMBL; CR857162; CAH89463.1; -; mRNA.
 PRT;
                             21-DEC-2004, sequence version 1.
07-FEB-2006, entry version 5.
Hypothetical protein DKFZp469K1522.
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nes 15; Conservative
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                                                                                                                                      NUCLEOTIDE SEQUENCE.
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                                                              Name=DKFZp469K1522;
                                                                                                                NCBI_TaxID=9600;
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QSRFJ4_PONPY
QSRFJ4;
                                                                                                                                                                                                                                                                                                  Hypothetical
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MEDLINE=2038835; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Rapleton M.J., Ugdin T.B., Poshiyuki S., Carninci P., Prange C.,

Rapa S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rosak S.A., McEwan P.J., McKernan K.J., Mallek J.A., Hulyk S.W.,

Rosak S.W., McEwan P.J., McKernan K.J., Mallek J.A., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rabas J., Helton B., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Ruterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rudin A., Schein J.E., Jones S.J.M., Marra M.A.;

Generation and initial analysis of more than 15,000 full-length human
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FUNCTION: Plays a critical role in MHC class II antigen processing by stabilizing peptide-free class II alpha/beta heterodimers in a complex soon after their synthesis and directing transport of the
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SUBUNIT: Nonamer composed of three alpha/beta/gamma heterotrimers.
SUBCELLUIAR LOCATION: Membrane; single-pass type II membrane
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                                                                                                                                                                                                 "Structure of the human Ia-associated invariant (gamma)-chain gene: identification of 5' sequences shared with major histocompatibility
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MEDLINE=96085023; PubMed=7477400; DOI=10.1038/378457a0;
Ghosh P., Amaya M., Mellins E., Wiley D.C.;
"The structure of an intermediate in class II MHC maturation: CLIP bound to HJA-DR3.";
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MEDLINE=93078879; PubMed=1448172; DOI=10.1038/360474a0;

MEDLINE=93070879; PubMed=1448172; DOI=10.1038/360474a0;

MEDLINE=PROTE OF THE OF THE
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MEDLINE=86233451; PubMed=3459184;
O'Sullivan D.M., Larhammar D., Wilson M.C., Peterson P.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM SHORT).
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Proc. Natl. Acad. Sci. U.S.A. 80:7395-7399(1983).
                                                                                                                                                                                                                                                                                                                                                       complex class II genes.";
Proc. Natl. Acad. Sci. U.S.A. 83:4484-4488(1986)
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IsoId=P04233-1; Sequence=Displayed;
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Claesson L., Larhammar D., Rask L.,
"CDNA clone for the human invariant
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103 PVSKMRMATPLLMQA 117
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ses 15; Conservative
                                  1194
1195
1195
206
217
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NCBI_TaxID=9606;
 RESULT 7
Q9MXD5 HORSE
ID . Q9MXD5_HORSE
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R GO; GO:0016021; C:integral to membrane; TAS.
R GO; GO:0016021; C:intracellular; TAS.
R GO; GO:001955; F:cytokine bluiding; IPI.
R GO; GO:0012289; F:cytokine bluiding; IPI.
R GO; GO:0042289; F:MHC class II protein binding; NAS.
R GO; GO:0018083; P:antigen presentation; endogenous antigen; NAS.
R GO; GO:0018083; P:antigen presentation; endogenous antigen; NAS.
R GO; GO:0018084; P:huncaral defense mechanism (sensu Vertebrata); ISS.
R GO; GO:0018086; P:intracellular protein transport; ISS.
R GO; GO:001806; P:negative regulation of apoptosis; IDA.
R GO; GO:001916; P:protein complex assembly; ISS.
R GO; GO:004506; P:regulation of macrophage activation; NAS.
R GO; GO:0045058; P:T cell selection; IDA.
R GO; GO:0045058; P:T cell selection; NAS.
R GO; GO:0045058; P:T cell selection; NAS.
R HITEFPO; IPRO11988; MHCII_invariant.
R FAM: PF00086; Thyroglobulin_1.
R FAM: PR0086; Thyroglobulin_1.
                                     Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00484; THYROGLOBULIN 1_1; 1.
PROSITE; PS51162; THYROGLOBULIN 1_2; 1.
3D-structure; Alternative splicing; Chaperone;
Direct protein sequencing; Glycoprotein; Immune response; Membrane;
Proteoglycan; Signal-anchor; Transmembrane.
CHAIN 1 296 HLA class II histocompatibility antigen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-linked (GlcNAc. .).
N-linked (GlcNAc. .).
O-linked (Xyl. ..) (glycosaminoglycan)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gamma chain.
/FTId=PRO 0000667954.
Cytoplasmic (Potential).
Signal-anchor for type II membrane protein (Potential).
Extracellular (Potential).
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/FTId=VSP_005331.
R -> T (in Ref. 2).
               -!- SIMILARITY: Contains 1 thyroglobulin type-1 domain.
                                                                    EMBL; K01144; AAA36304.1; -; MENA.
EMBL; X03339; CAA27046.1; -; Genomic_DNA.
EMBL; X0340; CAA27041.1; -; Genomic_DNA.
EMBL; X00497; CAA25192.1; -; MENA.
EMBL; X00497; CAA25193.1; -; MENA.
EMBL; X00497; CAA36033.1; -; Genomic_DNA.
EMBL; M13559; AAA36033.1; -j Genomic_DNA.
EMBL; M13559; AAA36033.1; JOINED; Genomic_DNA.
EMBL; BC019726.1; -; MRNA.
PDB; ILIE; NWR; A|B/C=134-208.
PDB; ILIE; NWR; A|B/C=134-208.
PDB; ILIE; NWR; A|B/C=134-208.
HIND; HXC00005015982; Homo sapiens.
HIND; H2C1697; CD74.
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By similarity.
By similarity.
     IsoId=P04233-2; Sequence=VSP 005331;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Characterization of peptides bound to extracellular and intracellular HLA-DR1 molecules.";
Hum. Immunol. 38:193-200(1993).
                                                                                                                                                                                                                                                                                                                      01-MAY-2000, integrated into UniProtKB/TrEMBL.
01-MAY-2000, sequence version 1.
07-FRB-2006, entry version 10.
HIAA-DR1-associated LI peptide.
HOMO sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN SEQUENCE.
MEDLINE=94148715; PubMed=8106277; DOI=10.1016/0198-8859(93)90540-H;
Max H., Halder T., Kropshofer H., Kalbus M., Muller C.A.,
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100.0%; Score 73; DB 1; Length 296; 100.0%; Pred. No. 3e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ensembl; ENSG00000019582; Homo sapiens.
SEQUENCE 20 AA; 2264 MW; D802F7C2C0FAE534 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 94.5%; Score 69; DB 2; Le Local Similarity 100.0%; Pred. No. 9.6e-06; nes 14; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            208 AA.
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                                                 Mismatches
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          100.0%; Pre-
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Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
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Alausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Appkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heishe F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldon M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brohards S., Worley K.C., Hale S., Garcinatane P.H.,
A Richards S., Worley K.C., Hale S., Garcinatane P.H.,
A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glbbs R.A.,
A Halton B.K., Ketreman M., Madan A., Rodrigues S., Sanchez A.,
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Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Bohnerch A., Schain J.E., Jones S.J.M., Marra M.A.;
T. "Generation and initial analysis of more than 15,000 full-length human
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Distributed under the Creative Commons Attribution-NoDerivs License
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Mammalia, Butheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                   Būkaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
MEDLINE=20353882; PubMed=10895327;
Tozaki T., Mashima S., Miura N., Tomita M.;
"The equine CD74 gene has a polymorphic (CAG)n repeat in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86.3%; Score 63; DB 2; Length 208; 80.0%; Pred. No. 0.0017; ive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0016620; C:membrane; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR011988; MHCII invariant.
SEQUENCE 208 AA; 23425 MW; 9739F801BE4050F8 CRC64;
                     -OCT-2000, integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2002, integrated into UniProtKB/TrEMBL.
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                                      01-0CT-2000, sequence version 1.
07-FEB-2006, entry version 10.
MHC class II associated invariant chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AB032166; BAA92343.1; -; mRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2002, sequence version 1.
07-FEB-2006, entry version 14.
Hypothetical protein.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                Anim. Genet. 31:239-240(2000).
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| PVSKIRVATPMLMQA 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 80.09
Marches 12; Conservative
                                                                                                           Equus caballus (Horse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P04233; IIIE.
SMR; Q9MXD5; 118-192.
                                                                                                                                                                                                                                                                                                                           untranslated region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090
                                                                                                                                                                                NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OBKOSB_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOUSE
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STRAIN=FVB/N; TISSUE=Colon, and Salivary gland;
MEDLINE=2288257; PubMed=12477932; DOI=10.1073/pnas.242603899;
A Strausberg R.L., Feingold E.A., Grouse L.H., Derged J.G.,
A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S. Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Williadon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Butterffield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
                                                                                                                                                                                                                                                  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-MAY-2005, sequence version 1.
07-FEB-2006, entry version 11.
14-associated invariant Lebin (Adult male kidney cDNA, RIKEN full-length enriched library, clone:0610006B16 product:1a-associated invariant chain, full insert sequence) (Cd74 protein).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 84.9%; Score 62; DB 2; Length 208; Local Similarity 73.3%; Pred. No. 0.0027; nes 11; Conservative 4; Mismatches 0; Indels
                                                                                                                                             Strausberg R.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
SEQUENCE 208 AA; 23590 MW; FF36F7835228A596 CRC64;
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                                                                                                                   STRAIN=FVB/N; TISSUE=Salivary gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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87 PLSKMRVATPMMMQA 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 PVSKMRMATPLLMQA 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=Cd74; Synonyms=Ii;
Mus musculus (Mouse)
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                                                                   NUCLEOTIDE SEQUENCE.
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Ry Dubded-1614072; DOI-10.1126/Science.112014;
Ry Carninci Pt. 762.0210.1126/Science.112014;
Ry Carninci Pt. 762.0210.1126/Science.112014;
Ry Bajto V.B. Brenner S.E. Batalov S., Forrest A.R., Shinokawa K., Radiato V. Allen J.E.,
Ry Davis M.J. Wilming L.G., Addinis V. Allen J.E.,
Ry Davis M.J. Wilming L.G., Apweiler R., Aturaliya R.M., Bailey T.L.,
Ry Bansei Impionbato A. Apweiler R., Aturaliya R.M., Banley T.L.,
Ry Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
Ry Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
Ry Gustincich S., Dalrymple B.P., Regiolini M., Faulkner G.,
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Ry Jak M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
Ry Aill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
Ry Kucockhi I.V., Lazarevic D., Lipovich L., Liu J.,
Ry Kucockhi I.V., Lazarevic D., Lipovich L., Liu J.,
Ry Mutegui-Tabar S., Mulder M., Makano W., Makchionni L.,
Matsuda H., Matsuzawa S., Miki H., Mignone R., Miyake S., Morris K.,
Ry Norlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
Ry Chando V., Pang K.C., Pavan W.J., Schneider C.,
Schiguchi K., Semille K., Semille R., Schneider C., Schiguchi K., Semille R., Schiguchi K., Semille R., Shinada H., Shinada K., Silva D., Shinada Y., Talki R.,
Schubach C., Schiguchi K., Semille R., Shinada H., Shinada K., Silva D., Shinada Y., Tan S.L., Tang S., Taylor M.S., Tagene J., Takinka Y.,
Ry Mannishi H., Zabarcovsky E., Zhu S., Hume J., Hude W., Wannishi H.,
Ry Amanishi H., Zabarcovsky E., Zhu S., Hume J., Kawaja H., Kawasashi J.,
Ry Ry Ramashima T., Kojima M., Kato T., Kawaji H., Kawasashi J.,
Ry Ramashima T., Kojima M., Kato T., Kawaji H., Kawasashi J., Ramashima T., Kojima M., Kato T., Kawaji H., Kawasashi J., Suzuki H., Kawashima T., Kojima M., Kato T., Kawaji H., Kawasashi J., Suzuki Y.,
Ry Hayashizaki Y.,
Ry Ha WOULD TISSUE-Kidney;

MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

Mikaido I., Casto N., Saiuka T., Adachi J., Bono H., Kondo S., Nikaido I., Osato N., Saiuko R., Suzuki H., Yamanaka I., Kiyosawa H., Yaqi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Baldarelli R., Hill D.P., Bult C., Hume D.A., Corbani L.E., Cousins S., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., Gaasterland T., Gariboddi M., Gissi C., Godzif A., Gough J., Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jaryis E.D., Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., STRAIN=C57BL/6J; TISSUE=Kidney;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninoi P., Hayashizaki Y.;
High-efficiency full-length cDNA cloning.";
Methods Enzymol. 303:19-44(1999). STRAIN=CS7BL/6J; TISSUE=Kidney; PubMed=16141073; DOI=10.1126/science.1112009; PubMed=16141073; DOI=10.1126/science.1112009; RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium; "Antiseense Transcription in the Mammalian Transcriptome."; Science 309:1564-1566(2005). "The transcriptional landscape of the mammalian genome."; Science 109:1559-1563 (2005). STRAIN-C57BL/6J; TISSUE-Kidney; PubMed=16141072; DOI=10.1126/science.1112014; NUCLEOTIDE SEQUENCE. NUCLEOTIDE SEQUENCE (3)
NUCLEOTIDE SEQUENCE. NUCLEOTIDE SEQUENCE 

Maglott D.R., Waltels L., Marchioum L., McKnatis L., Mikhi R.

Maglott D.R., Waltels L., Marchioum L., McKnatis L., Mikhi R.

Maglott D.R., Maltels L., Marchioum L., 10, D.D., Beanchandton R.

Mandelin A., Schmeider C., Sepule C.A., Setow M., Shinada K.,

Sandelin R., Takenka Y., Taylor M.S., Tesada R. B., Tomits M.,

Mystard R., Magner L., Mahlested C., Magg Y., Maranes Y., Mariane W., Hayahi K., Mariane W., Hayahi K., Mariane Y., Mariane W., Mariane W., Mariane W., Hayahi K., Mariane W., Mariane W., Mariane W., Mariane W., Mar

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+
       NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM LONG).

STRAIN=129; TISSUB-Mammary gland;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Itachul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Baht N.K.,
A Itachul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Baht N.K.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
B Rohastein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gluba R.A.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Blakeeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M., Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K., Sanbata K., Shibata K., Shibata K., Shibata K., Shibata K., Shibata Y., Shinagawa A., Shiraki T., Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tejima Y., TOya T., Yamamura T., Yamuni Y., Toya T., Yamamura T., Yamuni M., Hayashizaki Y., Yoshino M., Muramatsu M., Hayashizaki Y.
                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Koch N., Lauer W., Habicht J., Dobberstein B.;
"Primary structure of the gene for the murine Ia antigen-associated
invariant chains (Ii). An alternatively spliced exon encodes a
cysteine-rich domain highly homologous to a repetitive sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-AUG-1987, integrated into UniProtKB/Swiss-Prot.
13-AUG-1987, integrated into UniProtKB/Swiss-Prot.
01-NOV-1991, sequence version 3.
07-MAR-2006, entry version 63.
H-2 class II histocompatibility antigen, gamma chain (MHC class II-associated invariant chain) (Ia antigen-associated invariant chain)
                                                                                                                                                                                                                                                                                                                                         .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhu L., Jones P.P.; "Complete sequence of the murine invariant chain (Ii) gene."; Nucleic Acids Res. 17:447-448(1989).
                                                                                                                                                                                                                                                                                   Score 61; DB 2; Length 215;
Pred. No. 0.0044;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE, AND ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=AKR; TISSUE=Liver;
MEDLINE=89098406; PubMed=2492095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=87275861; PubMed=3038530;
                                                                                                                                                                                                                                                                                     83.6%;
85.7%;
                                                                                                                                                                                                                STRAIN=FVB/N; TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBO J. 6:1677-1683(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                  86 PVSOMRMATPLLMR 99
                                                                                                                                                                                                                                                                                                                                         12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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Name=Cd74; Synonyms=Ii;
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                                                                                                                                                                                         NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                           NIH MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thyroglobulin.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HG2A MOUSE
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HG2A MOUSE
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-!- FUNCTION: Plays a critical role in MHC class II antigen processing by stabilizing peptide-free class II alpha/beta heterodimers in a complex soon after their synthesis and directing transport of the complex from the endoplasmic reticulum to compartments where peptide loading of class II takes place.
-!- SUBUNIT: Nonamer composed of three alpha/beta/gamma heterotrimers
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=84207946; PubMed=6327293; Singer P. Lipp J., Koch N., Singer P. A., Lauer W., Demblc Z., Mayer W.E., Lipp J., Koch N., Hammerling G., Klein J., Doberstein B.; Structure of the murine Ia-associated invariant (Ii) chain as deduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-90257363; PubMed=2111346;
Eades A.-M., Litfin M., Rahmsdorf H.J.;
"The IFN-gamma response of the murine invariant chain gene is mediated
by a complex enhancer that includes several MHC class II consensus
                                                                                                                                                                                                                                                                  Stone J., Perry R., Todd J.A., McDevitt H.O.;
"Nucleotide sequences of the murine la-associated invariant chain (Ii)
and I-E (H-2S, Beta) chain expressible cDNA clones.";
Submitted (MAR-1988) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=88144436; PubMed=3422739; Miller J., Hatch J.A., Simonis S., Cullen S.E.; "Identification of the glycosaminoglycan-attachment site of invariant-chain proteoglycan core protein by site-directed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ensembl; ENSWUSGO0000024610; Mus musculus.
MGI; MGI:96534; Ii.
GO; GO:0005783; C:endoplasmic reticulum; IDA.
GO; GO:0009897; C:external side of plasma membrane; IDA.
GO; GO:0005794; C:Golgi apparatus; IDA.
GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0005764; C:lysosome; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ISOId=P0441-2; Sequence=VSP 005332;
-!- SIMILARITY: Contains 1 thyroglobulin type-1 domain.
                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomic_DNA.
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EMBL; X07129; CAA30141.1; -; mRNA.
EMBL; X05429; CAA29010.1; -; Genomic_DNA.
EMBL; X05429; CAA29012.1; -; Genomic_DNA.
EMBL; X05430; CAB37297.1; -; Genomic_DNA.
EMBL; BC003476; AAH03476.1; -; mRNA.
EMBL; X13444; -; NOT_ANNOTATED_CDS; Genomic_EMBL; M38972; AAA37897.1; -; Genomic_DNA.
PIR; B27866; HLHMSG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE OF 47-191 AND 256-279
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[7]
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SMR; P04441; 117-191, 193-256.
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                                                                                                                        cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from a cDNA clone.";
EMBO J. 3:873-877(1984).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein (Potential)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mutagenesis."
                                                                                                                        and mouse
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NCBI_TaxID=10090;
              NAMES OF THE PROPERTY OF THE P
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                                                                         Prantigen presentation; IDA.
Prantigen presentation, exogenous antigen via . . .; IMP.
Prantigen processing, exogenous antigen via M. . .; IMP.
Predli proliferation; ISS.
Prchaperone cofactor dependent protein folding; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gamma chain.

/FTId=PRO 000067955.

Cytoplasmic (Potential).
Signal-anchor for type II membrane protein (Potential).

Extracellular (Potential).
Thyroglobulin type-..) (Potential).
N-linked (GloNAc...) (Potential).
N-linked (GloNAc...) (Potential).
N-linked (Xyl...) (glycosaminoglycan).
By similarity.
By similarity.
By similarity.
Krid=VSP 005332.
S-A: No addition of glycosaminoglycan;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-FEB-2006, entry version 5. NOD-derived CDIIC +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F630001K12 product:Ia-associated invariant chain, full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                          GO:0006952; P:defense response; IMP.
GO:0016064; P:humoral defense mechanism (sensu Vertebrata); IMP.
GO:00160696; P:intracellular protein transport; IDA.
GO:0043066; P:inegative regulation of apoptosis; ISS.
GO:004581; P:negative regulation of T cell differentiation; IMP.
GO:0045582; P:positive regulation of T cell differentiation; IMP.
GO:0045582; P:positive thymic T cell selection; IMP.
GO:0045059; P:positive thymic T cell selection; IMP.
GO:0004515; P:prostaglandin biosynthesis; ISS.
GO:0004511; P:prostaglandin biosynthesis; ISS.
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N -> M (in Ref. 1).
N -> Q (in Ref. 2).
STG -> RHC (in Ref. 2).
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R GO; GO:0005771; C:multivesicular body; IDA.
R GO; GO:0019955; F:cytokine binding; ISS.
R GO; GO:0019985; P:antigen presentation, IDA.
R GO; GO:0019886; P:antigen presentation, exogenous antigen via.
R GO; GO:0019886; P:antigen presentation, exogenous antigen via R GO; GO:0010886; P:antigen processing, exogenous antigen via M.
GO; GO:0001085; P:claperone cofactor dependent protein folding GO; GO:0001085; P:defense response; IMP.
R GO; GO:0010866; P:humoral defense mechanism (sensu Vertebrata)
R GO; GO:0010866; P:negative regulation of apoptosis; ISS.
R GO; GO:0045581; P:negative regulation of T cell differentiation
R GO; GO:0045582; P:positive regulation of T cell differentiation
R GO; GO:0045582; P:positive thymic T cell selection; IMP.
R GO; GO:0045582; P:positive thymic T cell selection; IMP.
R GO; GO:0045059; P:positive thymic T cell selection; IMP.
R GO; GO:0043030; P:regulation of macrophage activation; ISS.
R HITEPPRO; IPR001188; MHCII invariant.
R FRAMRT; SM00211, TY; II.
R FMART; SM00211, TY; II.
R FMART; SM00211, TY; II.
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Pred. No. 0.0058;
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11-0CT-2005, sequence version 1.
17-EB-2006, entry version 5.
NOD-derived CD11c +ve dendritic cells cDNA, RI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               279 AA
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Q3U4Q8;
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85.7%;
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Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
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Birney E., Hayashizaki Y.;
M. "Analysis of the mouse transcriptome based on functional annotation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIATION OF THE STATE OF THE S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Muramatsu M., Hayashizaki Y.; Wormalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA lbraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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Arakwa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
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Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequencing pipeline with 384 multicapillary sequencer."; Genome Res. 10:1757-1771 (2000).
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MCG GO: 0005783; C:endoplasmic reticulum; IDA.

MCG GO: 0005783; C:endoplasmic reticulum; IDA.

MCG GO: 0005784; C:external side of plasma membrane; IDA.

MCG GO: 0005784; C:integral to plasma membrane; IDA.

MCG GO: 0005784; C:integral to plasma membrane; TAS.

MCG GO: 0005771; C:multivesicular body; IDA.

MCG GO: 0005771; C:multivesicular body; IDA.

MCG GO: 0005771; C:multivesicular body; IDA.

MCG GO: 0005785; P: protein binding; IDA.

MCG GO: 0005887; P: protein binding; IDA.

MCG GO: 0005887; P:mutigen presentation; IMP.

MCG GO: 0005886; P:mutigen presentation; MMP.

MCG GO: 0019886; P:mutigen presentation; MMP.

MCG GO: 0016086; P:protein presentation; MMP.

MCG GO: 0005886; P:intracellular protein folding; IMP.

MCG GO: 0006886; P:intracellular protein transport; IMP.

MCG GO: 00045581; P:negative regulation of T cell differentiation; IMP.

MCG GO: 00045582; P:positive thymic T cell selection; IMP.

MCG GO: 00045089; P:positive thymic T cell selection; IMP.

MCG GO: 00045089; P:protein complex assembly; IDA.

MCG GO: 00045089; P:protein complex assembly; IDA.
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                                                                                                                                        Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A., Muxamatsu M., Hayashizaki Y.;
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Ruminantia;
Pecora, Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Japanese Black; TISSUE=Tumorus lymph node;
BDDLINES=6512904; PubMed=6630076; DOL=10.1006/bbrc.1996.0689;
Niimi M., Nakai Y., Aida Y.;
"Identification of bovine invariant chain (Ii) gene by nucleotide
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Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
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; 31557 MW; 300A85014F170792 CRC64;
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Pred. No. 0.0058;
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                                                                                                                                                                                                                                             EMBL; AK154096; BAE32373.1; -; mRNA.
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TISSUE=Pituitary gland;

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see http://www.uniprot.org/terms
Attribution-NoDerivs License
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CD74 antigen (Invariant polpypeptide of major histocompatibility class
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82.2%; Score 60; DB 2; Length 204; 73.3%; Pred. No. 0.0065; ive 4; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       204 AA; 23146 MW; 0FD00643BCA82BFA CRC64;
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                                                                                                                                        EMBL; BC102368; AA102389.1; -; mRNA.
EMBL; BT021489; AAX46336.1; -; mRNA.
PIR; JC4796; JC4796.
HSSP; Q29633; 11IE.
SMR; Q29630; 116-190.
Ensembl; ENSBTAG0000015228; Bos taurus.
                                                                                                                                                                                                                                                                                                                                                          GO, GO:0016020, C:membrane, IEA.
GO, GO:0006955, P:immune response, IEA.
InterPro, IPR011988; MHCII_invariant.
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                                                                                                              EMBL; D83962; BAA12156.1; -; mRNA
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PMSQMRMATPMLMRA 101
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Name=Cd74;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein.
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Best Local Similarity
Matches 11; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical
SEQUENCE 20
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07-FEB-2006,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Heaton M.P., Keele J.W., Snelling W.M., Weidmann R.T., Smith T.P.L.;
"Sequencing and analysis of Bos taurus full-length insert CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Moore S., Alexander L., Brownstein M., Guan L., Lobo S., Meng Y., Tanaguchi M., Wang Z., Yu J., Prange C., Schreiber K., Shenmen C., Tanaguchi M., Barbazuk S., Barber S., Babakaiff R., Beland J., Chun E., Del Rio L., Gibson S., Hanson R., Kirkpatrick R., Liu J., Matsou C., Mayo M., Sancos R.R., Stott J., Tsai M., Wong D., Siddiqui A., Holt R., Jones S.J., Marra M.A.; Submitted (AUG-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Japanese Black; TISSUE=Tumorus lymph node;
MEDLINE=96212904; PubMed=8630076; DOI=10.1006/bbrc.1996.0689;
Niimi M., Nakai Y., Aida Y., "Aida Y." Indentification of bovine invariant chain (Ii) gene by nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996, sequence version 1.
07-MAR-2006, entry version 26.
Invariant chain (Hypothetical protein MGC127643) (Invariant gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus (Bovine).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Butheria, Laurasiatheria, Cetartiodactyla, Ruminantia;
Pecora, Bovidae; Bovinae; Bos.
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0
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Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                          190 AA; 21660 MW; DA3AD746DCD649FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem. Biophys. Res. Commun. 222:7-12(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82.2%; Score 60; DB 2; 73.3%; Pred. No. 0.006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q29630_BOVIN PRELIMINARY; PRT; 204 AA. Q29630; 01-NOV-1996, integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                           EMBL; D83961; BAA12155.1; -; mRNA.
SMR; Q7JFY1; 109-183.
Ensembl; ENSBTGG0000015228; Bos taurus.
G0; G0:0016020; C:membrane; IEA.
G0; G0:0006955; P:immune response; IEA.
InterPro; IPR011988; MHCII_invariant.
              Copyrighted by the UniProt Consortium,
                                                       Distributed under the Creative Commons
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Mamm. Genome 13:373-379(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=MGC127643; Synonyms=CD74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 PVSKMRMATPLLMQA 15
|:|:||||||:||:||
30 PMSQMRMATPMLMRA 94
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les 11; Conserv
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C29630 BOV
C29630 BOV
C2963 AC
C2066 AC
C2076 A
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Henkes W., Syha J., Reske K.;
"Nucleotide sequence of rat invariant gamma chain cDNA clone pLR gamma
                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE [MRNA].
STRAIN-FVG X DA; TISSUE-Spleen;
MEDLINE-89282409; PubMed=2499873;
McKnight A.J., Mason D.W., Barclay A.N.;
Sequence of a rat MHC class II-associated invariant chain cDNA clone containing a 64 amino acid thyroglobulin-like domain.";
Nucleic Acids Res. 17:3993-3984(1989).
                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
                                                                                   Gaps
                                                                                                                                                                                                 01-FEB-1991, sequence version 2.
07-MAR-2006, entry version 53.
H-2 class II histocompatibility antigen, gamma chain (MHC class II-
associated invariant chain) (Ia antigen-associated invariant chain)
                                                                                   ;
0
                                                               Score 59; DB 2; Length 216;
Pred. No. 0.011;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: Contains 1 thyroglobulin type-1 domain.
                GO; GG:0016020; C:membrane; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR011988; MHCII invariant.
SEQUENCE 216 AA; 24503 MW; 33677FA259B84F8E CRC64;
                                                                                                                                                                                        01-JUL-1989, integrated into UniProtKB/Swiss-Prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE [MRNA] OF 1-192 AND 257-280.
                                                                                                                                                                      280 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                soId=P10247-2; Sequence=VSP_005333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=P10247-1; Sequence=Displayed;
EMBL; BC059152; AAH59152.1; -; mRNA.
                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X14254; CAA32468.1; -; mRNA.
BERL; X13044; CAA31450.1; -; mRNA.
PRF; S04362; S04362.
HSSP; P04233; 11CF.
                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=89098337; PubMed=3264906;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMR; P10247; 118-192, 194-257
                                                                80.8%;
ilarity 85.7%;
Conservative
                                                                                                               ||| ||||||||:
87 PVSPMRMATPLLMR 100
                                                                                                    1 PVSKMRMATPLLMQ 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein (Potential).
ALTERNATIVE PRODUCTS:
                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
                                                      (Ii) (CD74 antigen).
Name=Cd74;
         Q6GT70; 118-192
                                                                                                                                                                                                                                                                                             NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=Short;
                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Lewis
                                                                                                                                                           HG2A_RAT
ID HG2A_RAT
                                                                                                                                                                              P10247;
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(By
                                                                                                                                                                                                                                                                                                                                       gamma chain.
/FTId=PRO 000067956.
Cytoplasmic (Potential).
Syloal-anchor for type II membrane protein (Potential).
Extracellular (Potential).
Thyroglobulin type-1.
N-linked (GLONAC. ..) (Potential).
N-linked (GLONAC. ..) (Potential).
O-linked (XIONAC. ..) (Potential).
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                             PROSITE; PS00484; THYROGLOBULIN 1 1; 1.
PROSITE; PS51162; THYROGLOBULIN 2; 1.
Alternative splicing; Chaperone; Glycoprotein; Immune response;
Membrane; Proteoglycan; Signal-anchor; Transmembrane.
CHAIN 1 280 H-2 class II histocompatibility antigen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=14681463; DOI=10.1093/nar/gkh037; Uenishi H., Eguchi T., Suzuki K., Sawazaki T., Toki D., Shinkai H., Okumura N., Hamasima N., Awata T.; Cokumura BST Data Explored: construction of a database for ESTs derived from porcine full-length cDNA libraries."; Nucleic Acids Res. 32:D484-D488(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                 GO; GO:0008283; F:cytokine binding; ISS.
GO; GO:0008283; P:cell proliferation; ISS.
GO; GO:0008283; P:cell proliferation of apoptosis; ISS.
GO; GO:0001516; P:prostaglandin biosynthesis; ISS.
GO; GO:001516; P:prostaglandin biosynthesis; ISS.
GO; GO:0043030; P:regulation of macrophage activation; ISS.
InterPro; IPR011988; MHCII invariant.
Pfam; PP00086; Thyroglobulin_1.
Ffam; PP00086; Thyroglobulin_1.
SMART; SM00211; TY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D935D169A98B5732 CRC64;
ENSRNOG00000018735; Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0s-JUL-2004, integrated into UniProtKB/TrEMBL. 05-JUL-2004, sequence version 1. 07-FEB-2006, entry version 9.
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Pred. No. 0.014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        By similarity.
By similarity.
Missing (in iso.
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR011988; MHCII_invariant.
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Best Local Similarity 85...
Local 2; Conservative
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114
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194
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Q764N1_PIG
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TRANSMEM
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CARBOHYD
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Query Match
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Q3G4U7 9DE
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Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Etgu P., Lee J.M.,
Toriumi M., Yu G., Brooks S., Chao Q., Chen H., Karlin-Neumann G.,
Kim C., Lam B., Miranda M., Nguyen M., Palm C.J., Shinn P.,
Southwick A., Davis R.W., Ecker J.R., Theologis A.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Town C.D., Haas B.J., Wu D., Maiti R., Hannick L.I., Chan A.P., Tallon L.J., Rooney T., Utterback T.R., VanAken S.E., Feldblyum T.V., White O., Fraser C.M.; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21417794; PubMed=11526245; DOI=10.1073/pnas.181304598;
Motchashi R., Nagata N., Ito T., Takahashi S., Hobo T., Yoshida S.,
Shinozaki K.;
                                                                                                                                                                                                                                                                                                                                                                                                                      Name=apg2; OrderedLocusNames=At2g01110;
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptoohyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
                                      76.7%; Score 56; DB 2; Length 214; 66.7%; Pred. No. 0.04; ive 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Summer E.J., McCaffery M.W., Cline K.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
[9]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Town C.D., Kaul S.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases
E5347DE04885524F CRC64;
                                                                                                                                                                                                                                                                                  QSSJVS ARATH PRELIMINARY; PRT; 340 AA. QSSJVS; Q9XF14; 01-MAY-2000, integrated into UniProtKB/TrEMBL. 01-JUN-2002, sequence version 2. 07-FEB-2006, entry version 22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 annotation.";
Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002)
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24118 MW;
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PLSKMRVSAPMLMQA 101
                                                                                                                                  1 PVSKMRMATPLLMQA 15
                                                                                      10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAR-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
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  214 AA;
                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                    TATC (CpTatC)
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Feldmann K.
  SEQUENCE
                                           Query Match
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Q95JV5 ARR
ID Q95JV5

DQ Q95JV

AC Q95JV

DT O1-MA

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Distributed under the Creative Commons Attribution-NoDerivs License
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US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T., Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome and assembly of Pelobacter propionicus DSM 2379.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US DOE Joint Genome Institute (JGI-ORNL);
Larimer F., Land M.;
"Annotation of the draft genome assembly of Pelobacter propionicus DSM
Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K., Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J., Miranda M., Narusaka M., Nayyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
Pelobacteraceae; Pelobacter.
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Submitted (AUG-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                     Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 340 AA; 37367 MW; 1429C265BFEDB281 CRC64;
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Pred. No. 34;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-NOV-2005, integrated into UniProtKB/TrEMBL.
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                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF360172; AAK25882.1; -; mRNA.
EMBL; AC006837; AAF18659.2; -; Genomic_DNA.
EMBL; AB054096; BAB62074.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF145045; AAD33946.1; -; mRNA.
EMBL; AY084784; AAM61351.1; -; mRNA.
EMBL, AY056347; AAL07196.1; -; mRNA.
PIR; T44583; T44583.
TAIR; At2901110; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-NOV-2005, sequence version 1.
07-FFB-2006, entry version 3.
Hydrophobe/amphiphile efflux-1 HAB1.
ORFNAmes=PproDRAFT_2759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro, IPR002033; Translocase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pelobacter propionicus DSM 2379.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR01840; TATCFAMILY.
TIGRFAMS; TIGR00945; tatC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.5%;
66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Conservative
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[1]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity)
                                                                                                                                                                                                                                                                                                                                        QSYUF1_NOCFA
                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                       Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T., Hammon N., Israni S., Pitluck S., Martinez M., Schmutz J., Larimer F., Land M., Ryrpides N., Ivanova N., Richardson P.; "Complete sequence of Synechococcus sp. CC9902."; Submitted (AUG-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                     Gaps
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Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Pasteurella.
                                                                                                                                                                                                                                                                       22-NOV-2005, integrated into UniProtKB/TrEMBL.
22-NOV-2005, sequence version 1.
07-FEB-2006, entry version 3.
YGGT family, conserved hypothetical integral membrane protein.
                                                                                                                             Score 42; DB 2; Length 1054;
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56.2%; Score 41; DB 2; Length 110; 72.7%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                   1; Indels
                                                                                             TIGRFAMS; TIGRO0915; 2A0602; 1.
SEQUENCE 1054 AA; 114349 MW; 5F57EC6404F4F839 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110 AA; 12043 MW; A220BA2C0EA9653F CRC64;
                                                                                                                                                                                                                                                                                                                             Synechococous sp. [strain CC9902].
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-AUG-2003, integrated into UniProtKB/Swiss-Prot
            Genomic DNA.
                   GO; GO:0016021; C:integral to membrane; IEA
GO; GO:0005215; F:transporter activity; IEA
GO; GO:0006810; P:transport; IEA.
InterPro; IPR001036; Acrflvin_res.
InterPro; IPR004764; HABI.
PEam; PF00873; ACR tran; 1.
PRINTS; PR00702; ACRIFLAVINRP.
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                                                                                                                                                   4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; CP000097; ABB25390.1; -; Genomic_DNA.
GO; GO:0016020; C:membrane; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
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07-MAR-2006, entry version 14.
Hypothetical protein PMO291 precursor.
OrderedLocusNames=PM0291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                    PRT;
           EMBL; AAJH01000006; EA036965.1; -;
                                                                                                                                                                                                                                                                                                                 ORFNames=Syncc9902 0420;
Synechococcus sp. (strain CC9902)
                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CC9902;
US DOE Joint Genome Institute;
                                                                                                                              57.5%;
61.5%;
                                                                                                                                                                                                                                                    PRELIMINARY;
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109 NKLQLATPLLPQA 121
                                                                                                                                                                          3 SKMRMATPLLMQA 15
                                                                                                                                         Best Local Similarity 61.5
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=316279;
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Y291 PASMU
ID Y291 PASMU
AC Q9CNYO;
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                                                                                                                              Query Match
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PubMed=15466710; DOI=10.1073/pnas.0406410101;
Ishlkawa J., Yamashita A., Mikami Y., Hoshino Y., Kurita H., Hotta K., Shiba T., Hattori M.;
"The complete genomic sequence of Nocardia farcinica IFM 10152.";
Proc. Natl. Acad. Sci. U.S.A. 101:14925-14930(2004).
-: SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016620; C:membrane; IEA.

GO; GO:0015520; F:tetracycline:hydrogen antiporter activity; IEA.

GO; GO:0015521; F:tetracycline transport; IEA.

GO; GO:0015904; P:tetracycline transport; IEA.

GO; GO:00180191; MFS.

InterPro; IPR011701; MFS.

InterPro; IPR011701; MFS.

InterPro; IPR011701; MFS.

InterPro; IPR011701; MFS.
STRAIN=PM70;
MEDLINE=21145866; PubMed=11248100; DOI=10.1073/pnas.051634598;
MAY B.U., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur "Complete genomic sequence of Pasteurella multocida Pm70.";
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
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Corynebacterineae, Nocardiaceae, Nocardia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56.2%; Score 41; DB 1; Length 238; 57.1%; Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein PM0291./FTId=PRO 0000014174.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
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                                                                                                                                                                                                                                                                                                      EMBL; AE006064; AAK02375.1; -; Genomic_DNA.
GenomeReviews; AE004439 GR; PM0291.
BioCyc; PMUL747:PM0291-MONOMER; -.
Complete proteome; Hypothetical protein; Signal.
SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OrderedLocusNames=nfa33430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 PVSKMRMATPLLMQ 14
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PROSITE; PS50850; MFS; 1.
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[2]
NUCLEOTIDE SEQUENCE.
                                                                                                          STRAIN=TM1040
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=PEST;
                                                                                 NUCLEOTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANOGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q709V4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 24
Q7Q9V4_ANC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3est
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; T03471; T03471.
InterPro; IRR07208; MrpF_PhaF.
Pfam; PF04066; MrpF_PhaF; 1.
Antiport; Hydrogen Ton transport; Membrane; Potassium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antiport; Hydrogen 1001 community. Transport.
Potassium transport; Transmembrane; Transport.
CHAIN 1 92 Probable K(+)/H(+) antiporter subunit F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Capainatus Sci. U.S.A. 94:9384-9388(1997).
-!- FUNCTION: Part of a K(+) efflux system involved in pH adaptation (By similarity).
-!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fonstein M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Belongs to the CPA3 antiporters (TC 2.A.63) subunit
                                                                                                                                                                                                                                                                                                                                                                                                                 (pH adaptation potassium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORFNames-RoseDRAFT 2168;
Silicibacter sp. TM1040.
Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales,
Rhodobacteraceae, Rhodobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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"Sequence of a 189-kb segment of the chromosome of Rhodobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 40; DB 1; Length 92,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Indels
                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     953B3509FB542A2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhodobacter capsulatus (Rhodopseudomonas capsulata)
                                                                                                                                                                                                                                                                                                                            integrated into UniProtKB/Swiss-Prot.
                                 ..
..
                                                                                                                                                                                                                                                                                                                                                                                  07-FEB-2006, entry version 26.
Probable K(+)/H(+) antiporter subunit F (pH ada
efflux system protein F) (Pha system subunit F)
Name=phaF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-OCT-2005, integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                                                                                                             92 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           335 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF010496; AAC16124.1; -; Genomic_DNA PIR; T03471; T03471.
  ed. No. 75;
Mismatches
  Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-0CT-2005, sequence version 1.
07-FEB-2006, entry version 3.
Inner-membrane translocator precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Potential
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                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE [GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=SB1003 / St Louis;
MEDLINE=97404404; PubMed=9256491;
                                                                                                                                                                                                                                                                                                                                                           sequence version 1.
                                 .,
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57.1%;
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269 PVGAIQLVTPMIMQS 283
40.08;
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                                                                                 1 PVSKMRMATPLLMQA 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                              6; Conservative
                                                                                                                                                                                                                                                                             STANDARD;
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57
82
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Proc. Natl. Acad. Sci
  Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1061;
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Q3QS54;
                                                                                                                                                                                                                                                                                                                                                              01-AUG-1998,
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                                                                                                                                                                                                                                                                                                   068038;
                                                                                                                                                                                                                     RESULT 22
ID HAAF RHOCA
ID HAAR CA
AC O68038
DT 30-MAY
DT 07-FEB
DE Probab
DE Probab
DE Rhodob
OC PL - FU
OC - - - SI
CC - - - - - SI
CC - - - - SI
CC - - - - SI
CC - - - - - SI
CC - - - - - SI
CC - - - -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q3QS54
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                                                                                                                                                                                                                                                                                                                                                                                                                                      "Annotation of the draft genome assembly of Silicibacter sp. TM1040."; Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
Anophelinae; Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=TM1040;
US DOE Joint Genome Institute (JGI-PGF);
US DOE Joint Genome Institute (JGI-PGF);
Hammon N., Israni S., Pitluck S., Richardson P.;
Submitted (JUN-205) to the EMBL/GenBank/DBBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                              Detter C., Glavina T.,
                                                                                                                                    US DOE Joint Genome Institute (JGI-PGF);
COpeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina
Hammon N., Israni S., Pitluck S., Richardson P.,
"Sequencing of the draft genome and assembly of Silicibacter sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
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Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                        Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56 Potential.
35328 MW; 3DD256F4FAB77A60 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AAFG02000005; EAN56679.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 40; DB 2;
Pred. No. 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-DEC-2003, integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO, GO:0016020; C:membrane; IEA.
GO; GO:0005215; F:transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR001851; Bac_inmem_transp.
Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    350 AA.
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                                                                                                                                                                                                                                                                                                                                                              STRAIN=IM1040;
US DOE JOINT Genome Institute (JGI-ORNL);
Latimer F., Land M.;
"Annotation of the draft genome assembly of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The Anopheles gambiae Sequence Committee;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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Rhodobacteraceae; Silicibacter.
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ENSANGP00000021807 (Fragment)
ORFNames=ENSANGG00000019318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.8%;
72.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       preliminary data.
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NUCLEOTIDE SEQUENCE
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                                                                                   SEQUENCE
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                    NCBI TaxID=292414;
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Query Match
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UVRD_SALTY
                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                          Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OrderedLocusNames=At2g23190;
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TAXID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rounsley S.D., Lin X., Ketchum K.A., Crosby M.L., Brandon R.C., Sykes S.M., Kaul S., Mason T.M., Kerlavage A.R., Adams M.D., Somerville C.R., Venter J.C., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                    The Anopheles gambiae Sequence Committee;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54.8%; Score 40; DB 2; Length 350; 70.0%; Pred. No. 85; ive 1; Mismatches 2; Indels
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Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the cytochrome P450 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              350 AA; 38908 MW; 3DF953760C0688B8 CRC64;
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GO; GO: 0016020; C: membrane; IEA.
GO; GO: 0020037; F: heme binding; IEA.
GO; GO: 0005506; F: iron ion binding; IEA.
GO; GO: 0004897; F: metal ion binding; IEA.
GO; GO: 0004497; F: metal ion binding; IEA.
GO; GO: 0006118; P: electron transport; IEA.
InterPro; IPR001128; Cytochrome_P450.
InterPro; IPR001401; EP4501.
PANTHER; PTHR19383; Cytochrome_P450; 1.
                                                                                                                                                                                                                                                                                                                         EMBL; AAAB01008900; EAA09481.2; -; Genomic_DNA.
GO; GO:0008270; F: sith c ion binding; IEA.
INCEPERO; IPR002048; EF hand Ca_bd.
InterPro; IPR004181; ZnF_MIZ.
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01-JAN-1998, sequence version 1.
21-FEB-2006, entry version 31.
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PIR; T00513; T00513.
HSSP, P14779; 1UPZ.
TAIR; At2g23190; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF02891; zf-MIZ; 1.
PROSITE; PS00018; EF HAND 1; UNKNOWN 1.
PROSITE; PS51044; ZF SP_RING; 1.
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                                                                                                                                                                preliminary data.
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nes 7; Conserv
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=1462427; DOI=10.1371/journal.pbio.0000045; Stein L.D., Bao Z., Blasiar D., Blumenthal T., Brent M.R., Chen N., Chinwalla A., Clarke L., Clee C., Cophlan A., Coulson A., Griffiths-Jones S., Harris T.W., Hillier L.W., Kamath R., Kuwabara P.E., Mardis E.R., Marra M.A., Miner T.L., Minx P., Mullikin J.C., Plumb R.W., Rogers J., Schein J.E., Sohrmann M., Waterston R.H.;
Pfam; PF00067; p450; 1.

PRINTS; PR00463; EP4501.

PRINTS; PR00385; P450.

PROSITE; PS00085; CYTOCHROME P450; UNKNOWN 1.

PROSITE; PS00086; CYTOCHROME P450; UNKNOWN 1.

SEQUENCE 543 AA; 62777 MW; 06332D6C090FDB12 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLOS Biol. 1:166-192(2003).
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The genome sequence of Caenorhabditis briggsae: a platform for comparative genomics.";
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                                                                                                                                                                                      54.8%; Score 40; DB 2; Length 543
66.7%; Pred. No. 1.4e+02;
iive 2; Mismatches 2; Indels
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63.6%; Pred. No. 1.7e+02;
ive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS51044; ZF SP RING; 1.
Complete proteome; Hypothetical protein.
SEQUENCE 675 AA; 75900 MW; BF2633230A44B877 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UVRD_SALTY STANDARD; PRT; 720 AA. Q05311; Q9L6P3; 01-0CT-1994, integrated into UniProtKB/Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; CAAC01000060; CAE67038.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-NOV-2004, integrated into UniProtKB/TrEMBL. 23-NOV-2004, sequence version 1. 07-FEB-2006, entry version 7. Hypothetical protein CBG12444.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            675 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0008270; F:zinc ion binding; IEA. InterPro; IPR004181; Znf MIZ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                   1 PVSKMRMATPLL 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis briggsae.
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267 PLSKIRMKTPV 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=CBG12444;
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Q61DK9;
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NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN=ATCC 9150 / SARB42;
STRAIN=ATCC 9150 / SARB42;
STRAIN=ATCC 9150 / SARB42;
STRAIN=ATCC 9150 / SARB42;
SA PubMed=1531882;
DA McClelland M., Sanderson K.E., Cliert T., Ozersky P., McLellan M., Porwollik S., Sabo A., Meyer R., Bieri T., Ozersky P., McLellan M., Harkins C.R., Wang C., Nguyen C., Berghoff A., Elliott G., A., Kremizki C., Layman D., Leonard S., Sun H., Fulton L., Nash W., Miner T., Minx P., Delehaunty K., Fronick C., Magrini V., Nhan M., Warren W., Florea L., Spieth J., Wilson R., T., Spieth J., Wilson R., T., Comparison of genome degradation in Paratyphi A and Typhi, human-restricted serovars of Salmonella enterica that cause typhoid.";
Nat. Genet. 36:1268-1274(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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                                                                                                                                                                                                                                                            Chiu C.-H., Tang P., Chu C., Hu S., Bao Q., Yu J., Chou Y.-Y., Wang H.-S., Lee Y.-S.; rithe genome sequence of Salmonella enterica serovar Choleraesuis, highly invasive and resistent zoonotic pathogen."; Nucleic Acids Res. 33:1690-1698(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name-uvrD; OrderedLocusNames=SPA3792;
Salmonella paratyphi-a.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE017220; AAX67756.1; -; Genomic_DNA.

QO; GO:0005737; C:cytoplasm; IEA.

GO; GO:0005737; C:cytoplasm; IEA.

GO; GO:0005737; F:ATP-dependent DNA helicase activity; IEA.

GO; GO:0003677; F:DNA binding; IEA.

GO; GO:0006268; F:Nelicase activity; IEA.

GO; GO:0006268; P:DNA repair; IEA.

GO; GO:0006268; P:DNA unwinding during replication; IEA.

InterPro; IPR00575; UvrD-helicase.

R PANTHER; PTHR11070; UvrD-helicase; 1.

R FAMTHER; PTHR11070; UvrD-helicase; 1.

R TIGREAMS; TIGR01075; UvrD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 40; DB 2; Length 720;
Pred. No. 1.9e+02;
0; Mismatches 3; Indels
07-FEB-2006, entry version 4.
DNA-dependent ArPase I and helicase II.
Name=uvrD; CrderedicousNames=SC3850; ORFNames=SCH_3850;
Salmonella choleraesuis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome, Helicase.
SEQUENCE 720 AA, 81953 MW; CBBE8D126B03D80C CRC64;
                                                                                                                                                                           [1]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-JAN-2005, integrated into UniProtKB/TrEMBL.
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                                                                                                                                                                                                                                                PubMed=15781495; DOI=10.1093/nar/gki297;
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07-FEB-2006, entry version 8.
DNA helicase II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.8%;
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Best Local Similarity 72.7
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATP-binding; Complete proteome; DNA damage; DNA repair; DNA replication; DNA-binding; Helicase; Hydrolase; Nucleotide-binding; SOS response.
                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; Pubmed=11677609; DOI=10.1038/35101614;
MEDLINE=21534948; Pubmed=11677609; DOI=10.1038/35101614;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D. Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K., "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-93300795; PubMed-a14774; Smith R.L., Banks J.L., Snavely M.D., Maguire M.E.; Smith R.L., Banks J.L., Snavely M.D., Maguire M.E.; Squence and topology of the CorA magnesium transport systems of "Sequence and topology of the CorA magnesium transport systems of almorella typhimurium and Escherichia coli. Identification of a new class of transport protein."; J. B.D. Chem. 268:14071-14080(1993).

-!-FUNCTION: Has both ATPase and helicase activities. Unwinds DNA duplexes with 3 to 5' polarity with respect to the bound strand and initiates unwinding most effectively when a single-stranded region is present. Involved in the post-incision events of region is present. Involved in the post-incision events of region is planty: Belongs to the helicase family. UvrD subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                              07-MAR-2006, entry version 41.
DNA helicase II (EC 3.6.1.-).
Name=uvrD; OrderedLocusNames=STM3951; ORFNames=STMD1.39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 720 DNA helicase II.
/FTId=PRO 000102073.
29 36 ATP (Potential).
720 AA; 81981 MW; CE6D60296392511C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 40; DB 1; I
Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 708-720.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 720 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; L11043; AAA02965.1; -; Unassigned_DNA HSSP; P09980; 1UAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF233324; AAF33441.1; -; Genomic DNA.
EMBL; AE008884; AAL22795.1; -; Genomic DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GenomeReviews, AE006468 GR; STM3951.
StyGene, SG10414; uvrD.
BioCyc; STYP99287:STM3951-MONOMER; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro, IPR005753; UvrD.
Interpro; IPR000212; UvrD-helicase.
PANTHER: PTHR11070; UvrD-helicase; 1.
Pfam; PF00580; UvrD-helicase; 1.
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Q57HQ6_SALCH PRELIMINARY; PRT;
Q57HQ6;
          29-AUG-2001, sequence version 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                           Salmonella typhimurium.
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es 8; Conserv
                                                                                                                                                                                NCBI_TaxID=602
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SEQUENCE
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10-MAY-2005, integrated into UniProtKB/TrEMBL. 10-MAY-2005, sequence version 1.

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QZIRQ8_RHOPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=TY2 / ATC 700931;
MEDLINE=22531357; PUMPGG=12644504;
DOI=10.1128/JB.185.7.2330-2337.2003;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Bashaman D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin W., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria, Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                 EMBL, CP000026, AAV79568.1; -; Genomic_DNA.
GO; GO:0005737; C:cytoplasm; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004003; F:ATP binding; IEA.
GO; GO:0004003; F:ATP binding; IEA.
GO; GO:000486; F:ATP binding; IEA.
GO; GO:000488; F:ATP binding; IEA.
GO; GO:0006281; P:DNA repair; IEA.
GO; GO:0006281; P:DNA mwinding during replication; IEA.
InterPro; IPR005212; Uvrb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54.8%; Score 40; DB 2; Length 720; 72.7%; Pred. No. 1.9e+02; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome, Helicase.
SEQUENCE 720 AA; 81953 MW; CBBE8D126B03D80C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QB23B0 SALTI PRELIMINARY; PRT; 720 AA. QB23B0; Q7C6W2; 01-MAR-2002, integrated into UniProtKB/TrEMBL. 01-MAR-2002, sequence version 1. DYAR-2006, entry version 23. DNA helicase II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=uvrD; OrderedLocusNames=STY3608, t3346; Salmonella typhi.
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EMBL; AE014613; AAO70874.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                 PANTHER; PTHR11070; UVrD-helicase; 1.
Pfam; PF00580; UVrD-helicase; 1.
TIGRFAMs; TIGR01075; uvrD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Bacteriol. 185:2330-2337(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 72.7*;
Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    653 PVSHQRMGTPL 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 413:848-852(2001)
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HSSP; P09980; 1UAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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07-MR-2006, sequence version 1.
07-MR-2006, entry version 1.
Aldehyde oxidase and xanthine dehydrogenase, molybdopterin binding.
ORFNAmmes=RPB 4416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Rhodopseudomonas.
                                                                                                      GO; GO:0005737; C:cytoplasm; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0006281; P:DNA repair; IEA.
GO; GO:0006281; P:DNA repair; IEA.
InterPro; IPR00573; Uvrb.
InterPro; IPR005212; Uvrb.helicase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 40; DB 2; Length 720;
Pred. No. 1.9e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54.8%; Score 40; DB 2; Length 755; 50.0%; Pred. No. 2e+02;
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SEQUENCE 720 AA; 82110 MW; 9E926B873D9CE672 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; CP000250; ABD09102.1; -; Genomic_DNA.
SEQUENCE 755 AA; 79136 MW; 611FD147885CA0F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9BZT1;
01-JUN-2001, integrated into UniProtKB/TrEMBL.
01-JUN-2001, sequence version 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Mismatches
BioCyc; SENT209261:T3346-MONOMER-; -. BioCyc; SENT90370:STY3608-MONOME-; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PANTHER; PTHR11070; UvrD-helicase; 1.
Pfam; PF00580; UvrD-helicase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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US DOE Joint Genome Institute;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGRFAMS; TIGR01075; uvrD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9BZTI HUMAN
ID Q9BZTI HUMAN PRELIMINARY;
AC Q9BZTI HUMAN OF CONTROL OF CONTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 72...,
Best Local Similarity 72...,
Best Local Similarity 72...,
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237 PIAKVRIITPLI 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 PVSKMRMATPLL 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             653 PVSHORMGTPL 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PVSKMRMATPL 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
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CTRAIN-C2A / ATCC 35395 | DSM 3084;

XX MEDLINE-21929760; PubMed=11932238; DOI=10.1101/gr.223902;

XX MEDLINE-21929760; PubMed=11932238; DOI=10.1101/gr.223902;

XX Galagan J.E., Nusbaum C., Roy A., Enddizzi M.G., Macdonald P.,

XX Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,

XX Linch I., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,

XX Limer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,

XX Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,

XX Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,

XX Springer T.A., Umayam L.A., White O., White R.H., Daulsen I.T.,

XX Perry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.T.,

XX Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,

XX The genome of Methanosarcina acetivorans reveals extensive metabolic

XX The genome of Methanosarcina acetivorans reveals extensive metabolic
                                                                                                                                                                                                                                                                                                                                                                                                                     Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                  MEDLINE=99069613; PubMed=9851916; DOI=10.1126/science.282.5396.2012;
                                                                                         Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                        investigating biology.";
Science 282:2012-2018(1998).
-!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMEL, Z78410; CAB01637.2; -; Genomic_DNA.

PIR, T20133; T20133.

Bansembl; CSIE3.5; Caenorhabditis elegans.

WormBase; WBGeneo00008251; CSIE3.5.

WormPep; CSIE3.5; CE37815.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:001684; F:rhodopsin-like receptor activity; IEA.

GO; GO:000186; P:G-protein coupled receptor protein signalin. Interpro; IPR000276; GPCR Rhodops.

PROSITE; PSG0262; GPROFIN RECEP_F1_2; 1.

Complete protecome; Hypothetical protein.

SEQUENCE 304 AA; 34320 MW; 28DF98B71CCE198D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Methanosarcīna acetivorans.
Archaea, Euryarchaeota, Methanomicrobia, Methanosarcinales;
Methanosarcinaceae, Methanosarcina.
                                                                                                                                                                                                                                                             The C. elegans sequencing consortium; "Genome sequence of the nematode C. elegans: a platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53.4%; Score 39; DB 2; I
57.1%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2002, integrated into UniProtKB/TrEMBL
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                                                                                                                                                                                       NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               411 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QBTP38 METAC PRELIMINARY; PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2002, sequence version 1. 07-MAR-2006, entry version 18.
                                             Name=srsx-30, ORFNames=C51E3.5, Caenorhabditis elegans.
21-FEB-2006, entry version 31. Hypothetical protein srsx-30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cation efflux system protein.
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                                                                                                                                                                                                                  STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=2214;
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                                                                                                                                              NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                 similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
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                                                                                                                                                                                                                                                                                                           Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US DOE Joint Genome Institute;
Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T., Hammon N., Israni S., Pitluck S., Di Bartolo G., Chain P., Schmutz J., Larimer F., Land M., Lykidis A., Richardson P.;
"Complete sequence of Thermobifida fusca YX.";
Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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Streptosporangineae, Nocardiopsaceae, Thermobifida.
NCBI_TaxID=269800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.4%; Score 39; DB 2; Length 141; 53.3%; Pred. No. 50; 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  53.4%; Score 39; DB 2; Length 140; 64.3%; Pred. No. 49; 1; Mismatches 4; Indels
                                                                                                                                                                                       NUCLECTIDE SEQUENCE.

Yu W.-Q., Sun B.-Z., Chai Y.-B., Zhu F., Liu X.-S., Li Z
Yan W., Yang H., Zhao Z.-L.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               141 AA; 14666 MW; CC24A2B46964BA77 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                   EMBL, AF274958; AAK07533.1; -; mRNA.
SEQUENCE 140 AA; 16335 MW; 68CCA7520ED6CE51 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q18767_CAEEL PRELIMINARY; PRT; 304 AA. Q18767; 01-NOV-1996, integrated into UniProtKB/TrEMBL.01-MAR-2005, sequence version 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74.75.32 THEFY PRELIMINARY; PRT; 141 AA. 047832.
13-SEP-2005, integrated into UniprotKB/TrEMBL. 13-SEP-2005, sequence version 1.
07-FEB-2006, entry version 4.
Putative ATP/GTP binding protein.
OrderedLocusNames=Tfu 0697; Thermobifida fusca (strain YX).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; CP000088; AAZ54735.1; -; Genomic_DNA.
GO; GO:0006950; P:response to stress; TEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 PVSKALAATPITLDA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 PVSKMRMATPLLMQA 15
            07-FEB-2006, entry version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 PVSKMRMATPLLMQ 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PVSVFRLATOLLHO 42
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nes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 64.3
les 9; Conservative
                                                     Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome. SEQUENCE 141 AA;
                                                                                                                                              NCBI_TaxID=9606;
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Q18767 CAE
ID Q1876
AC Q1876
DT 01-NO
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RESULT RE

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Matches

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Gaps

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Length 304; 4; Indels

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Indels

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STRAIN=RIB 40;

R. PubMed=16372010; DOI=10.1038/nature04300;

R. Rusumoto K., Arima T., Akita O., Kashiwagi Y., Abe K., Gomi K.,

R. Kusumoto K., Arima T., Akita O., Kashiwagi Y., Abe K., Gomi K.,

A. Horiuchi H., Kitamoto K., Kobayashi T., Takeuchi M., Denning D.W.,

A. Horiuchi H., Kitamoto K., Yu O., Archer D.B., Bennet J.W.,

B. Hatnagar D., Cleveland T.E., Fedorova N.D., Gotoh O., Horikawa H.,

Hosoyama A., Ichinomiya M., Igarashi R., Iwashita K., Juvvadi P.R.,

Akto M., Kato Y., Kin T., Kokubun A., Maeda H., Maeyama N.,

Amanyama J., Nagasaki H., Nakajima T., Oda K., Okada K., Paulsen I.,

Sakamoto K., Sawano T., Takahashi M., Takase K., Terabayashi Y.,

Mortman J.R., Yamada O., Yamagata Y., Anazawa H., Hata Y., Koide Y.,

Komori T., Koyama Y., Minetoki T., Suharnan S., Tanaka A., Isono K.,

Kuhara S., Ogasawara N., Kikuchi H.,

"Genome sequencing and analysis of Aspergillus oryzae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Fungi, Ascomycota, Pezizomycotina, Eurotiomycetes,
Burotiales, Trichocomaceae, mitosporic Trichocomaceae, Aspergillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mashreghi-Mohammadi M.;
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AP007169; BAE63971.1; -; Genomic DNA.
SEQUENCE 469 AA; 52120 MW; CC1BB0E8A6C9930D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 53.4%; Score 39; DB 2; I Local Similarity 66.7%; Pred. No. 1.8e+02; es 10; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                  24-JAN-2006, integrated into UniProtKB/TrEMBL.
24-JAN-2006, sequence version 1.
07-MAR-2006, entry version 3.
05-mayne F420-dependent NS.
ORFNames=A0090038000132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-DEC-2004, integrated into UniProtKB/TrEMBL.
07-DEC-2004, sequence version 1.
07-FBB-2006, entry version 11.
Name=FAF1; ORFNames=RP5-850015.2-003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          490 AA.
   Mismatches
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QSVTA2;
2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            223 PASKQR--TPLLFQA 235
                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 PVSKMRMATPLLMQA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 438:1157-1161(2005)
7; Conservative
                                                                                                                               378 PVSKLRIRTP 387
                                                            1 PVSKMRMATP 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aspergillus oryzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=5062;
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                                                                                                                                                                                                                                                           94 ASPOR
QZU394 ASPOR
Q2U394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Matches
                                                                                                                                                                                                                                RESULT 37
                                                                                                                                                                                                                                                              Q2U394
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                                                        Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53.4%; Score 39; DB 2; Length 411; 53.8%; Pred. No. 1.6e+02; ive 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53.4%; Score 39; DB 2; Length 464; 70.0%; Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      411 AA; 45126 MW; 64652A3A73BEEB94 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C3F730400AF6EC4F CRC64;
                                                                                                                                                                                                               GenomeReviews; AE010299 GR; MA2085.
BioCyc; MACE188937:MA2085-MONOMER; -.
GO; GO:0016620; C:membrane; IEA.
GO; GO:0008324; F:cation transporter activity; IEA.
GO; GO:0006812; P:cation transport; IEA.
InterPro; IPR002524; Cation efflux.
InterPro; IPR003731; FeMo.co_biosynth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AL603746; CAH72115.1; -; Genomic_DNA.
EMBL; AC118557; CAH72115.1; JOINED; Genomic_DNA.
EMBL; AL049637; CAH72115.1; JOINED; Genomic_DNA.
EMBL; AL049637; CA123012.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AC118557; CAI23012.1; JOINED; Genomic DNA
EMBL; AL603746; CAI23012.1; JOINED; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-DEC-2004, integrated into UniProtKB/TrEMBL. 07-DEC-2004, sequence version 1. 07-FBB-2006, entry version 11. Fas KTHRSF6) associated factor 1. Name=FAF1, ORFNAmes=FR5-850015.2-002; Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         464 AA.
                                                                                                                                                          EMBL; AE010299; AAM05485.1; -; Genomic_DNA
HSSP; Q9X2D6; 1013.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMR; QSVTA1; 375-433.
Ensembl; ENSG00000185104; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01545; Cation efflux; 1. Pfam; PF02579; Nitro Femo-Co; 1. TIGRFAMS; TIGR01297; CDF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53654 MW;
Genome Res. 12:532-542(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QSVTA1 HUMAN PRELIMINARY;
QSVTA1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  291 ISVMKIAVPVĽMO 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 53.8 Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR006577; UAS.
InterPro; IPR001012; UBX.
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SMART; SM00594; UAS; 1.
SMART; SM00166; UBX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mashreghi-Mohammadi M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UBX;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome
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RESULT 36

8 g ï

Gaps

7

Length 469; 3; Indels

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NCBI_TaxID=4952;
                                                                                                                                                                                                                                         QGCSN2_YARLI
ID QGCSN2_YARLI
AC QGCSN2;
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                                                                                    Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Capsicum annuum (Bell pepper).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamiids; Solanales; Solanaceae; Capsicum.
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                                                                                                                                                                                                                                                                                                                                                                                                 53.4%; Score 39; DB 2; Length 490; 70.0%; Pred. No. 1.9e+02; Live 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kim K.-W., Lee S.-W.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the cytochrome P450 family.
                    to the EMBL/GenBank/DDBJ databases.
                                                               to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                           490 AA; 55998 MW; 99CC7ED351A0C251 CRC64;
                                                                                                                     AL603746; CAH72114.1; -; Genomic_DNA.
AC091610; CAH72114.1; JOINED; GENOMic_DNA.
AC118557; CAH72114.1; JOINED; GENOMic_DNA.
AL049637; CAH72114.1; JOINED; GENOMIC_DNA.
AL059977; CAH72114.1; JOINED; GENOMIC_DNA.
                                                                                                                                                                                                    Genomic DNA
Genomic DNA
                                                                                                                                                                                                                       Genomic_DNA.
                                                                                                                                                                                                                                   CAH70190.1; -; Genomic_DNA.
CAH70190.1; JOINED; Genomic_DNA
                                                                                                                                                                                                                                                        CAH70190.1, JOINED, Genomic_DNA.CAH70190.1, JOINED, Genomic_DNA.CAH70190.1, JOINED, Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001, integrated into UniProtKB/TrEMBL 01-MAR-2001, sequence version 1. 07-FEB-2006, entry version 20. Cinnamic acid 4-hydroxylase.
                                                                                                                                                                             AL049637; CAI23010.1; -; Genomic_DNA.
AC091610; CAI23010.1; JOINED; Genomic_
AC118557; CAI23010.1; JOINED; Genomic_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        505 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF212318; AAG43824.1; -; mRNA.
GO; GO:0020037; F:heme binding; IEA.
GO; GO:0005506; F:iron ion binding; IEA.
GO; GO:0046872; F:metal ion binding; IEA.
                                                                                                                                                                                                                                                                                                    Ensembl; ENSG0000185104; Homo sapiens
                                                                                                                                                                                                             CAI23010.1; JOINED;
CAI23010.1; JOINED;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9FQY6_CAPAN PRELIMINARY;
Q9FQY6;
                                                                                                                                                                                                                                                                                                             InterPro; IPR006577; UAS.
InterPro; IPR001012; UBX.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  412 PVSKLRIRTP 421
                                                                                                                                                                                                                                                                                                                                                SMART; SM00594; UAS; 1.
SMART; SM00166; UBX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                              1 PVSKMRMATP 10
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SEQUENCE 490 AA; 55
                                                                                                                                                                                                                                                                                                                                   Pfam; PF00789; UBX; 1.
                       Submitted (MAY-2005)
                                                                Submitted (MAY-2005)
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                                                                          SMR; Q5VTA2; 409-490
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  NUCLEOTIDE SEQUENCE
                                             NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4072;
                                                                                                                                                                                                                                                         AC118557;
                                                                                                                                                                                                                                                                      AL049637;
                                                                                                                                                                                                                                                AC091610;
                                                                                                                                                                                                                                                                               AL603746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Root;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=C4H;
             Moore M.
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EMBL;
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EMBL;
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EMBL;
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XX Dibmed-15229592; DOI=10.1038/nature02579;
XX Dubmed-15229592; DOI=10.1038/nature02579;
XX Dubmed-15229592; DOI=10.1038/nature02579;
XX Duplon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
XX Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
XX Daffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
XX Banchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
XX Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruar A.,
XX Boisrame A., Boyer E., Fairhead C., Ferry-Dumazet H., Groppi A.,
XX Ferrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
XX Rerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Sullar H.,
XX Swennen D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
XX Seniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
XX Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
XX Genome evolution in yeasts.";
XX Genome evolution in yeasts.";
XX Nature 430:35-44(2004).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-AUG-2004, sequence version 1.
OryFBB-2006, entry version 12.
Similar to tr|O04472 Saccharomyces cerevisiae YMR115w.
OrderedLocusNames=YAL10E16621g;
Varrowia lipolytica (Gandida lipolytica).
Eukaryota; Rungi; Ascomycota; Saccharomycetis;
Saccharomycetales; Dipodascaceae; Yarrowia.
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GO; GO:0004497; F:monooxygenase activity; IEA.

GO; GO:0006118; P:electron transport; IEA.

A InterPro: IPR001128; Cytochrome_P450.

InterPro: IPR002401; PE4501.

PANTHER; PTHR19383; Cytochrome_P450; 1.

PEAM; PF00067; P450.

PRINTS; PR00483; EP450.

PRINTS; PR00485; P450.

PRINTS; PR00865; CYTOCHROME_P450; UNKNOWN 1.

PRINTS; PR01395; P450.

PRINTS; PR01395; P450.

PRINTS; PR0139; MONOOXygenase; Oxidoreductase.

Heme; Iron; Metal-binding; Monooxygenase; Oxidoreductase.

SEQUENCE 505 AA; 58020 MW; 38E61FCCE249FE0F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                    Length 505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                    53.4%; Score 39; DB 2; 70.0%; Pred. No. 2e+02; tive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-AUG-2004, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          524 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY; PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77 PVSKVRFRTILLLLA 91
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Best Local Similarity 70...
7; Conservative
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nes 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        366 RLRMATPLLV 375
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Aef30018 Lead Cere
Adr98917 Lung spec
Adv99213 Plant ful
Abb67142 Drosophil
Abb65704 Uman ORF
Ad323713 Zea mays
Aef30016 Lead Cere
Adi60138 Secreted
Abb69217 Drosophil
Adx8446 Plant ful
Adx8646 Plant ful
Adx96203 Plant ful
Adx96203 Plant ful
Adx96209 Protein o
Adx30500 Protein o
Adx0500 Protein o
Abb71564 Drosophil
Adx96399 Protein o
Adx96300 Protein o
Adx96300 Protein o
Abm87699 Rice abio
Abg23551 Novel hum
                                                                                                                                                                                                                                  Adi29006 Human MHC
Adi29007 Human MHC
Adi42025 Plant tra
Ado02575 Thalecres
Ado62214 Transcrip
                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                              7; Search time 89.924 Seconds (without alignments) 61.014 Million cell updates/sec
   GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                         Total number of hits satisfying chosen parameters:
                                                                                2589679 segs, 457216429 residues
                              22:37:17
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AD06214
AEF30018
ABF3013
ADY09213
ABB67142
ABB67142
ABB67142
ABB64188
ABB6570
AAG32713
AEF30016
                     protein search, using sw model
                                                                                                                                                                                                                                  AD129006
AD129007
AD142025
                                                                                                                                                                                                                                                                                              ADI60138
ABB69217
ADX78446
AAX06203
AAX05813
AAX020499
AAX020499
AAX020500
ABM87699
AAX20500
                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
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geneseqp1990s:*
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 ADD021598
 ADD021598

2

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Gaps

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0; Indels

Mismatches

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100.0%; 100.0%;

Query Match
Best Local Similarity luv.
Local 21 Conservative

1 AAMAAAAAAMA

Score 50; DB 8; Length 12; Pred. No. 0.23;

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The present invention describes an isolated MHC class II compound (I)

comprising: (a) an MHC class II component comprising at least a portion

comprising: (a) an MHC class II component comprising at least a portion

of an MHC class II alpha chain and at least a portion of an MHC class II beta

comprising the MHC class II alpha chain and MHC class II beta

chain form a peptide binding groove; (b) a spaceholder molecule; and (c)

an effector component, Also described; (l) a pharmaceutical composition

comprising the MHC class II molecule and a carrier; (2) a method of

producing an MHC class II compound; (3) a method of directly identifying

comprising the MHC class II compound; (3) a method of directly identifying

an antigen-specific T cell; (4) a method of tregulating an immune disorder in a subject;

in a subject; (5) a method of treating an immune disorder in a subject;

c) a method of treating an immune response ex vivo in a subject;

c) a method of treating an immune disorder ex vivo in a subject;

c) a method of treating an immune disorder ex vivo in a subject;

c) a method of treating an immune disorder ex vivo in a subject;

c) a method of treating an immune disorder ex vivo in a subject;

c) a method of treating an immune disorder ex vivo in a subject;

c) an etipacterial, antiparasitic, cytostatic and immunosuppressive

c) circuides, and can be used in gene therapy. The MHC class II compound

c) infections, peoplastic disease, autoimmunity or treating immune

c) and or opplastic disease, autoimmunity or treating immune

c) an MHC class II compound from the present invention.
                                                                                                                                                                                                                                                                                                                                                                    MHC class II compound; MHC class II component; MHC class II alpha chain; MHC class II beta chain; peptide binding groove; spaceholder molecule; effector component; immune response; immune disorder; virucide; antibacterial; antiparasitic; cytostatic; immunosuppressive; gene therapy; viral infections; bacterial infection; parasitic infection;
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Mou
POS
POS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New MHC class II compound, useful for preparing a composition for treating immune disorders e.g. viral infections, bacterial infections, parasitic infections, neoplastic disease, autoimmunity or toxicity.
                   House
                                                       Mouse
Adu68997 B
Adu68997 B
Adw87412 B
Adz66429 B
                                                                                                                                                                                                                                                                                                                                  Human MHC class II compound spaceholder molecule SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neoplastic disease; autoimmunity; toxicity; human.
                                                                                                                   ALIGNMENTS
 ADU73761
ADU68997
ADW87412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; SEQ ID NO 2; 92pp; English
                                                         ADZ66429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (DAND ) DANA FARBER CANCER INST INC.
                                                                                                                                                                                                                  ADI29006 standard; peptide; 12 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-JUL-2002; 2002US-0395494P.
22-JUL-2002; 2002US-0397893P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-JUL-2003; 2003WO-US021767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wucherpfenning KW, Seth N;
   (first entry)
   892
892
892
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   80.0
80.0
80.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
   0440
                                                                                                                                                                                                                                                        AD129006;
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MHC class II compound, MHC class II component, MHC class II alpha chain, MHC class II beta chain; peptide binding groove; spaceholder molecule; effector component, immune response; immune disorder; virucide; antibacterial; antiparastic; cytosteric; immunosuppressive; gene therapy; viral infections; bacterial infection; parasitic infection; neoplastic disease; autoimmunity; toxicity; human.

(DAND ) DANA FARBER CANCER INST INC.

Seth N;

Wucherpfenning KW,

11-JUL-2003; 2003WO-US021767. 12-JUL-2002; 2002US-0395494P. 22-JUL-2002; 2002US-0397893P.

WO2004007528-A2.

22-JAN-2004

sapiens.

Ношо

Synthetic

Human MHC class II compound spaceholder molecule SEQ ID NO:3.

15-APR-2004 (first entry)

ADI29007;

ADI29007 standard; peptide; 13 AA.

RESULT 2 ADI29007

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The present invention describes an isolated MHC class II compound (I)

comprising: (a) an MHC class II component comprising at least a portion

of an MHC class II alpha chain and at least a portion of an MHC class II beta

beta chain, such that the MHC class II alpha chain and MHC class II beta

comprising the MHC class II alpha chain and MHC class II beta

chain form a peptide binding groove; (b) a spaceholder molecule; and (c)

an effector component, Also described; (l) a pharmaceutical composition

comprising the MHC class II molecule and a carrier; (2) a method of

producing an MHC class II compound; (3) a method of directly identifying

comprising the MHC class II compound; (3) a method of directly identifying

an antigen-specific T cell; (4) a method of regulating an immune response ex vivo in a subject; and

(7) a method of regulating an immune response ex vivo in a subject; and

(7) a method of treating an immune disorder ex vivo in a subject; and

(7) a method of treating an immune disorder ex vivo in a subject; and

(7) a method of treating an immune disorder ex vivo in a subject; and

(8) a crivities, and can be used in gene therapy. The MHC class II compound

(1) can be used for preparing a composition for treating immune

(1) can be used for preparing a composition for treating immune

(1) can be used for preparing a composition for treating immune

(1) can be used for preparing a composition for treating immune

(2) disorders, e.g., viral infections, parasitic

(3) can offer a spaceholder molecule peptide, which can be used in

(3) can MHC class II compound from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New MHC class II compound, useful for preparing a composition for treating immune disorders e.g. viral infections, bacterial infections, parasitic infections, neoplastic disease, autoimmunity or toxicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11; SEQ ID NO 3; 92pp; English
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Sequence 13 AA;

Sequence 12 AA;

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09-AUG-2002; 209-AUG-2002; 217-DEC-2002; 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention describes a transgenic plant comprising a recombinant polynucleotide of any one of more than 500 nucleotide sequences fully defined in the specification or its complement. The method of the invention can be used to produced a plant having altered traits such as: enhanced tolerance to abiotic stress; glyphosphate tolerance; hormone sensitivity; disease resistance; sugar sensing; early or late flowering;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New transgenic plant comprising a recombinant polynucleotide of any one of more than 500 nucleotide sequences, useful in bioinformatic search
                                                                                                                                                                                        glyphosphate tolerance; hormone sensitivity; disease resistance; sugar sensing; flowering; flower structure; stem bifurcation; branching pattern; apical dominance; trichome; stem morphology; root prowth; root hair; seed development; cell proliferation; leaf morphology; seed morphology; seed morphology; seed morphology; seed morphology; seed an orphology; seed blochemistry; root anthocyanin; plant anthocyanin; light response; shade avoidance; bioinformatic; transcription factor; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haake V;
Keddie J, Broun PE;
                       Gaps
                       ;
0
    8; Length 13;
                      1; Indels
                                                                                                                                                                                  transgenic; plant; enhanced tolerance to abiotic stress;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heard JE, F. Reuber TL,
   Score 44; DB 8
Pred. No. 1.9;
                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adam LJ, Reun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 488; 435pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jiang C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratcliffe O, Adam L. Dubell AN, Pineda O,
                                                                                                                                                               Plant transcription factor #231.
                                                                                                       ADI42025 standard; protein; 233
                                                                                                                                                                                                                                                                                                                                                         18-APR-2001; 2001US-00837944.
                                                                                                                                                                                                                                                                                                                                      25-FEB-2003; 2003US-00374780.
   88.0%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Riechmann JL,
                                                                                                                                            (first entry)
Query Match
Best Local Similarity 91.7
Marches 11; Conservative
                                         12
                                                         AAMAAAAAAAA 12
                                                                                                                                                                                                                                                                                                                                                                                            JIANG C.
HEARD J E.
HAAKE V.
CREELMAN R A.
RATCLIFFE O.
                                                                                                                                                                                                                                                                                                                                                                          SHERMAN B K.
RIECHMANN J L.
                                                                                                                                                                                                                                                                                                                                                                                                                                          ADAM L J.
REUBER T L.
KEDDIE J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BROUN P E.
PILGRIM M L.
DUBELL A N.
PINEDA O.
YU G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Creelman RA,
Pilgrim ML,
                                                                                                                                                                                                                                                                              Oryza sativa.
                                                                                                                                            22-APR-2004
                                                                                                                                                                                                                                                                                                                   29-JAN-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sherman BK,
                                                                                                                           ADI42025;
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(CREE/)
(RATC/)
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(JIAN/)
(HEAR/)
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(YUGG/)
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(DUBE/)
                                                                                                                                                                                                                                                                                                                                                                           SHER/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (KEDD/)
                                                                                                                                                                                                                                                                                                                                                                                                                                           (ADAM/)
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                                                                                                ADI42025
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altered flower structure, change in stem bifurcations, altered branching pattern, reduced apical dominance, reduced trichome density; lack of trichomes reduced actopic trichome development; altered trithome development; increase in trichome number; altered stem morphology; increased root growth; increased root hairs; altered seed development; altered call proliferation or call differentiation; rapid development; premature senescence; increased necrosis; increase in seedling or plant size; decreased plant size; leaf morphology; seed morphology; seed biochemistry; increase in root anthocyanins; increase in plant anthocyanins, or alteration in light response or shade avoidance. The transgenic plant, polymucleotides and polypeptides are useful in bioinformatic search methods. This is the amino acid sequence of a plant transcription factor, and an orthologue of Arabiodopsis thaliana transcription factors isolated in the invention, that can be used in the creation of a transgenic plant with altered traits.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rice; transcription factor; plant; transgenic; abiotic stress; cold tolerance; heat tolerance; drought; osmotic stress; phosphate limitation; potassium limitation; nitrogen limitation; hormone sensitivity; disease resistance; sugar sensing; seed germination; flowering; inflorescence architectural change; meristem cell differentiation; phyllotaxy; apical dominance; trichome development; seed development; premature senescence; delayed senescence; lethality; necrosis; plant size; leaf morphology; secondary metabolism; light response; shade avoidance.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Length 233;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thalecress transcription factor, Rice orthologue #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 44; DB
Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AD002575 standard; protein; 233 AA.
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21-JAN-2000; 2000US-005489376.
22-MAR-2000; 2000US-00556720.
22-MAR-2000; 2000US-00533029.
22-MAR-2000; 2000US-00533392.
22-MAR-2000; 2000US-00533392.
22-MAR-2000; 2000US-00533648.
66-APR-2000; 2000US-00713994.
16-NOV-2000; 2001US-00819142.
17-APR-2001; 2001US-00819444.
17-APR-2001; 2001US-00819444.
17-APR-2001; 2001US-00819444.
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2002US-00225067.
2002US-00225068.
2002US-0434166P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88.0%;
91.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 91. ...
Best 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 233 AA;
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25-FEB-2003; 2003US-00374780.
       ZHANG J.
FROMM M E.
HEARD J E.
RIECHMANN J L.
                                         JIO G.
JIANG C.
SAMAHA R S.
PILGRIM M L.
                                                      CREELMAN R A
                                                             RATCLIFFE O. KUMIMOTO R.
                                                                     SHERMAN B K.
                                                                                               WPI; 2004-225755/21.
                            PINEDA O. REUBER T L. KEDDIE J S.
                     ADAM L J.
BROUN P E.
                                                          DUBELL A N.
                                                                            Zhang J, Fro
Pineda O, Ro
Pilgrim ML,
Sherman BK;
                            (PINE/)
(REUB/)
                                           (JIAN/)
                                                   (PILG/)
(CREE/)
                                                          (DUBE/)
(RATC/)
(KUMI/)
                                                                     (SHER/)
       ZHAN/)
                          BROU/)
                      (ADAM/)
                                        YUGG/)
                                    (KEDD/)
                  RIEC/
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Heard JE, Riechmann JL, Adam LJ, Broun PE; , Keddie JS, Yu G, Jiang C, Samaha RS; Fromm ME, Heard JE, Riechmann JL, Adam LJ, Broun Pf Reuber TL, Keddie JS, Yu G, Jiang C, Samaha RS; L, Creelman RA, Dubell AN, Ratcliffe O, Kumimoto R;

transgenic plant, useful in developing phenotypes with altered or improved characteristics or traits.

Claim 1; SEQ ID NO 989; 213pp; English

transcription relates to a transgence plant comprises a recombinant polymucleotide having a polymucleotide sequence or its complementary sequence comprising a sequence encoding a polymucleotide, that initiates transcription (i.e. a transcription factor) from Arabidopsis, Soybean, comprising as equence encoding a transgenic plant to agrow a progeny plant, an expression cassette (comprising as Abo01355). Also included are using a transgenic plant to grow a progeny plant, an expression cassette (comprising a constitutive inducible or tissue-specific promoter and a transgenic constitutive inducible or tissue-specific promoter and a transgenic cassette, producing a modified plant having a modified trait, identifying a factor that is modulated by or interacts with a polypoptide encoded by the polymucleotide sequence and identifying at least one downstream to plymucleotide sequence and identifying at least one downstream polymucleotide sequence and identifying a plant that has an altered transgenic plant is useful for producing a plant that has an altered transgenic plant is useful for producing a plant that has an altered transgenic plant is useful for producing a plant that has an altered transgenic plant is useful for producing a plant that has an altered transgenic plant is useful for producing a plant that has an altered transgenic plant is useful for producing a plant that has an altered transgenic plant is useful of drought, tolerance to obecased tolerance to drought, tolerance to obecased tolerance to prosphate limitation, colerance to potassium conformed transmittivity reduced sensitivity to bactical series and altered susceptibility to Fautoranium, altered susceptibility to Fautoranium, altered susceptibility to Fautoranium, altered susceptibility to seurodomonas syringae, altered susceptibility to series and massitum, altered susceptibility of plants increased for flowering, an inflorescence architectural change, altered susceptibility increased for hard morphology, altered susception of proiferation, alter The invention relates to a transgenic plant comprises a recombinant

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          content, an alteration of leaf glucosinolate content, change in seed biochemistry, an increase in seed oil content, decrease in seed faity acid content, increase in seed protein content, on seed protein content, increase in seed protein content, increase in seed protein in seed protein lipid content, increase in seed in seed in secondary metabolism, increase in root anthocyanins, increase in plant anthocyanins, and alteration in light response or shade avoidance. The present sequence represents an orthologue of a thalecress transcription factor isolated from Rice.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plant; transcription factor; transgenic plant; abiotic stress tolerance; osmotic stress tolerance; cold tolerance; heat tolerance; low nitrogen tolerance; low phosphate tolerance; fungal disease; glyphosate resistance; flowering; fertility; seed development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to novel plant transcription factor proteins (I) and nucleotide sequences (II) (ADO61534-ADO63778). The sequences can be used to produce transgenic plants, which overexpress on the transgenic plant has an altered trait as compared to a non-transgenic plant or wild-type plant. The transgenic plant comprises an altered trait selected from increased tolerance to abiotic stress, increased tolerance to cold, increased germination in cold, increased tolerance to heat, increased germination in heat, increased tolerance to heat, increased increased tolerance to low nitrogen conditions, increased tolerance to low nitrogen conditions, increased tolerance to low phosphate conditions, increased tolerance to disease, including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New recombinant polynucleotide encoding transcription factor polypeptides, useful for producing transgenic plants with advantageous properties compared to a reference plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reuber TL;
increased leaf anthocyanins, an alteration of leaf fatty acid
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                                                                                                                                                                                                                                                               Score 44; DB 8; Length 233;
Pred. No. 33;
0; Mismatches 1; Indels
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, Keddie JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 681; 510pp; English.
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Riechmann JL, Haake V, Dubell AN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADO62214 standard; protein; 233 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MEND-) MENDEL BIOTECHNOLOGY INC.
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                                                                                                                                                                                                                                                                       88.0%;
91.7%;
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                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                               Sequence 233 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza sativa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADO62214;
                                                                                                                                                                                                                                                                         Query Match
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Claim 1; SEQ ID NO 2218; 612pp; English.

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increased tolerance to multiple fungal pathogens, increased resistance to glyphosate, increased sensitivity to ABA, reduced sensitivity to ABA, conceased sensitivity to ABA, reduced sensitivity to ABA, conceased sensitivity to ABA, altered sensitivity to ABA, increased tolerance to sugars, altered carbon/nitrogen sensing; early flowering, latered flower structure, loss of flower determinacy, reduced fertility, altered selected branching pattern, altered stem morphology, altered density, altered branching pattern, apical dominance, altered trichome density, altered trichome development, altered seed trichome structure, altered seed trichome structure, altered seed coll profileration, altered seed development, altered seed call profileration, altered cell differentiation, altered seed cell profileration, altered cell destance, altered seed development, altered cell death, lethality when overexpressed, altered necrosis patterns, increased cell prize, increased blomass, large seedlings, dwarfed plants, dark green leaves, change in leaf shape, increased leaf size and mass, light green or gray leaves, glossy leaves, altered abaxial adaxial polarity, altered seed size, altered abexial polarity, altered seed shape, large altered seed coloration, altered seed size, altered abaxial polarity, altered seed shape, large altered seed soloration, altered seed shape, large altered seed seed coloration, altered seed size, altered abaxial polarity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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disease and particularly Erysiphe, Fusarium and Botrytis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
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91.7%;
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30-JUN-2004; 2004US-0584800P.
30-JUN-2004; 2004US-0584829P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JUN-2005; 2005WO-US023326.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 233 AA;
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The phenotypes and characteristics, comprising a nucleotide sequence that phenotypes and characteristics, comprising a nucleotide sequence that the nerodes an amino acid sequence exhibiting at leaf 8% sequence in the carbon an amino acid sequence in the sequence listing or in the critical and an amino acid sequence in the sequence listing or in the critical and an amino acid sequence in the sequence of the nucleotide sequence in (a) (auch that the reverse nucleotide sequence has a sequence order which is the reverse of the nucleotide sequence of the reverse of the nucleotide sequence of the sequence of the nucleotide sequence of the sequence of the nucleotide sequence of the sequence of sequence of the sequence of the sequence of sequence of sequence of
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                                       invention relates to an isolated nucleic acid molecule modifying
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88.0%; Score 44; DB 10; Length 233; 91.7%; Pred. No. 33;
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06-MAY-1999; 99US-00304517.
05-NOV-2001; 2001US-00985678.
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91.7%;
                                                                               28-APR-2003; 2003US-00425114
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ZHOU Y.
KOVALIC D K.
SCREEN S E.
                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-180133/17.
                                                                                                                                                                                                                                                                   TABASKA J E.
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US2004034888-A1
                                                                                                                                                                                                                                                                                          CAO Y.
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                                      19-FEB-2004,
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(CAOY/)
                                                                                                                                                                                 (LIUJ/)
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(SCRE/)
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                                                                                                                                                                                                                                                                                                                                 Liu J,
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                                                                                                                                                                                                                                                                                                                                                                                    molecule (I) comprising any of 113 fully defined nucleotide sequences given in the specification, their encoded protein sequences, sequences cgiven in the specification, their encoded protein sequences, sequences at least 60% identifying to the nucleotide sequences. The methods and cat least 60% identity to the nucleotide sequences. The methods and cat diagnosing, monitoring, staging, imaging and treating lung cancer and non-cancerous diseases of the lung. They are also used for identifying, tissue, monitoring and identifying and/or designing antagonists of the carrier of the invention, gene therapy, production of transgenic animals and production of engineered lung tissue for treatment and creater. Lung specific genes (LSGs) were identified by a systematic animals and production of engineered lung tissue for treatment and catalysis of gene expression adata in the LIFESEO Gold database using the data mining software package candidate lead automatic search program (CLASP). Genes were grouped into gene bins where each bin is a cluster of sequences grouped together where they share a common contig.

Composition of reach gene in libraries of normal tissues or non-tumour tissues from cancer patients were compared with the expression cumour tissues from cancer patients were compared with the expression levels in this unibraries associated with tumour or disease. This sequence represents a protein of the invention.
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                                                                                                                                                                                                                                               New isolated human lung specific nucleic acid molecule, useful for identifying, diagnosing, monitoring, staging, imaging and treating lung cancer and non-cancerous diseases of the lung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Pred. No. 40;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 202; 542pp; English
                                                                                                                                             Liu S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADY09213 standard; protein; 646 AA.
                                                                                                                                             Sun Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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91.7%;
                   06-DEC-2002; 2002US-0431307P.
06-DEC-2002; 2002US-0431510P.
06-DEC-2002; 2002US-0431516P.
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                                                                                                                                           Macina RA, Turner LR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
--nc 11; Conserva
                                                                                                  (DIAD-) DIADEXUS INC
                                                                                                                                                                                      WPI: 2004-635553/61
                                                                                                                                                                                                         N-PSDB; ADR98780
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The invention describes a recombinant DNA construct comprising a polymucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at the invention are also useful in physical arrays of molecules and as of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme compositions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, increased resistance to plant disease, for increasing the rate of homologous recombination in plants, for inpressing the rate of homologous recombination in plants, for introgen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This is the amino acid sequence of a plant full length insert polypeptide that can be used in the recombinant DNA construct of the
                                                                                                                              New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for improving yield.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila; developmental biology; cell signalling; insecticide;
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0
Cao Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 44; DB 8; Length 646;
Pred. No. 92;
0; Mismatches 1; Indels
Zhou Y, Kovalic DK, Screen SE, Tabaska JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster polypeptide SEQ ID NO 28218.
                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 65028; 15pp; English.
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WO200171042-A2

Unidentified

ADY09213;

RESULT 8

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Human, open reading frame, ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mallitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                                                                               The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
              detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes substantially purified human proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative,
                                                                                           Disclosure; SEQ ID NO 19356; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                Score 42; DB 4; Length 2857;
Pred. No. 7.9e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hyperproliferative disorders and autoimmune disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human ORFX protein sequence SEQ ID NO:13122.
                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
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29-AUG-2000; 2000US-0228716P.
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                New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                            10; Conservative
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                                                                                                                                                                                                                                                                                                                                                            Sequence 2857 AA;
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                                                        interactions
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                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABB37737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                              isolated nucleic acid detection reagent for detecting 1000 or more es from Drosophila and for elucidating cell signaling and cell-cell
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Pred. No. 1e+02;
2; Mismatches 0; Indels
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                                                    23-MAR-2001; 2001WO-US009231
                                                                                         23-MAR-2000; 2000US-0191637P.
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11-JUL-2000; 2000US-00614150.
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83.3%;
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                                                                                                                                                                                              Adams M,
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N-PSDB; ABL08291.
                                                                                                                                                                                                                                     WPI; 2001-656860/75
                                                                                                                                                      (PEKE ) PE CORP NY
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                                                                                                                                                                                                                                                          N-PSDB; ABL11245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 526 AA;
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                                                                                                                                                                                                                                                                                                                                          interactions.
                                                                                     23-MAR-2000;
              27-SEP-2001.
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Best Local 9
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Gaps

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Treating to as open reading trame, ORFX, where X is 1.11491 (see Table 1 in the specification). ABN15722 encode the human ORFX proteins given in ABP00010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder. ORFX polynucleotide disorder in humans, and in the manufacture of a medicament for treating a syndrome associated with ORFX-associated disorder. ORFX polynucleotide sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, costiasis, benign tumours, keloid, degenerative disorders, haemorrhage, osteoarthritis, neurodegenerative disorders, disorders related to organ cransplantation, cardiovascular diseases, diabetes mellitus, systemic lupus erythematosus, hyperthyroidism, cholesterol ester storage disease, various immune deficiencies and disorders, infectious carbinitis, autoimmune disorders such as multiple sclerosis, rheumatoid atheases, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also conseful for treating burns, incisions, ulcers, for treating osteoporosis, bone degeneration and treatment of lung or liver fibrosis, corporection or regeneration and treatment of lung or liver fibrosis, systemic cytokine damage. NB. The sequence data for this patent did not for mpart of the printed specification, but was obtained in electronic form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
(referred to as open reading frame, ORFX, where X is 1-11491 (see Table
                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                          82.0%; Score 41; DB 5; Length 129; 83.3%; Pred. No. 51; ive 1; Mismatches 1; Indels
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99US-0123548P.
99US-0123548P.
99US-0126264P.
99US-0126785P.
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99US-0126785P.
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99US-0130510P.
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99US-0131449P.
99US-0132048P.
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nes 10; Conservative
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11 AALAAAAAAA 22
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29-MAR-1999
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16-APR-1999
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99US-0142920P.
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990S-0144352P.
990S-0144632P.
990S-0144884P.
990S-0145086P.
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99US-0144331P.
99US-0144332P.
990S-0132484P
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990S-0132863P
990S-0134218P
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990S-0134941P
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9905-0137502P.
9905-0138034P.
9905-0138540P.
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99US-0139492P.
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99US-0140354P.
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16-JUL-1999;
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9905-0145192P

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9905-0149319P

9905-0151080P

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990S-0158029P.
990S-0158232P.
990S-0159293P.
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99US-0160741P
                    22-JUL-1999;
22-JUL-1999;
23-JUL-1999;
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02-AUG-1999;
02-AUG-1999;
03-AUG-1999;
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05-AUG-1999;
06-AUG-1999;
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09-AUG-1999;
09-AUG-1999;
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-OCT-1999;
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26-AUG-1999;
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18-AUG-1999
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20-SEP-1999
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The invention relates to an isolated nucleic acid molecule modifying plant phenotypes and characteristics, comprising a nucleotide sequence that encodes an amino acid sequence exhibiting at least 85% sequence identity to an amino acid sequence in the sequence listing or in the ortholog alignments of Figure 1, a nucleic acid, which is a complement of (a), a nucleic acid, which is the reverse of the nucleotide sequence in (a) (such that the reverse nucleotide sequence has a sequence order which is the reverse of the sequence order of (a)) or a nucleic acid capable of
                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         plant; transgenic plant; crop improvement; abiotic stress tolerance; plant growth regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid molecule modifying plant phenotypes and characteristics and the polypeptide it encodes, useful for making transgenic plants with improved characteristics.
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                                                                                                                                                                                                                             Length 156;
                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         Lead_CeresClone681222 protein homolog SEQ ID NO:2216.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Feldmann K;
                                                                                                                                                                                                                              DB 3;
62;
                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                Score 41;
Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mascia P,
                                                                                                                                                                                                                                                                                                                                                                  AEF30016 standard; protein; 243 AA.
        990S-0160768P-
990S-0160710P-
990S-0160814P-
990S-0160980P-
990S-0160981P-
990S-0161404P-
990S-0161406P-
990S-0161406P-
990S-0161406P-
990S-0161406P-
                                                                                                                                                                              99US-0161992P.
99US-0161993P.
99US-0162142P.
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30-JUN-2004; 2004US-0584800P.
30-JUN-2004; 2004US-0584829P.
                                                                                                                                                       99US-0161361P.
99US-0161920P.
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                                                                                                                                                                                                                              82.0%;
99US-0160767P
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nes 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Triticum aestivum.
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                    21-0CT-1999;
21-0CT-1999;
22-0CT-1999;
22-0CT-1999;
25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
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26-0CT-1999;
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28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
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Matches
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ID AEF3
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hybridizing (a-c), under conditions that permit formation of a nucleic acid duplex at a temperature of 40-48 degrees C below the melting temperature of the nucleic acid duplex. Also included are a vector construct (comprising a first nucleic acid having a regulatory sequence of capable of causing transcription and/or translation in a plant, operably linked to a second nucleic acid having the sequence of the isolated nucleic acid molecule that is flanked by exogenous sequence, a host cell comprising the isolated nucleic acid molecule that is flanked by exogenous sequence, a host cell comprising the vector construct, an isolated polypeptide comprising an aniho acid sequence exhibiting at least 85* sequence identity to those cited above, introducing an isolated nucleic acid into a host cell, transforming a comprising the nucleic acid molecule, a plant generated from the plant cell or seed, a plant (plant cell, plant material or seed) comprising the nucleic acid molecule, a plant paying plant compared to a wild type plant), improving plant characteristics in a plant comprising transforming the plant with the nucleic acid sequence, and a transgenic plant having a gene construct (comprising the nucleic component operably linked to a plant promoter so that the component operably linked to a plant promoter so that the component operably linked to a plant promoter so that the component operably linked to a plant promoter so that the component to maturation, greater fruit or seed yield, higher tolerance to low phosphate concentration, or higher tolerance to low phosphate concentration, or higher tolerance to progenitor plant are cultivated under identical environmental conditions, where the component is any one of the polypeptides of the above. The nucleic acid molecules are useful for producing transgenic plants are useful for producing transgenic plants with a plant nucleic acid molecules are useful for producing transgenic plants.
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Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82.0%; Score 41; DB 10; Length 243; 83.3%; Pred. No. 96; 1; Mismatches 1; Indels
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16-SEP-2002; 2002US-00323349.
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Matches 10, Conservative
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Ghosh M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADI60138;
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The invention relates to novel isolated polynucleotides or a sequence encoding a polypeptide with biological activity, where the polynucleotide hybridization conditions or has greater than 99% sequence identity with the polynucleotide. The polynucleotides and polypeptides are useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders and other traits, to assess biodiversity, as nutritional sources or supplements. The polynucleotides may also be used as molecular weight markers, chromosome markers or map related gene positions, or as an antigen to raise anti-DNA antibodies or elicit immune response. The polypeptides are useful for raising antibodies, as markers for tissues in which the corresponding polypeptide is expressed, for re-engineering damaged or diseased tissues, for treating myeloid or lymphoid cell calsoners, in home cartilage, tendon, ligament and/or nerve tissue growth cr regeneration, in wound healing, in tissue repair and replacement, in healing of burns, incisions and ulcers, and in treating cancer. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                         New polynuclectides and secreted proteins, useful for treating myeloid or lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve tissue growth or regeneration, in wound healing, and in tissue repair and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence corresponds to a protein sequence of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 41; DB 7; Length 2/0. Pred. No. 1.18+02; O; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster polypeptide SEQ ID NO 34443.
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                                                                                                                                                  claim 20; SEQ ID NO 173; 243pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.0%;
75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Conservative
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5 AALSAAAAAALA 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-656860/75.
            WPI; 2003-354601/33.
N-PSDB; ADI60483.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 276 AA;
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                                                                                                                     replacement
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ABB69217
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Claim 1; SEQ ID NO 47812; 15pp; English.
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                                                                                                                                                                                                                                                 Sequence 333 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US2004034888-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unidentified
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                                                                                                                                                                                                         invention.
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                                                                                                                                                                                                                                                                      Query Match
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(ZHOU/)
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(SCRE/)
(TABA/)
(CAOY/)
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                                      The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16175, ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737) and ABB2072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for improving yield.
                                                                                                                                                                                                                                                                                                                                                                                                 plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; heat tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; yalatcomannan production; lighin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield; protein content.
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                    Disclosure; SEQ ID NO 34443; 21pp + Sequence Listing; English.
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                                                                                                                                                                                 82.0%; Score 41; DB 4; Length 328; 100.0%; Pred. No. 1.3e+02;
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                                                                                                                                                                                                                                                                                                      ADX78446 standard; protein; 333 AA.
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05-NOV-2001; 2001US-00985678.
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                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 10, Conservative
                                                                                                                                                                                                                                               98 AAMAAAAAA 107
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CAO Y.
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                                                                                                                                                            Sequence 328 AA;
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21-APR-2005
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(SCRE/)
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(CAOY/)
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The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at a vailable in electronic form from the US patent office at the polynucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme camotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, lignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of the cell by modification of photosynthesis or carbohydrate, mitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or centent. This is the amino acid sequence of a plant full length insert polypeptide that can be used in the recombinant DNA construct of the
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Pred. No. 1.3e+02;
1; Mismatches 1; Indels
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05-NOV-2001; 2001US-00985678.
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157 SAMAAAAAAAA 168
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Hes 10; Conservative
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ZHOU Y.
KOVALIC D K.
SCREEN S E.
TABASKA J E.
CAO Y.
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                                                                                                                           The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at t.p. seqdata.uspto.gov/sequence.html?DocID:2004034088. The polynucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme someotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing glaactomannan, increased resistance to plant disease, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This is the amino acid sequence of a plant full length insert in the recombinant DNA construct of the
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                         recombinant DNA construct, useful for improving plant tolerance to , heat, drought, herbicides, extreme osmotic conditions, pathogens or s, for conferring increased resistance to plant disease, or for
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                                                                                                                                                                                                                                                                                                                                                                                                                                             82.0%; Score 41; DB 8; Length 429;
100.0%; Pred. No. 1.7e+02;
.ive 0; Mismatches 0; Indels
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/note= "DNA-binding HMG domain"
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(SLOK ) SLOAN KETTERING INST CANCER RES.
(CORR ) CORNELL RES FOUND INC.
                                                                                                      Claim 1; SEQ ID NO 58867; 15pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE05813 standard; protein; 443 AA.
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 WPI; 2004-180133/17.
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                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 429 AA;
                                                                          improving yield.
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                                                                                                                                                                                                                                                                                                                                                                                         invention.
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                                                                                                                                                                    The invention relates to nucleic acids and encoded polypeptides which are cancer associated antigens expressed in patients afflicted with small cell lung cancer. The molecules provided by the invention can be used in the diagnosis, monitoring, research or treatment of conditions characterised by the expression of one or more cancer associated antigens. The polypeptide is used to treat a disorder characterised by expression of an expression of an abnormal amount of a protein encoded by a nucleic acid (NA) Group I molecule. The disorders are small and non-small cell lung cancer, melanoma, colon, breast, head and neck, or transitional cancer, leimyosarcoma or synovial sarcoma. The present sequence is human SOX3 protein, encoded by a small cell lung cancer associated gene designated as NY-SCLC-9
                                                 Isolated polypeptide, used to treat or prognose a disorder characterized by expression of a hCAAP e.g. cancer, is encoded by an isolated nucleic acid comprising an NA Group 3 or 4 molecule.
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Pred. No. 1.7e+02;
1; Mismatches 1;
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                                                                                                                                         Disclosure, Fig 1; 152pp, English
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11-JUL-2000; 2000US-00614150.
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N-PSDB; ABL15667.
2001-457597/49.
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WPI; 2001-457597/
N-PSDB; AAD11118.
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Matches
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protein of the APP related human homologue hCP41313 #1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neuroprotective; nootropic; transgenic fly; Alzheimer's disease; Abeta; amyloid precursor protein; tissue-specific expression control; human APP; APP pathway modulator; gene therapy.
useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL3631), expressed DNA sequences (ABL0176-ABL3631), expressed DNA sequences (ABL0176-ABL3631), expressed DNA ABB2072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New transgenic fly, containing DNA encoding an Abeta portion of human APP, useful for identifying agents which modulate the APP pathway and which can be used to treat Alzheimer's disease.
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                                                                                                                                                                                                     Score 41; DB 4; Length 524
Pred. No. 2.1e+02;
" Mismatches 1; Indels
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(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
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                                                                                                                                                                                                                                                                                                                                                                                                                       AAO20499 standard; protein; 593 AA.
                                                                                                                                                                                                             82.0%;
83.3%;
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14-JUN-2001; 2001US-0298309P.
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                                                                                                                                                                        Sequence 524 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200226820-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA020499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cohen D,
                                                                                                                                                                                                                                                                                                                                                                                    RESULT 20
                                                                                                                                                                                                                                                                                                                                                                                                       AAO20499
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                                                                                                                                                                                                                                                                                                                                                  Neuroprotective; nootropic; transgenic fly; Alzheimer's disease; Abeta; amyloid precursor protein; tissue-specific expression control; human APP; APP pathway modulator; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               stranded Manlecule, Tibozyme, or particularly an antibody. It is used to treat conditions such as Alzheimer's disease. The agent can be used as an APP pathway modulator or in gene therapy. This sequence represents the protein of the APP related human homologue hCP41313 #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a transgenic fly whose genome comprises DNA encoding a polypeptide having the Abeta portion of human amyloid precursor protein (APP), fused to a signal sequence. The DNA sequence encodes a 133 (Abeta40) or 129 (Abeta42) amino acid sequence, given in the specification. The DNA sequence is operably linked to a tissue-specific expression control sequence. Expression of the sequence gives the fly an altered phenotype. The purpose of the invention is for identifying agents that inhibit or promote the expression and/or function of genes or encoded polypeptides which modify the APP pathway. The agent is a compound, triple helix DNA, antisense oligonuclectide, double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New transgenic fly, containing DNA encoding an Abeta portion of human APP, useful for identifying agents which modulate the APP pathway and
                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Konsolaki M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 645;
                               Length 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                0; Indels
                                                                                                                                                                                                                                                                                                                    Protein of APP related human homologue hCP41313 #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cohen D, Dengler UJ, Finelli AL, Freuler F, Reinhardt MWHM, Zusman S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82.0%; Score 41; DB 5; I 75.0%; Pred. No. 2.5e+02; ive 3; Mismatches 0.
                               Score 41; DB 5; Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                which can be used to treat Alzheimer's disease.
                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 25; Page 92-93; 129pp; English.
                                                                                                                                                                                                                  AA020500 standard; protein; 645 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2001; 2001WO-EP011345.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-SEP-2000; 2000US-0236893P.
14-JUN-2001; 2001US-0298309P.
                               82.0%;
75.0%;
                                                                                                                                                                                                                                                                                   27-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          508 SSMASAAAAAA 519
                                                                9; Conservative
                                                                                                 12
                                                                                               1 AAMAAAAAAAA
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N-PSDB; AAK99394.
                                Query Match
Best Local Similarity
Sequence 593 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 645 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200226820-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-APR-2002.
                                                                                                                                                                                                                                                    AAO20500;
                                                                 Matches
                                                                                                                                                                                    RESULT 21
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(first entry)

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Human, chromosome mapping, gene mapping, gene therapy, forensic; food supplement, medical imaging, diagnostic, genetic disorder.
                                                                               Novel human diagnostic protein #23542.
                                                                                                                                                                                                                                                                                                        31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                      30-MAR-2001; 2001WO-US008631
                                                                                                                                                                                                                                                                                                                                                                                                Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC.
                                                                                                                                                                                                     WO200175067-A2.
                                                                                                                                                                       Homo sapiens.
                                              18-FEB-2002
                                                                                                                                                                                                                                         11-OCT-2001.
              ABG23551;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and polypeptides. Also disclosed are vectors, expression cassettes, host cells, and plants containing such polynucleotides. Also disclosed are nethods for using the polynucleotides and polypeptides to alter the responsiveness of a plant to abiotic stress. The invention is useful in agriculture. The nucleic acid is useful for determining whether a test plant has been exposed to an abiotic stress condition. It is also useful for selecting an agent that alters abiotic stress regulated polynucleotide expression in a plant cell, and to identify a homolog or ortholog to an abiotic stress responsive polynucleotide. The nucleic acid molecule and the polypeptide encoded by it are useful in altering the responsiveness of a plant to an abiotic stress, such as cold stress, sattess, osmotic stress or any of their combinations. The present sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New stress-responsive nucleic acid, useful for altering the responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold stress, salt stress or osmotic stress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to novel abiotic stress responsive polynucleotides
                                                                                                                                                                                                                                                                           abiotic stress tolerance; transgenic plant; plant; cereal; agriculture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Katagiri F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                         Rice abiotic stress responsive polypeptide SEQ ID NO:5945.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goff SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glazebrook J,
), Zhu T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       claim 1; SEQ ID NO 5945; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SYGN ) SYNGENTA PARTICIPATIONS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cooper B, G.
N, Ricke D,
                                                                                                                                      ABM87699 standard; protein; 648 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-JUN-2001; 2001US-0300112P.
24-AUG-2001; 2001US-0314662P.
26-SEP-2001; 2001US-0325277P.
21-NOV-2001; 2001US-0332132P.
                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUN-2002; 2002WO-US019668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 83.3
Marches 10; Conservative
                                                                                                                                                                                                          (first entry)
                                     ::||:|||||||
558 SSMASAAAAAMA 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kreps J, Briggs SP, Coo
Moughamer T, Provart N,
                   1 AAMAAAAAAMA 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-248011/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 648 AA;
                                                                                                                                                                                                                                                                                                                                                   WO2003008540-A2.
                                                                                                                                                                                                                                                                                                                   Oryza sativa
                                                                                                                                                                                                            02-JUN-2005
                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2003
                                                                                                                                                                        ABM87699;
                                                                                                      RESULT 27
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Tang YT;

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed constitution of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed activity of (II) or to treat disease states involving (II). (II) is constituted in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging cyllypeptide in tissue, as molecular weight markers and as a food states expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders of sites expression or biological activity. The polypeptide and polynucleotide sequences have applications in cresponsible for genetic disorders or other trails to assess biodiversity and to produce other types of data and products dependent on DNA and canno acid sequences of the invention. Note: The sequence data for this mino acid sequences of the invention. Note: The sequence data for this center tid not appear in the printed specification, but was obtained in celectronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 41; DB 4; Length 791;
Pred. No. 3.18+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                      Claim 20; SEQ ID NO 53910; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADD02808 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.0%;
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Best Local Similarity
Local Similarity
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WPI; 2001-639362/73.
                                     N-PSDB; AAS87738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 791 AA;
                                                                                                                                                                                                                          biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADD02808;
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ABG23551 standard; protein; 791 AA.

RESULT 23 ABG23551 ID ABG

553 AAAAAAAAALA 564

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1 AAMAAAAAAAA 12

Peptide useful for coded probe useful in biomolecule analysis.

(first entry)

29-JUL-2004

ADO43159;

ADO43159 standard; peptide; 30 AA.

AD043159

Nano-barcode; scanning probe microscopy; probe.

/note= "C-terminal amide"

WO2004038037-A2

06-MAY-2004

Modified-site

Synthetic

22-SEP-2003; 2003WO-US029726 20-SEP-2002; 2002US-00251152 19-SEP-2003; 2003US-00667004

Yamakawa M;

Su X,

Chan S,

(ITLC ) INTEL CORP

WPI; 2004-399960/37.

Location/Qualifiers

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The present invention describes a superantigen binding site within the CD28 molecule that specifically and directly binds to a superantigen. Also described: (1) a method for treating a superantigen-related disorder in a mammalian subject; (2) a method of inhibiting pyrogenic exotoxin-mediated activation of Th1-1ymphocytes and protecting against toxic shock induced by a pyrogenic exotoxin or by a mixture of pyrogenic exotoxins, in a subject; (3) a method of eliciting protective immunity against toxic shock induced by a pyrogenic exotoxin in a subject; (4) a substance that inhibits the binding of a superantigen to a superantigen binding site in CD28; (5) a pharmaceutical composition for treating or preventing superantigen-related disorders comprising the substance that inhibits the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        preparing a pharmaceutical composition for treating superantigen-related disorders caused by Staphylococcus aureus or Streptococcus pyogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               direct interaction between CD28 molecule and the pyrogenic exotoxin, which leads to antagonising of toxin-mediated activation of Thi hyphocytes; (6) an isolated and purified peptide having an amino acid sequence homologous to an amino acid sequence comprised within a sequence comprised within a servening for a test substance which specifically binds to the CD28 molecule and is capable of antagonising pyrogenic exotoxin-mediated activation of Thi lymphocytes and optionally of eliciting protective immunity against toxic shock induced by a pyrogenic exotoxin or by a mixture of at least two pyrogenic exotoxins; and (8) a method of preparing a therapeutic composition for treating a superantigen-related disorder in a mammalian subject. The substance and pharmaceutical composition have antibacterial activities, and can be used in gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New superantigen binding site within the CD28 molecule, useful for
                                                                                                                                                                                          superantigen binding site; CD28; superantigen; antibacterial; gene therapy; superantigen-related disorder; epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         therapy. The substance, peptide or CD28 molecule can be used
                                                                                               SCD28 molecule related motif peptide SEQ ID NO:7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 8; SEQ ID NO 7; 160pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2003WO-IL000278.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34-APR-2002; 2002IL-00148993
     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-APR-2003;
01-JAN-2004
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                                                                                                                                                                                                                                                                                                                                           Synthetic
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preparing a pharmaceutical composition for treating superantigen-related disorders caused by Staphylococcus aureus or Streptococcus pyogenes. The present sequence represents an sCD28 molecule related peptide motif, which is used in the exemplification of the present invention.
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                                                                                                                                                                                  .
0
                                                                                                                                        Score 40; DB 7; Length 16;
                                                                                                                                                                                Indels
                                                                                                                                                                                  1;
                                                                                                                                                          Pred. No. 9.1;
0; Mismatches
                                                                                                                                                        90.98;
                                                                                                                                          80.08;
                                                                                                                                                                              10; Conservative
                                                                                                                                                                                                                      1 AAMAAAAAAM 11
                                                                                                                                                            Similarity
                                                                                                                                        Query Match
Best Local S
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1 AAAAAAAAAM 11

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The present sequence is that of a peptide of potential use for production of a coded probe useful in the method of the invention. The sequence was obtained by solid-phase peptide synthesis, and is predicted to be an alpha helix. The invention provides methods, apparatus and compositions for the detection, identification and/or sequencing of biomolecules, such as nucleic acids or proteins. Coded probes comprising a probe molecule attached to one or more nano-barcodes are allowed to bind to target molecule (s). After binding and separation from unbound coded probes, the bound coded probes are aligned on a surface and analysed by scanning probe microscopy (SPM). The nano-barcodes may be any molecule or complex that is distinguishable by SPM, such as carbon nanotubes, fullarenes; submaritner metallic barcodes, nanoparticle or quantum dots. The methods allow the sequencing of long nucleic acids equences in a single sequencing run, high speed of obtaining sequence data, low cost of sequencing and high efficiency in terms of operator time, and sensitive and accurate detection and/or identification of nucleic acids with low incidence of false positive results.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detecting, identifying and sequencing of biomolecules using controlled alignment of nano-barcodes encoding specific information for scanning probe microscopy, useful in the fields of molecular biology.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; SEQ ID NO 1; 63pp; English
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The invention relates to a method for determining a nucleotide sequence of a nucleic acid. The method comprises: (a) providing one or more coded oligonucleotide probes, each coded oligonucleotide probes comprising an oligonucleotide associated with at least one nanocode comprising a detectable non-encoding feature, (b) contacting a target nucleotide acid with the one or more coded oligonucleotide probes; and (c) identifying coded oligonucleotide probes; and (c) identifying using scanning probe microscopy (SPM) to detect the nanocode and the detectable non-encoding feature. Nanocodes of the invention in certain aspects include detectable features beyond the arrangement of tags that encode information about the barcoded object. The tags that encode information about the barcoded object. The detectable features include structures of a nanocode or associated with a nanocode, referred to as detectable feature tags, for error.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       checking/error correction, encryption and data reduction/compression. The present sequence represents a synthetic peptide which connects four buckeyballs on graphite in an example from the present invention, where the example is about the synthesis and SPM scanning of a nanocode.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying target nucleic acid sequence, by contacting target nucleic acid with coded oligonucleotide probes, and identifying probes binding to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human prostate/colon/lung/breast cancer-related protein 1442, SEQ:1499.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; cancer; tumour; prostate cancer; colon cancer; lung cancer;
                                                                   nucleic acid determination; scanning probe microscopy; nanocode.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  target nucleic acid using scanning probe microscopy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; SEQ ID NO 1; 29pp; English.
                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADN13984 standard; protein; 92 AA.
                               Synthetic peptide SEQ ID NO:1.
                                                                                                                                                                      /note= "-CONH2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80.0%;
                                                                                                                                                                                                                                                                             31-DEC-2003; 2003US-00750515.
                                                                                                                                                                                                                                                                                                             31-DEC-2003; 2003US-00750515
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                 Berlin A;
                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2005-511772/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                             (ITLC ) INTEL CORP.
                                                                                                                                                                                                          US2005147981-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 30 AA;
                                                                                                                                                      Modified-site
08-SEP-2005
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                                                                                                                                                                                                                                                                                                                                                                                 Yamakawa M,
                                                                                                                                                                                                                                            07-JUL-2005
                                                                                                     Synthetic
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human prostate, colon, lung and breast cancer CDNA libraries, and to 57 proteins (ADNI3971-ADNI4027) encoded by a subset of these CDNA sequences proteins (ADNI3971-ADNI4027) encoded by a subset of these CDNA sequences (ADNI3914-ADNI3970). The invention also relates to vectors and host cells comprising a nucleic acid of the invention; a method for the recombinant production of a protein of the invention; a method for the recombinant protein of the invention; a method for detecting a cancerous cell by PCR or probe hybridisation; inhibiting at least concervous concerved electrically aberrant proliferation) of a cell; a method of chencype (particularly aberrant proliferation) of a cell; a method of product differentially expressed in a cancerous cell; and a method of treating a cancerous concerved interesting a cancerous concerved interesting a cancer with a contain cell; and a method of treating a cancer patient using the agent commal cell; and a method of treating a cancer patient using the agent of normal cell; and a method of treating a cancer patient using the agent of concerved interesting a cancer patient using the agent of prognose, treat or prevent cancers such as prostate, colon, lung or breast cancer, and can also be used to screen for drugs for the treatment of cancers. The nucleic acids can also be used for gene mapping, tissue to propried and tissue profiling. The present sequence represents a cyping and tissue profiling. The present commance data for this patent did not form part of the printed prom when was obtained in electronic form at the printed form was obtained in a lengtronic format directly from with the printed promise.
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                                                                                                                                                                                                                                                                                                                                                                                                                               profiling, as diagnostic reagents, and for gene mapping or tissue typing or e.g. prostate, colon, or breast cancer.
breast cancer; drug screening; diagnosis; prognosis; prevention; gene mapping; tissue typing; tissue profiling; cytostatic; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention relates to nucleic acids (ADN12486-ADN13970) isolated
                                                                                                                                                                                                                                                                                                                                          Garcia PD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; gene expression; single exon probe; microarray; alternative splicing event; genomic alteration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human genome derived single exon protein #4601.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                            Zhang G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 18; SEQ ID NO 1499; 190pp; English
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABO58367 standard; protein; 109 AA.
                                                                                                                                                                                                                                                                                                                                            Kassam A,
                                                                                                                                                                                               16-MAY-2003; 2003WO-US015465.
                                                                                                                                                                                                                                      17-MAY-2002; 2002US-0381533P.
04-FEB-2003; 2003US-0445222P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80.08;
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Best Local Similarity 90.9
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                              Scott EM, Lamson G,
                                                                                                                                                                                                                                                                                                                                                                                     2004-376173/35.
                                                                                                                                                                                                                                                                                                     (CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ADN13927
                                                                                                            WO2004039943-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 92 AA;
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                                                                     Homo sapiens
                                                                                                                                                   13-MAY-2004
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Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.

Novel human diagnostic protein #15492.

(first entry)

18-FEB-2002

ABG15501;

ABG15501 standard; protein; 112 AA.

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RESULT 29
ABG15501
                                                              The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acids acquences ("Illy defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule expression (comprising a plurality of probes for measuring human cells or tissues. Also included are a spatially—adversable set of single exon nucleic acid probes for measuring human gene expression, a method of and addressably isolatable or amplifiable from the plurality, a single exon addressably isolatable or amplifiable from the plurality, a single exon addressably isolatable or amplifiable from the plurality, a single exon addressably isolatable or amplifiable from the plurality, a single exon addressably isolatable or amplifiable from the plurality, a single exon probe cited above, where each of the plurality of probes cited above, where seed of the above—mentioned amino acid of contiguous amino acids of any of the above—mentioned amino acid of contiguous amino acids of any of the above—mentioned amino acid of sequences (optionally with conservative amino acid substitutions), an isolated antibody that binds specifically to a peptide cited above, methods of selling and/or licensing single exon probes or microarrays to a customer desiring to measure gene expression, a method of providing human gene expression data by subscription, and a computer-readable expression analysis. The probes may be used as tools for surveying clack above. The probes may be used as tools for surveying clack above. The probes are used in identifying and characterising cross of the probes are used in identifying and characterising secure. In addition, the probes are used in identifying and characterising calternative splicing events, in priming the synthesis of nucleic acids. In expressing the ORF-encoded peptide.
                                                                                                                                                                                                                                                                                      New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 8; Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            segdata.uspto.gov/seguence.html?DocID=20030194704
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Pred. No. 61;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                     Claim 45; SEQ ID NO 32001; 80pp; English.
                                                                                                                                                                                                                             Penn SG, Rank DR, Hanzel DK;
                                                                                                      03-APR-2002; 2002US-00029386.
                                                                                                                                    03-APR-2002; 2002US-00029386
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Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                (PENN/) PENN S G.
(RANK/) RANK D R.
(HANZ/) HANZEL D K.
                                                                                                                                                                                                                                                           WPI; 2004-119264/12
                                                                                                                                                                                                                                                                                                                                       surveying tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 109 AA;
                                             US2003194704-A1
               Homo sapiens.
                                                                         16-OCT-2003
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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess

biodiversity.

Tang YT;

Drmanac RT, Liu C, WPI; 2001-639362/73.

N-PSDB; AAS79688.

(HYSE-) HYSEQ INC.

30-MAR-2001; 2001WO-US008631. 31-MAR-2000; 2000US-00540217.

WO200175067-A2.

11-OCT-2001.

Homo sapiens.

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain acaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed control in gene therapy techniques to reserve normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a cupylement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (II) and (II) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in disorders responsible for genetic disorders or other traits to assess biodiversity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and to produce other types of data and products dependent on DNA and amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at fit, wipo.int/pub/published_pct_sequences
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Claim 20; SEQ ID NO 45860; 103pp; English.
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RESULT 30 AAG35185

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9905-014793P.
9905-014793P.
9905-0148319P.
9905-0148341P.
9905-0149368P.
9905-0149368P.
9905-014975P.
9905-014975P.
9908-0139461P.
9908-0139462P.
9908-0139762P.
9908-0139763P.
9908-0139763P.
9908-0140353P.
9908-0140353P.
9908-014032P.
9908-014032P.
9908-014237P.
9908-014237P.
9908-014237P.
9908-0144332P.
9908-014508P.
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13-AUG-1999;
13-AUG-1999;
16-AUG-1999;
17-AUG-1999;
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20-AUG-1999;
23-AUG-1999;
18 - JUN - 1999;
22 - JUN - 1999;
23 - JUN - 1999;
23 - JUN - 1999;
24 - JUN - 1999;
28 - JUN - 1999;
29 - JUN - 1999;
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28-JUL-1999;
02-AUG-1999;
02-AUG-1999;
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                                                                                      30-JUN-1999
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  Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
                                            Zea mays protein fragment SEQ ID NO: 42946.
   AAG35185 standard; protein; 126 AA.
                                                                                                                                               9905-0121825P.
9905-0123180P.
9905-0125788P.
9905-0126784P.
9905-0126784P.
9905-012874P.
9905-012874P.
9905-0130077P.
9905-0130077P.
9905-0130081P.
9905-0131449P.
9905-0132447P.
9905-0132487P.
9905-0134228P.
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9905-0134228P.
9905-0134238P.
9905-0134238P.
9905-0134238P.
9905-0136782P.
                                                                                                                                  25-FEB-2000; 2000EP-00301439
                              18-OCT-2000 (first entry)
                                                                                        Zea mays subsp. mays
                                                                                                                                               25-FEB-1999;

05-MAR-1999;

23-MAR-1999;

25-MAR-1999;

101-APR-1999;

06-APR-1999;

06-APR-1999;

10-APR-1999;

21-APR-1999;

21-APR-1999;

21-APR-1999;

23-APR-1999;

06-MAY-1999;

06-MAY-1999;

06-MAY-1999;

06-MAY-1999;

06-MAY-1999;

06-MAY-1999;

11-MAY-1999;
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14-MAY-1999;
14-MAY-1999;
18-MAY-1999;
19-MAY-1999;
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25-MAY-1999;
27-MAY-1999;
28-MAY-1999;
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07-JUN-1999;
08-JUN-1999;
10-JUN-1999;
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                                                                                                                     06-SEP-2000
                AAG35185;
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capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-ABB77072). The sequence data for this patent did not form part of the from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                     New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytostatic; antipsoriatic; antiinflammatory; gene therapy; Nanodisc; proliferative disorder; inflammatory disorder; immune disorder; metabolic disorder; bone disorder; CNS disorder; cancer; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid detection reagent
                              Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 35520; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Length 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 40; DB
Pred. No. 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                      Li PWD, Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human polypeptide seqid 1053.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADU02586 standard; protein; 191 AA.
                                                                                                                                              23-MAR-2001; 2001WO-US009231
                                                                                                                                                                      23-MAR-2000; 2000US-0191637P, 11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80.0%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-APR-2004; 2004WO-US012047
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ulcerative colitis; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97 AAAAAAAAAA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AAMAAAAAAMA 12
                                                                     Drosophila melanogaster
                                                                                                                                                                                                                                      Adams M,
                                                                                                                                                                                                                                                              WPI; 2001-656860/75.
                                                                                                                                                                                                          (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 158 AA;
                                                                                                                                                                                                                                                                            N-PSDB; ABL13679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2004093804-A2
                                                                                            WO200171042-A2
                                            pharmaceutical
                                                                                                                                                                                                                                                                                                                              interactions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-NOV-2004.
                                                                                                                     27-SEP-2001.
                                                                                                                                                                                                                                      Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADU02586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
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                99US-0149930P.
99US-015066P.
99US-0151065P.
99US-0151066P.
99US-0151080P.
99US-0151030P.
99US-0151930P.
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990S-0155659P.
990S-0156596P.
990S-0157117P.
990S-015713P.
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99US-0153070P.
99US-015408P.
99US-0154039P.
99US-0154739P.
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99US-0158369P.
99US-0159294P.
99US-0159295P.
99US-0159329P.
99US-0159339P.
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990S-0159638P-
990S-0165964P-
990S-0160768P-
990S-0160768P-
990S-0160814P-
990S-0160814P-
990S-0160819P-
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99US-0161405P.
99US-0161406P.
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99US-0161993P.
99US-0162142P.
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99US-0161920P.
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hes 10; Conservative
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                                                                                                                                                                                                                                                                                                     -OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                          -OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                        -OCT-1999;
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ID ABB6
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AC ABB6
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DT 26-N
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Gaps

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Length 191; 1; Indels

Sequence 191 AA;

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08-SEP-2003; 2003US-0505059P
                       WPI; 2004-775861/76.
                        N-PSDB; ADU01854.
  02-MAY-2003;
02-MAY-2003;
                    Lee E,
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invention.

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The invention relates a recombinant DNA construct comprising a CC polymucleotide having any of 5544 mucleotide sequences (CDNAs SEQ ID NO: CD polymucleotide having any of 5544 mucleotide sequences (CDNAs SEQ ID NO: 5545-11088). The CDNAs and procteins are from corn. Soybean, CSC (SEQ ID NO: 5545-11088). The CDNAs and procteins are from corn. Soybean, CSC (SEQ ID NO: 5545-11088). The CDNAs and procteins are from corn. Soybean, CSC producing a plant having an improved property, comprising transforming a plant having an improved property, comprising transforming a plant with a recombinant DNA construct comprising promoter region (CC plant) in a plant cell operably joined to a polymucleotide encoding a COLYpeptide associated with the property, and growing the transformed collymptide associated with the property, and growing the transformed collamingulating growth rate in plant cells by modification of the cell cycle pathway, for improving plant tolerance to plant disease, for galactomannan production, for production of plant sowth regulators, for improving plant tolerance to herbicides, for increasing the rate of improving plant tolerance to herbicides, for increasing the rate of homologous recombination in plants, for lighn production, for improving plant tolerance to extreme osmotic conditions, for improving plant tolerance to extreme osmotic conditions, for improving plant tolerance to pathogens or pests, for yield improvement by modification of collection of carbohydrate, nitrogen or phosphorus use and/or uptake and for yield improvement by providing improved plant growth and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New recombinant DNA constructs useful in the field of biochemistry and genetics, and in particular for producing transgenic plants with improved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plant; transgenic; cold tolerance; growth rate; drought tolerance; disease resistance; galactomannan production; plant growth regulator; heat tolerance; herbicide tolerance; lignin production; extreme osmotic condition tolerance; pathogens resistance; pest resistance; yield improvement; seed oil yield; seed protein yield.
  Score 40; DB 8; I
Pred. No. 1.1e+02;
                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; SEQ ID NO 7771; 14pp; English.
                                                                                                                                                                                                                                                                                                                      ADT57694 standard; protein; 227 AA.
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28-APR-2003; 2003US-00425115.
80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genetics, and in particular
biological characteristics.
                                                                                                                                                                                                                                                                                                                                                                                                                                   13-JAN-2005 (first entry)
                                                                Conservative
                                                                                                                     1 AAMAAAAAAM 11
                                                                                                                                                                         20 AAAAAAAAM 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (KOVA/) KOVALIC D K.
                       Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                 ADT57694;
  Query Match
                                                                                                                                                                                                                                                                 RESULT 33
                                                                                                                                                                                                                                                                                               ADT57694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention describes a new first nucleic acid molecule comprising a polynucleotide sequence given in the specification. Also described are: an animal injected with the nucleic acid molecule, a second nucleic acid molecule and an animal injected with the nucleic acid molecule or that bybridises to the first polynucleotide sequence that is at least about 70.80 so or 54 homologous to the first nucleic acid molecule and stringeror complicitions; a vector comprising the nucleic acid molecule and a promocer that drives the expression of the nucleic acid molecule and a promocer that drives the expression of the nucleic acid molecule and a promocer that drives the expression of the nucleic acid molecule and a bybridises to more compositions comprising the nucleic acid molecule; a nucleic acid composition comprising a carrier of molecule, vector or nore compositions comprising the nucleic acid molecule; and one or more compositions comprising the nucleic acid molecule; and a carrier or buffer and one or more compositions comprising the nucleic acid molecule; and a carrier or buffer and one or more compositions composition comprising the polypeptide and carrier or buffer; a cell a candinal injected with the polypeptide and a carrier or buffer; a cell a cransfecred or infected books cell; synthesising Nanodiscs simultaneously conductions of crystal structure; paparing a hydrophobic protein cransfecred or infected books cell; synthesising a non-human animal; correening for modulators of hydrophobic protein acivity; a diagnostic composition comprising the parternal particle; and patient; an antibody specifically recognising, binding to or modulating the animody is displayed on the bacteriophage; a non-human animal injected with the antibody diagnosing a disease, disorder; synthesis and encoded by a nucleic composition; a host cell that secretes the antibody diagnosing a disease, disorder; synthesis and encoded by anitodic comprising cancer; or proliferative, inflammatory, immune, metabolic comprising a disease, the polyp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New first nucleic acid molecule comprising a polynucleotide sequence given in the specification, useful in preparing a composition for diagnosing or treating e.g., cancer, psoriasis or ulcerative colitis.
                                                                                                                                                                                                                                                                                                                                                                                                              Williams LT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 14; SEQ ID NO 1053; 291pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                 Hestir K, Chu K, Masuoka L,
                                                                                                                                                                                                                                                                                                                                                         (FIVE-) FIVE PRIME THERAPEUTICS INC.
                                02-MAY-2003; 2003US-0467230P.

19-MAY-2003; 2003US-0471306P.

19-MAY-2003; 2003US-0471336P.

08-JUL-2003; 2003US-0485224P.

08-JUL-2003; 2003US-0486446P.

14-JUL-2003; 2003US-0486480P.

08-AUG-2003; 2003US-0486480P.

08-AUG-2003; 2003US-0493573P.
           2003US-0467199P
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HAAKE V.
                               FROMM
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                                                                             Century K;
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                               (FROM/)
                      SHER/)
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development under at least one stress condition. The polynucleotide may also encode a plant transcription factor. The methods and compositions of the present invention are useful in the field of blochemistry and centrollar for producing transgenic plants with improved biological characteristics such as increased yield, improved nitrogen flow, increasing plant tolerance to cold or heat, improving plant tolerance to extreme osmotic and drought conditions, and improving plant tolerance to plant pests or pathogens. They can also be used in physical arrays of molecules, plant breeding markers, computer-based storage and analysis systems. The present sequence is one of the 5544 plant protein nequences of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in sequence. Lettronic format directly from USPTO at
                                                                                                                                                                                     Gaps
                                                                                                                                                                                     ..
                                                                                                                                                                                                                                                                                                                                                  Plant, C-repeat/DRE binding factor; CBF; transgenic; biomass; cold inducible promoter; environmental stress; cold tolerance; cell injury; growth inhibition; drought; high salt condition.
                                                                                                                                                                 80.0%; Score 40; DB 8; Length 227; 83.3%; Pred. No. 1.3e+02;
                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                Corn C-repeat/DRE binding factor (CBF) G3441.
                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                        ADH75874 standard; protein; 231 AA.
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98US-00018235.
98US-00198119.
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98US-00017816.
98US-00018227.
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2000US-00580377
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                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                    10; Conservative
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G
                                                                                                                                                                           Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GILMOUR S
ZARKA D.
JIANG C.
ZHANG J.
                                                                                                                                              Sequence 227 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JAGLO K.
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                                                                                                                                                                                                                                                                                                              15-APR-2004
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28-JAN-1999;
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(ZHAN/)
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(ZARK/)
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The invention relates to a transgenic plant having an altered trait as compared to a wild type or untransformed plant. The trait is altered, i.e. increasing or decreasing levels of at least one cell protectant in cells of the transgenic plant to raltered, i.e. increasing or decreasing levels of biomass, where the transgenic plant is transformed with a cells of blomass, where the transgenic plant is transformed with a creombinant polymucleotide comprising an AP2 domain. Also a Crepeat/DRE binding factor (CRP) comprising an AP2 domain. Also included are a cold inducible promoter comprising an AP2 domain. Also control of the Rable or Dreb2a promoters, a method of inducible protectant in a cell, a method for inducible levels of a cell protectant in a cell, a method for controling the levels of a cell protectant in a plant cell, a method for improving the tolerance and a method of altering the biomass of a plant. The improved environmental stress is selected from a decrease in certain of of a plant is or a cell is injury, plant is growth inhibition, increase in survival response to freezing temperatures, survival rate after exposure to freezing temperatures, cextent of a plant after exposure to drought conditions, cextent of a plant after exposure to drought conditions, cextent of a plant after exposure to drought conditions, cextent of a plant after exposure to drought conditions, cextent of a plant after exposure to drought conditions, cextent of a plant after exposure to drought conditions, cextent of a plant after exposure to high salt conditions, and which has an increased tolerance be an environmental stress, e.g. drought, cold, the present sequence represents a plant CBF or handled an environmental stress, e.g. drought, cold, the present sequence represents a plant CBF or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New transgenic plants comprising C-repeat/DRE binding factor, useful in producing phenotypes with increased tolerance to an environmental stress. e.g. drought, cold, freezing or high salt.
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Riechmann JL, Sherman BK, Fromm M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transgenic; plant; enhanced tolerance to abiotic stress;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 20; SEQ ID NO 314; 223pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADI42782 standard; protein; 231 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plant transcription factor #450.
                                                                                                                                                                                                                                            Thomashow M, Stockinger EJ,
Jiang C, Zhang J, Haake V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170 AAAAAAAAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AAMAAAAAAM 11
RIECHMANN J L.
SHERMAN B K.
                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-070474/07.
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                                                                                                                                                     (CENT/) CENTURY K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 231 AA;
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The invention describes a transgenic plant comprising a recombinant polynucleotide of any one of more than 500 nucleotide sequences fully defined in the specification or its complement. The method of the invention can be used to produced a plant having altered traits such as: enhanced tolerance to abiotic stress; glyphosphate tolerance; hormone sensitivity; disease resistance; sugar sensing; early or late flowering; altered flower structure, change in stem biturcations, altered branching pattern, reduced apical dominance, reduced trichome density; lack of trichomes; reduced ectopic trichome development; altered trichome development; increase in trichome number; altered stem morphology; increased root growth; increased root hairs; altered seed development; premature senescence; increased nor cell differentiation; rapid development; premature senescence; increased morphology; seed development; premature senescence; increased morphology; seed size; decreased plant size; leaf morphology; seed plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       biochemistry; increase in root anthocyanins; increase in plant anthocyanins, or alteration in light response or shade avoidance. The transgenic plant, polymucleotides and polymeptides are useful in bioinformatic search methods. This is the amino acid sequence of a plant transcription factor, and an orthologue of Arabiodopsis thaliana transcription factors isolated in the invention, that can be used in the creation of a transgenic plant with altered traits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New transgenic plant comprising a recombinant polynucleotide of any one of more than 500 nucleotide sequences, useful in bioinformatic search
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haake V;
Keddie J, Broun PE;
plant anthocyanin; light response; shade avoidance; bioinformatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Heard JE, F
Reuber TL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jiang C, Heard
Adam LJ, Reube
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 1245; 435pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Creelman RA, Ratcliffe O, Adam LJ
Pilgrim ML, Dubell AN, Pineda O,
                  transcription factor; gene; ds.
                                                                                                                                                25-FEB-2003; 2003US-00374780.
                                                                                                                                                                                  18-APR-2001; 2001US-00837944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Riechmann JL,
                                                                                                                                                                                                                   SHERMAN B K.
RIECHMANN J L.
                                                                                                                                                                                                                                                  JIANG C.
HEARD J E.
HAAKE V.
CREELMAN R A.
                                                                                                                                                                                                                                                                                                                  RATCLIFFE O. ADAM L J. REUBER T L. KEDDIE J.
                                                                                                                                                                                                                                                                                                                                                                                   BROUN P E.
PILGRIM M L.
DUBELL A N.
PINEDA O.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 231 AA;
                                                                                  US2004019927-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        YU G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pilgrim ML,
                                                                                                                   29-JAN-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sherman BK,
                                                     Zea mays.
                                                                                                                                                                                                                                                                                                                                     (ADAM/)
(REUB/)
                                                                                                                                                                                                                                                                                                                                                                                                                      (DUBE/)
(PINE/)
                                                                                                                                                                                                                   SHER/)
                                                                                                                                                                                                                                                                                                      CREE/)
                                                                                                                                                                                                                                                                                                                     (RATC/)
                                                                                                                                                                                                                                                                                                                                                                       (KEDD/)
                                                                                                                                                                                                                                                                                                                                                                                       (BROU/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (XIGG/)
                                                                                                                                                                                                                                                                                                                                                                                                        PILG/)
                                                                                                                                                                                                                                    RIEC/)
                                                                                                                                                                                                                                                                                     (HAAK/)
                                                                                                                                                                                                                                                      JIAN/
                                                                                                                                                                                                                                                                     HEAR/
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Producing transformed plant, by transforming a target plant with a firs polynuclectide, which is a member of the CBF clade of transcription factors, and which is mutagenized, and identifying a transformed plant.

Canella D;

Cook DD,

Gilmour SJ,

Thomashow M,

WPI; 2006-010542/01.

N-PSDB; AEE27924.

19-MAY-2005; 2005WO-US017583.

WO2005112608-A2.

Zea mays

01-DEC-2005

21-MAY-2004; 2004US-0573443P (UNMS ) UNIV MICHIGAN STATE

transformation; transgenic plant; plant; abiotic stress tolerance; transcription factor; CBF.

CBF clade transcription factor G3441 SEQ ID NO 178.

(first entry)

09-FEB-2006

AEE27925;

AEE27925 standard; protein; 231 AA.

RESULT 36

AEE27925

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polynucleotide; and a transgenic plant comprising a recombinant, overexpressed mutated polynucleotide that encodes a mutant member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CBF clade of transcription factor polypeptides, where the transgenic plant exhibits fewer or reduced adverse morphological or developmental effects than a plant that overexpresses a wild-type form of the mutated polynucleotide. The method is useful for producing a transformed plant having increased abiotic stress tolerance, as compared to wild type or control plants. This is the amino acid sequence of a CBF clade
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 40; DB 10; Length 231;
Pred. No. 1.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 9; SEQ ID NO 178; 225pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   170 AAAAAAAAAM 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transcription factor
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 231 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AEE27977
SXXX
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Gaps

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Score 40; DB 8; Length 231; Pred. No. 1.3e+02; 0; Mismatches 1; Indels

80.0%; 90.9%;

Query Match Best Local Similarity

10; Conservative

Matches

8

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ADU40376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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  8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                     The invention describes a method of producing a transformed plant comprises transforming a target plant with the first polynucleotide, which is a member of the Case of transcription factors, and iss mutagenized to produce a second or a third polynucleotide, where the second or third polypeptide has an amino acid sequence different than the first polypeptide, and identifying a transformed plant comprising the second polynucleotide and identifying a transformed plant comprising the transgenic plant produced by the method above; a seed produced by the transgenic plant, where the seed comprises the second or third overexpressed mutated polynucleotide that encodes a mutant member of the CBF clade of transcription factor polypeptides, where the transgenic
                                                                                                                                                                                                                                                                   Producing transformed plant, by transforming a target plant with a first polynucleotide, which is a member of the CBF clade of transcription factors, and which is mutagenized, and identifying a transformed plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              plant exhibits fewer or reduced adverse morphological or developmental effects than a plant that overexpresses a wild-type form of the mutated polymucleotide. The method is useful for producing a transformed plant having increased abiotic stress tolerance, as compared to wild type or control plants. This is the amino acid sequence of a CBF clade transcription factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      novel gene; novel protein; tissue marker; molecular weight marker; chromosome marker; genetic disorder.
                                            transformation; transgenic plant; plant; abiotic stress tolerance; transcription factor; CBF.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40; DB 10; Length 231;
Pred. No. 1.3e+02;
); Mismatches 1; Indels
                                                                                                                                                                                                                          Canella D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                       CBF clade transcription factor G3441.
                                                                                                                                                                                                                        Thomashow M, Gilmour SJ, Cook DD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADE08006 standard; protein; 232 AA.
                                                                                                                                                                                                                                                                                                                  Disclosure, Fig 3; 225pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80.08;
                                                                                                                                                   19-MAY-2005; 2005WO-US017583.
                                                                                                                                                                        21-MAY-2004; 2004US-0573443P.
                                                                                                                                                                                                (UNMS ) UNIV MICHIGAN STATE
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 170 AAAAAAAAAM 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AAMAAAAAAM 11
                                                                                                                                                                                                                                              WPI; 2006-010542/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 231 AA;
                                                                                                    WO2005112608-A2.
                                                                               Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified
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                                                                                                                           01-DEC-2005
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anticonvulsant; cerebroprofective; vasotropic; gene therapy; gene mapping; forensic; mutation identification; biodiversity; cancer; gene mapping; forensic; mutation identification; biodiversity; cancer; autoimmune disorder; multiple sclerosis; rheumatoid arthritis; myasthenia gravis; tissue growth; tissue regeneration; tissue repair; tissue replacement; burn; incision; ulcer; osteoporosis; osteoarthritis; bone degenerative disorder; periodontal disease; nervous system disease; neuropathy; mechanical disorder; traumatic disorder; nerve injury; Alzheimer's disease; Parkinson's disease; Huntington's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotides, useful for expressing recombinant proteins for analysis, characterization or therapeutic use, or as markers for tissues in which the corresponding protein is preferentially expressed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention comprises the amino acid and coding sequences of novel proteins. The DNA and protein sequences of the invention are useful as: markers for tissues in which the corresponding protein is preferentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expressed; as molecular weight markers on gels; as chromosome markers or tags; to identify chromosomes or to map related gene positions; and to compare with endogenous DNA sequences in patients to identify potential genetic disorders. The present amino acid sequence represents a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhao QA, Wang J;
anac RT, Wang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antirheumatic; antiarthritic; muscular; osteopathic; vulnerary; antiulcer; antiinflammatory; CNS; nootropic; antiparkinsonian;
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ou P, Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytostatic; antianemic; immunosuppressive; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 40; DB 7; Length 232; Pred. No. 1.3e+02; O; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ren F, Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tang YT, Asundi V, Goodrich RW, Ren F,
Ghosh M, Xue AJ, Wehrman T, Weng G, Zh
Ma Y, Wang D, Chen R, Xu C, Boyle BJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 20; SEQ ID NO 1072; 1177pp; English.
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                                                                                                                                                                                               10-DEC-2001; 2001US-0339739P.

11-DEC-2001; 2001US-0339453P.

14-MAR-2002; 2002US-036591P.

14-MAR-2002; 2002US-0365384P.

12-APR-2002; 2002US-0372381P.

12-APR-2002; 2002US-037261SP.

22-APR-2002; 2002US-0012858.

24-APR-2002; 2002US-0012858.
                                                                                                                                     10-DEC-2002; 2002WO-US039555
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ADE07095
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WO2003054152-A2
                                                                    03-JUL-2003.
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Sequence 232 AA;

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The invention describes an isolated polynucleotide comprising a nucleotide sequence selected from 124 nucleotide sequences (SEQ ID NO: 1-
124), or a polynuclectide encoding a polypeptide with biological
cetivity, where the polynucleotide hybridises to the nucleotide sequence
under stringent hybridisation conditions or has greater than 99% sequence
condensity with the nucleotide sequence. The polynucleotide or the encoded
condensity with the nucleotide sequence. The polynucleotide or the encoded
condensity with the nucleotide sequence. The polynucleotide or the encoded
condensity dentification of mutations responsible for genetic
disorders or other traits, to assess biodiversity, and to produce many
cother types of data and products dependent on DNA and amino acid
consists. The polynucleotide or the polypeptide is useful in methods for
sequences. The polynucleotide or the polypeptide is useful in methods for
corporating and/or treating disorders and for treating
contribution or biological activity e.g., cancer, as nutritional sources or
supplements. The polypeptide is useful for regulating hematopoiesis and
control manned disorders such as multiple sclerosis, rheumatoid architis,
autoimmune disorders such as multiple sclerosis, rheumatoid architis,
contominance of regeneration, as well as in wound healing and tissue
crepair and replacement, and in healing of burns, incisions and ulsers,
for treating osteoporosis, osteoarthritis, bone degenerative disorders,
cor periodontal disease. The composition is useful in assays for
corporiserating nerve and or harding second nervel for reating centerating nerve and for periodontal and praint state is an exposite or experient and replacement, and the health of the confosition and differentiation, for proliferating centeral disease. The composition is useful in assays for
corporation and differentiation of various hematopoietic lines, assays
conditions and replacement and replacement and composition is useful and praint and replacement and composition is useful and praint an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue, particularly diseases such as peripheral neuropathy and localised neuropathies, Alzheimer's disease, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy'-Drager syndrome, as well as stroke. This sequence represents a novel polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          isolated polynucleotide, useful in therapeutic (i.e. for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e.g., cancer, neurodegenerative disorders), diagnostic (as expressed sequence tags for identifying expressed genes) and research methods
amyotrophic lateral sclerosis; Shy-Drager syndrome; stroke; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Boyle BJ,
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25-JAN-2001; 2001WO-US00263.
05-FEB-2001; 2001WO-US003800.
26-FEB-2001; 2001WO-US004927.
05-MAR-2001; 2001WO-US004941.
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18-APR-2001; 2001WO-US008656.
11-DEC-2001; 2001US-0339453P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2005-010094/01.
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DRMANAC R T.
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WANG Z.
WENG G.
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                                                                                                       Homo sapiens.
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25-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treating a mammal having a tumor of glial origin comprising cells that express a type A or B glial tumor antigen by contacting the cells with a composition comprising first and second binding agents.
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                                                                                                                                                                                                                                                                                                                 cytostatic; diagnosis; therapy; tumor;
tumor-associated antigenic target polypeptide; TAT.
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Pred. No. 1.3e+02;
Score 40; DB 9; I
Pred. No. 1.3e+02;
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                     Pred. No. 1.3e
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                                                                                                                                                                                     ADV70174 standard; protein; 236 AA.
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27-FEB-2004; 2004US-0548299P.
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90.9%;
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      80.08;
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                   Best Local Similarity 90.5
Matches 10; Conservative
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N-PSDB; ADV70078.
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                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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